us-09-832-929-18\_copy\_478\_486.rapb

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1 TESLVNRRP 9
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US-09-832-501-18
US-09-833-117-18
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                                                                                                         MEDIUM TIFE: LICE, OMBITIE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/984,010
FILING DATE: 12-DG-1998
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 12-DEC-1996
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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VIS-09-33-041-18

Sequence 18, Application US/09833041

Sequence 18, Application US/09833041

GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF545
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR PILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 79

SOFTWARE PRIOR DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 79

LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTT-SENGE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-984-010-26
                                                             ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
    CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo Sapiens
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RESULT 12

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Sequence 445, Application US/09932322
Publication No. US20030194743A1
Sequence 445, Application No. US20030194743A1
Sequence 45, Application No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Beltzer, James P.
APPLICANT: Petter, M. Daniel
APPLICANT: Pleming, Tony U.
APPLICANT: Ladner, Robert Charles
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: Dyx-018.1 PCT; DYX-018.1 US
CURRENT PILLING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTHARE: Patentin version 3.1
SEQ ID NO 445
LENGTH: 585
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US-09-833-117-18
Sequence 18, Application US/09833117
Publication No. US20030171267A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Prosen, Craig A.
APPLICANT: Profor, Christopher P.
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Albumin Fusion Froteins
FILE REFERENCE: PF543
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SEQ TURNER: PARENTIN Ver. 2.1
SEQ TURNER: PARENTIN Ver. 2.1
SEQ TURNER: PARENTIN VER. 20.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ballance, David J. APPLICANT: Sleep, Darrell
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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CRGANISM: Homo Sapiens
US-09-833-117-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: HomoSapiens
US-09-932-322-445
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100.0%; Score 45; DB 11; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels (
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Sequence 19, Application US/09833118
Sequence 19, Application US/09833118
Sequence 10, Application US/09833118
Sequence 10, Application US/09833118
SEQUENCE 10 NOTATION:
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF54
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 585
TYPE: PRI OR Sapiens
US-09-833-118-18
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homa
APPLICANT: Sadeghi, Homa
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF542
CURRENT APPLICATION NUMBER: 06/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-31
PRIOR FILING DATE: 2000-14-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATCHIN Ver. 2.1
SEQ ID NO 18
LENGTH: S85
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo Sapiens
US-09-832-501-18
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Search completed: April 19, 2004, 12:55:00 Job time : 4.78947 secs

478 TESLVNRRP 486

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RESULT 1
US-08-153-799-14
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Appli
                                                                                                      April 19, 2004, 11:40:29; Search time 1.3795 Seconds (without alignments) 336.813 Million cell updates/sec
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Sequence 3,
Sequence 4,
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Sequence 7
Sequence 9
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Sequence 2
Sequence 2
Sequence 3
Sequence 3
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
. /cgn2 6/ptodata/2/iaa/5A COMB.pep:*
. /cgn2 6/ptodata/2/iaa/5B COMB.pep:*
. /cgn2 6/ptodata/2/iaa/6A COMB.pep:*
. /cgn2 6/ptodata/2/iaa/6B COMB.pep:*
. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-964-186-2
US-10-153-064-96
US-10-153-064-99
US-10-153-064-99
US-10-153-064-135
US-10-153-064-131
US-10-153-064-131
US-10-153-064-131
US-10-153-064-131
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US-08-448-196A-3
US-08-448-196A-3
US-08-702-572-2
US-08-769-746-2
US-08-22-619-3
US-08-433-037-4
US-08-897-956A-2
US-08-976-594-977
US-09-976-594-977
PCT-US95-04075-3
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                            US-09-832-929-18_COPY_439_447
51
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                              1 KHPEAKRMP 9
                                                                                                                                                                              Title:
Perfect score:
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                                                                                                         Run on:
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No.
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Sequence 127, App Sequence 125, App Sequence 125, App Sequence 123, App Sequence 92, Appl Sequence 2, Appli Sequence 10, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17911 Appli Sequence 17911 Appli Sequence 17911 Appli Sequence 17911 Appli Sequence 11, Appli	
US-10-153-064-127 US-10-153-064-125 US-10-153-064-125 US-10-153-064-123 US-10-153-064-101 US-08-25-938-2 US-08-25-938-2 US-08-79-689-16 US-08-79-689-16 US-09-984-186-16 US-09-984-186-16 US-09-915-064-89 US-09-918-19791 US-09-333-729A-12 US-09-333-729A-12 US-09-335-409-18	
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## ALIGNMENTS

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US-105-199-14

US-105-199-14

Detent No. 576683

Patent No. 576683

Patent No. 576683

CREALICANT: Goodey, Andrew R

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Marray Hill
STRATE: New Jersey

COUNTRY: USA

ZIP: 07974

COMPUTER: Ploppy disk

COMPUTER: Thopy disk

COMPUTER: Thopy Of sk

COMPUTER: Thopy Of sk

COMPUTER: Thopy Of sk

COMPUTER: Thopy Of sk

COMPUTER: DATE: OF NAR-1992

REDICATION NUMBER: US/08/153,799

FILING DATE: OF-MR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/84795

FILING DATE: 29-APR-1999

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952

FILING DATE: 29-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB90/00650

FILING DATE: 29-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB90/00650

FILING DATE: 29-APR-1990

PRIOR APPLICATION DATA: ARB-1990

PRIOR APPLICATION NUMBER: US 07/775952

FILING DATE: 29-APR-1990

PRIOR APPLICATION NUMBER: BCT/GB90/00650

FILING DATE: 29-APR-1990

ATTORNEY ARRAYTERISTICS:

LENGTH: 58-APR-1990

TELEFAR ATTORNEY ATTORNEY
```

```
Sequence 1, Application US/08984176

Sequence 1, Application US/08984176

Patent No. 5948609

GENERAL INFORMATION:
APPLICANT: GATER, DANIEL C

APPLICANT: HO, JOSEPH X

APPLICANT: HO, JOSEPH X

TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

FILE REPERBRÜCE: 08/984,176

CURRENT APPLICATION NUMBER: US/08/984,176

CURRENT APPLICATION NUMBER: US/08/984,176

CURRENT FILING DATE: 1997-12-03

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTH: 585

TYPE: PATENTH: 585

TYPE: PATENTH: HOMO Sapiens

US-08-984-176-1
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Sequence 2, Application US/08702572

Patent No. 596536

GENERAL INFORMATION:
APPLICANT: Kerry-Williams, Sean M
APPLICANT: Gilbert, Sarah C
TITLE OF INVENTION: Yeast Strains and Modified Albumins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDERSS:
ADDRESSED: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
CUNTRY: Wing of Prussia
CITY: Ming of Prussia
CITY: Wing of Prussia
COMPTRY: Pennsylvania
COMPTRY: Rand of Prussia
STATE: Pennsylvania
COMPTRY: BPLOGATION
STATE: Pennsylvania
COMPTRY: ISP Compatible
COMPTRY: ISP COMPATE: ISP COMP
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100.0%; Score 51; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 KHPEAKRMP 447
                                                              439 KHPEAKRMP 447
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1 KHPEAKRMP 9
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US-08-702-572-2
                                                                                                                                                                                    RESULT 3
US-08-984-176-1
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APPLICANT: CARTER, DANIEL C.

APPLICANT: CARTER, DANIEL C.

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS

TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR

TITLE OF INVENTION: RELATED PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NASA

STREET: MARSHALL SPACE FLIGHT CENTER

CITY: HUNTSVILLE

STATE: ALABAWA

COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 1; Length 585; 100.0%; Pred, No. 0.065; tive 0; Mismatches 0; Indels
                                                                                                      PEATURE:
| NAME/KEX: Region | LOCATION: 369.419 |
| OTHER INFORMATION: HSA(1-n) |
| FEATURE: | NAME/KEX: Region |
| OTHER INFORMATION: HSA(1-n) |
| FEATURE: | NAME/KEX: Region |
| LOCATION: 1.585 |
| OCATION: 1.585 |
| OTHER INFORMATION: | Anaino acid sequence of |
| OTHER INFORMATION: | natural HSA" |
| US-08-153-799-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSIFICATION NUMBER: US/08/448,196A
ATTORNEY/AGBMT INFORMATION:
NAME: BROAD UR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELEPHONE: 205-544-0021
TELEPHONE: 105-505-544-0021
TELEPHONE: 205-544-0021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08448196A Patent No. 5780594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
           protein
NO
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                                           HYPOTHETICAL: N
ORIGINAL SOURCE:
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US-08-448-196A-3
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Gaps
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Sequence 3, Application US/08222619
Patent No. 5652352
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDECE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: Amgen Center, Patent Operations/RRC
STREET: Us.
COMPTRY: Thousand Oaks
STATE: California
COMPTRY: U.S.
COMPTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC COMPATE:
FLING DATE:
CLASSIFICATION NUMBER: US/08/222,619
FILING DATE:
CLASSIFICATION NUMBER: US/08/222,619
FILING DATE:
SEQUENCE CRASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CRASSIFICATION:
TYPE: amino acid
STRANDEDBRESS: unknown
TYPE: amino acid
STRANDEDBRESS: unknown
TOPICATV. unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 51; DB 1; Length 609; 100.0%; Pred. No. 0.068;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 4, Application US/08433037

Patent No. 5707828

GENERAL NPORMATION:

APPLICANT: Sreekrishna, Kotikanyadan
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Best Local Similarity 100.
Matches 9; Conservative
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US-08-433-037-4
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US-08-769-746.

Sequence 2, Application US/08769746

Patent No. 6274305

GENERAL INFORMATION

APPLICANT: Somenschein, Carlos

APPLICANT: Somenschein, Carlos

APPLICANT: Soco, Ana M.

TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells

NUMBER OF SEQUENCES: CORRESEE: Medlen & Carroll, LLP

STREET: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/769,746

CLASSIFICATION: 435-1996

CLASSIFICATION: 435-1996

CLASSIFICATION 19-DEC G.

REGISTRATION NUMBER: 32,837

REGISTRATION NUMBER: 32,837

REGISTRATION NUMBER: 32,837

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELECHOMIC CHARACTERISTICS:

LENGTH SEG : Mino acids

TELENGTH SEG : Mino acids

TELENGTH SEG : Mino acids
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Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           Query Match
100.0%; Score 51; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-153-064-5
Sequence 5, Application US/10153064
Patent No. 6663485
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVERTION:
FILE REFERENCE: PF556
             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 KHPEAKRMP 447
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US-08-769-746-2
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Sequence 977, Application US/09976594

Sequence 977, Application US/09976594

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT PILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PELL PROGRAM
SEQ ID NO 977

LENGTH: 609
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Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 51; DB 4; Length 609; 100.0%; Pred. No. 0.068; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                     Sequence 7, Application US/10153064;
Patent No. 6663485;
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION:
FILE REPERENCE: PFS56
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24;
PRIOR PILING DATE: 2001-05-25;
NUMBER OF SEQ ID NOS: 137;
SOFTWARE: Patentin version 3.1;
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                   463 KHPEAKRMP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Homo Sapiens US-10-153-064-7
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US-10-153-064-7
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APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Trohlopp, Juerg P.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: ALONG CArden City Plaza
CITY: Garden City
STARET: New York
COUNTRY: U.S.A.
CITY: Garden City
STARET: New York
COUNTRY: IS NO CARDENDES
CONDUTER READABLE FORM:
MEDIUM TYPES: Floppy disk
COUNTRY: IS NO COMPATION:
COUNTRY: IS NO COMPATION:
COUNTRY: IS NO COMPATION:
MEDIUM TYPES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 31,346
TELECOMMUNICATION INFORMATION:
TELECHOME: (516) 742-4343
TELECHOME: (516) 742-4343
TELECHOME: (516) 742-4366
TTELEX: 230 901 SANS UR
SURGITHE COPAMINO CITY
TELERAX: (516) 742-4366
TTELEX: LING DATE: DIGGET TELEX: 1100 CITY
TELERAX: (516) 742-4366
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-4363
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-4366
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-4363
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-4363
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-4363
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-4366
TTELEX: 1100 COPAMINO CITY
TELERAX: (516) 742-436
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Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 2, Application US/08897956A

PRIERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-433-037-4
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KHPEAKRMP 9
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US-08-897-956A-2
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Sequence 3, Application PC/TUS9504075; GENERAL INFORMATION: APPLICANT: AMGEN INC.

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Query Match
100.0%; Score 51; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels

US-08-897-956A-2

RESULT 12 PCT-US95-04075-3

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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09984186

Sequence 1, Application US/09984186

Patent No. 6686179

GENERAL INFORMATION:
FOURTHER, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
Yeh, Patrice
Yeh, Patrice
Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 51; DB 2; Length 610; 100.0%; Pred. No. 0.069;
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintcsh
CLASSIFICATION NUMBER: US/09/97,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: F-38,619
REFERENCE/DOCKET NUMBER: F-38,619
REFERENCE/DOCKET NUMBER: F-38,619
TELLEPAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                             APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
RECISTRATION WUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10454-3839
TELECAX: (610) 454-3839
TELECAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACATERISTICS:
LENGTH: 610 amino acids
TYPE: amino acids
                                                        UMBER: PCT/FR93/00085
28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 KHPEAKRMP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KHPEAKRMP 9
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Best Local Similarity
Matches 9; Conserva
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US-09-984-186-2
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Jequence 2, Application US/08797689

Patent No. 5876699

APPLICANT: Fleer, Reinhard

APPLICANT: Guitton, Jean-Dominique

APPLICANT: Guitton, Jean-Dominique

APPLICANT: Guitton, Jean-Dominique

APPLICANT: WING GERARD

APPLICANT: WING GERARD

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES

TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE 3. 36

CITY: COLLOGEVILE ROAD ACOLE ROAD 3043

CITY: COLLOGEVILE ROAD ACOLE ROAD 3043

CITY: COLLOGEVILE PORM:

MEDIUM TYPE: PA

CONDUTER READABLE FORM:

MEDIUM TYPE: PA

COMPUTER: MACINICOS

CORPUTER: MACINICOS

CORPUTER: MACINICOS

CORPUTER: MACINICOS

CORPUTER: APPLICATION DATA:

APPLICATION NUMBER: US (08/797, 689)

FILING DATE: 28-JUL-1994

PRIOR APPLICATION NUMBER: US (08/256, 927)

FILING DATE: 31-348-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PR 92/01064

FILING DATE: 31-348-1992
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
CONDUTEX: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
CONDUTEX: U.S.
ZIP: 91320-1789
COMPUTER: FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION STEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION NUMBER: PCT/US95/04075
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: Unknown
PCT-US9S-04075-3
INDOMATION TYPE: Protein
PCT-US9S-04075-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-797-689-2
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Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-153-064-133
| Sequence 133, Application US/10153064
| Patent No. 6663485
| GENERAL INFORMATION:
| APPLICANT: Bell et al. |
| TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins File Reference: PF556
| CURRENT APPLICATION NUMBER: US/10/153,064
| CURRENT APPLICATION NUMBER: 60/293,212
| PRIOR PILING DATE: 2001-05-25
| NUMBER OF SEQ ID NOS: 137
| SEQ ID NO 133
| SEQ ID NO 133
LENGTH: 610 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2
                                                                                                                                                                                                                                                                463 KHPEAKRMP 471
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CORGANISM: Homo sapiens
US-10-153-064-133
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Search completed: April 19, 2004, 12:05:21 Job time : 2.3795 secs

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Mon Apr 19 13:27:23 2004

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                                                                                                              April 19, 2004, 11:37:59; Search time 1.70637 Seconds (without alignments) 789.208 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                         US-09-832-929-18_COPY_462_475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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S65948	1778	581	T16546	G96616	T38176	875776	T47732	T50773	T50774	AJFFPM	T31102	T3110S	A81439	1961	T09748
365	A3	S42	116	969	138	S7	T4	73	13	Ā	H3.	13	A8.	84	Ţ
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30 37 52.	ß						37		37	37	37	37	36	36	45 36 50

## AL IGNMENTS

RESULT 1
estum albumin precursor. Vallached) - numan N.Alternate names: preproalbumin
N; Contains: kinetensin
C;Species: Homo sapiens (man)
C.DACTER 29-4011-1904 H SHEQUENCE TEVINEDIO 3-1-041-1934 FEST-141-1904 FEST-141-1904 FEST-141-1904 FEST-141-1904 FEST-159286 FEST-159313 G01747; \$55314; A01420; \$06422; \$34
Rilawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seebu:
Nucleic Acids Res. 9, 6103-6114, 1981
Affitle: The sequence of human serum albumin cDNA and its expression in Escherichae co A.Reference number: A91743: MUID:82081882; PMID:617178
 A,Accession: A93743
A MOLECULE TYPE I MENU A 11-600 JING
A) Kabiluwesi 1-11, N. 1-11-2005 A.B. (D8:L00132; GB:L00133; NID:G28591; PIDN:CAA2: A):Cross-references: BMBL:V00495; GB:G00139; GB:L00133; NID:G28591; PIDN:CAA2:
R, Dugaiczyk, A.; Law, S.W.; Dennison, O.E.
Proc. Matt. Acad. Sci. U.S.A. /y, /l.f.) 1982. N.T.:le. M. Clearing and the encoded amino acids of human serum albumin MRNA.
A,Accession: A93936
 A; Molecule type: mRNA
 A;Residues: 1-120,/5/, 122-609 < DUGA PROPERTY OF THE PROPERTY
 Ajidosa-Ideleriandesi Emblivouquay, Nilojigoobooy, riunkichazbiob.ii riungadoboo Ajitosoo V. Matanaho K. Gakai M. Tamaoki T. Diitoo
 A (Junio), Chem. 261, 3244-3251, 1986
Ailile: The human albumin gene. Characterization of the 5' and 3' flanking regions and
A;Reference number: I39427; MUID:86140099; PMID:2419329
A;Accession: I39427
A)Status: translation not shown
A MOLECULE TYPE: UNA
A.Cross-references: GB:M13075; NID:q178330; PIDN:AAA51688.1; PID:g553173
R; Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994
A)TILE: A NUCLECTION INSERTION AND TRANSMILL CAUSE ANALOUMINEMIA IM AN ILCALIAN CAULTY.
A; Reference number: 199200; MOLD: 941015); FOLD: 040450; A: Accession: 155286
A;Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A) REBIOURS: A64-250, NSTRING COMMISS OF PIDN: AAB30282.1: PID:G546033
A, Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia
R; Madison, J.; Galliano, M.; Warkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putnam,
PIOC. NATL: Acad. Sci. 0.5.4. 11 04.700400, 1554 ***********************************
A. Reference number: 159313; MUID:94294404; PMID:8022807
A; Accession: 159313
A;Status: translated from GB/BMBL/DDBJ
A, Molecule type: DNA
A; restudes; 30-7-30-7, Archivolution (NIC) 6547231; PIDN: AAB31177.1; PID: 9547232

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A; Gene: GDB: ALB
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serum albumin precursor [validated] - bovine
NyAlternate names: 67K protein; preproalbumin
(Species: Bos primigenius tautus (cattle)
C,Species: Bos primigenius tautus (cattle)
C,Accession: A38885, A36401; A31258; B60808; S10780; D45800; A26693; A90309; A91458; A9
C,Accession: A38885, A36401; A31258; B60808; S10780; D45800; A26693; A90309; A91458; A9
submitted to the EMBL Data Library, August 1991
A,Description: Bovine serum albumin: cDNA sequence and expression.
A,Reference number: A38885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 1; Length 605;
Pred. No. 0.0015;
2; Mismatches 0; Indels
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A;Residues: 1-607 <HOL>
A;Cross-references: EMBL:M73215
K;Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara,
Biochem. Biophys. Res. Commun. 173, 639-646, 1990
                             90.1%;
85.7%;
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Best Local Similarity 85.7
Matches 12, Conservative
                                                                                                             12; Conservative
                     Query Match
Best Local Similarity
Matches 12; Conserv
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C.Species: Felis silvestris catus (domestic cat)

C.Species: Felis silvestris catus (domestic cat)

C.Species: Felis silvestris catus

C.Species: Felis silvestris catus

C.Species: Felis silvestris catus

C.Species: Felis silvestris

C.Species: Felis silvestris

R.Hilger, C.; Grigioni, F.; Hentges, F.

Gene 169, 295-296, 1996

A.7Itle: Sequence of the gene encoding cat (Felis domesticus) serum albumin.

A.7Reference number: JC4660; MUID:96194824; PMID:8647469

A.7Recession: JC4660

A.7Accession: JC4660

A.7Accessi
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A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in bilitu A;Reference number: A47391; MUD:93211971; PMID:8460152
A;Contents: B/B homozygote
A;Accession: A47391
F;166-174/Product: Kinetensin #status experimental <KIP>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;77/Binding site: copper (His) #status predicted
F;77-86;99-115;114-125;146-193;192-201,224-270,269-277,289-303;302-313;340-385;384-393,
F;214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIP:128281)
C;Superfamily: serum albumin; serum albumin repeat homology
F;21-194/Domain: serum albumin repeat homology <8A1>
F;213-386/Domain: serum albumin repeat homology <8A2>
F;405-584/Domain: serum albumin repeat homology <8A3>
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Ajmolecule type: mRNA; protein
AjResidues: 1-600 <WAT>
Ajcross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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Gaps

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A, nocesolute type: protein
A, Residues: 23-51, YX, 53-54; XXXGY, 146, 'E', 148, 'E', 150-151, 'XVN', 155 < LIM>
A, Residues: 23-51, 'X', 53-54; XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 < LIM>
A, Experimental source: dental ename!
A, Experimental source: dental ename!
A, Experimental source: dental ename!
A, Note: albumin and other serum proteins are also found in bone
C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membracy Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; metal binding; plasma
F; 11-25/Domain: propeptide # status predicted < NAT>
F; 23-605/Product: serum albumin repeat homology < SA1>
F; 218-39/Domain: serum albumin repeat homology < SA2>
F; 410-589/Domain: serum albumin repeat homology < SA3>
F; 410-589/Domain serum albumin 
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A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-605 <MBID: AMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
A;Cross-references: BMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
B;Limbback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
B;Done Miner. Res. 4, 235-241, 1989
A;Title: Serum albumin and its acid hydrolysis peptides dominate preparations of minera
A;Reference number: A61006; MUID:89269769; PMID:2728927
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S01382; A6106
R;Weinstock, J; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Title: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:3174440
                                                                                                                                                   Gaps
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0
Score 64; DB 2; Length 600;
Pred. No. 0.0015;
2; Mismatches 0; Indels
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A; Accession: A93872
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Antities Papid confirmation and revision of the primary structure of bovine serum albumant Ancessaion 134600 Accession 136000 Accession 136000
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A. Accession: 80636
A. Molecule type: mRNA
C. Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
C. Superfamily: serum albumin; serum albumin repeat homology
C. Keywords: carrier protein; duplication; metal binding; plasma
F. 19-24/Domain: serum albumin fatatus predicted A. MIO
F. 20-70/Product: serum albumin repeat homology A. SA1>
F. 20-201/Domain: serum albumin repeat homology A. SA3>
F. 21-201/Domain: serum albumin repeat homo
C;Keywords: carrier protein; copper binding; duplication; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;29-201/Domain: propeptide #status experimental <MPT>
F;25-607/Product: serum albumin repeat homology <SA1>
F;20-393/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,
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A;Residues: 1-608 <SAR>
A;Cross-references: GB:V01222; GB:J00698; NID:G55627; PIDN:CAA24532.1; PID:G55628
R;Straus-W. Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 252, 6846-6855, 1977
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NyAlternate names: preproalbumin
C;Species: Nature
C;Species: Nature
C;Species: Nature
C;Date: 31.May-1979 #sequence revision 31-May-1979 #text_change 22-Jun-1999
C;Accession: A93872; A92211; Ā91946; A91940; C45800; I57621; A03233
R;Sargent, T.D.; Yang, M.; Bonner, J.
R;Sargent, T.D.; Yang, M.; Bonner, J.
A;Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUID:81223722; PMID:7017712
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C)Accession: S06936
R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:90098888; PMID:2602160
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90.1%; Score 64; DB 1; Length 607;
Best Local Similarity 85.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 0; Indels
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serum albumin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O5-Jun-1987 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A05139; 148638
R;Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
Mol. Biol. Evol. 2, 347-358, 1386
A;Fittle: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudocy A;Reference number: A93055; MUID:88216123; PMID:2452956
A;Accession: A05139
A;Accession: A05139
A;Accession: MOS139
A;Accession: MOS139
A;Accession: MOS139
A;Accession: Deschartette, J.; Meunier-Rotival, M.
Gene 89, 181-186, 1990
A;Attle: Empty and occupied insertion site of the truncated LINE-1 repeat located in the A;Reference number: 148638; MUID:90269606; PMID:1971802
                                            A. Molecule type: mRNA
A. Residues: 1-607 cHOA
C. Resi
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DNA Res. 4, 351-354, 1997

A/Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in threference number: JC5838; MUID:98116663; PMID:9455485

A;Accession: JC5838

A;Residues: J-609 < xOS>
A;Residues: 1-609 < xOS>
A;Residues: 1-609 < xOS>
A;Coss-references: DDBJ:AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278

A;Residues: 1-609 < xOS>
A;Coss-references: liver
C;Superfamily: serum albumin; serum albumin repeat homology
F;222-395/Domain: serum albumin repeat homology <SA2>
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C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 05-Mar.1998 #sequence_revision 13-Mar.1998 #text_change 19-May-2000
C;Accession: UC5838
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Pred. No. 0.0023;
3; Mismatches 0; Indels
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Best Local Similarity 78.6
Matches 11; Conservative
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Matches 11
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Aftitle: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analys Asteremene number: ASZIL MUDI:748657; PMID:83447

Ancression: ASZIL MUDI:77211 MUDI:7748657; PMID:83447

Ancression: ASZIL MUDI:77211 MUDI:7748657; PMID:84445

Ancression: ASZIL MUDI:77211 MUDI:7748657; PMID:84445

Ancression: ASZIL MUDI:77210405

Ancression: ASZIL MUDI:772104107

Ancression: ASZIL MUDI:772104105

Ancression: ASZIL MUDI:77210406

Ancression: AS
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R;Ho, J.X.; Holowachuk, E.W.; Norton, B.J.; Twigg, P.D.; Carter, D.C.
Eur. J. Blochem. 215, 205-212, 1993
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
A;Reference number: S34053; MUID:93345495; PMID:8344282
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C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
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Pred. No. 0.0015;
2; Mismatches 0; Indels
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Best Local Similarity 85.7%;
Matches 12; Conservative
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A;Molecule type: DNA
A;Residues: 1-34 CAND.
A;Cross-references: EMBL:271686; NID:g1302605; PID:g1302606; GSPDB:GN00014; MIPS:YNR0710
A;Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000612; GB:AE000511; NID:g2314188; PIDN:AAD08087.1; PID:g23141:
C;Superfamily: regulatory protein lcrD
                                                                                                                                                                                                                                                                                                                                        C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Go-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 24-Sep-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 24-Sep-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 24-Sep-1999
C;Accession: Aside50
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sthalak, H.G.; Glodek, A.; McKenn, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L. Nature: 388, 539-547, 1997
Conform M.S.; Borodovsky, M.; Fujli, C.; Bowman, C.; Watthey, L. Nature: 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W. S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: Ad4520; MUID:97394467; PMID:9252185
A;Accession: Ad4550
A;Accession: Ad4550
A;Accession: Ad4550
A;Accession: Application not shown
A;Molecule type: DNA
A;Residues: 1-73 *TOMA
A;Accession: Ad4500
A;Accession: Ad4500
A;Accession: Ad4500
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N,Alternate names: hypothetical protein N3605
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr.1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C;Accession: S63404
R;Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.; Vissers, S.
A;Reference number: S62920
A;Reference number: S62920
A;Accession: S63404
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ö
                                                                                                                                                                                                                                                                                                    flagellar biosynthesis protein - Helicobacter pylori (strain 26695)
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   Indels
       <u>س</u>
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19;
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Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
       Mismatches
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Pred. No.
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nilarity 80.0%;
Conservative 0
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53.8%;
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C,Superfamily: aldose 1-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MIPS:YNR071c
A;Cross-references: SGD:S0005354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           577 LLHEKIPIKDMLT 589
                                                                                                                   :|||| |: | :|
577 LLHEKIPIKDMLT 589
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Best Local Similarity 53.0.
Best Accelerative
Ti Conservative
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                                                                    1 VLHEKTPVSDRVT 13
          7; Conservative
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Best Local Similarity
Matches 8; Conserv
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          Matches
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C;Species: Pseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Accession: B3840
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Attereror number: A82950; MUD:20437337; PMID:10984043
A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-553 <STO>
A;Cross-references: GB:AE004444; GB:AE004091; NID:g9945863; PIDN:AAG03439.1; GSPDB:GN001
C;Genetics:
A;Gene: PA0049
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A;Variety: strain J99
A;Variety: strain J99
C;Date: 12. Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Sep-1999
C;Date: 12. F1937
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Jros, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Accession: E71937
A;Status: preliminary
A;Molecule type: DNA
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A;Residues: 1-733 <ARN>
A;Cross-references: GB:AE001473; GB:AE001439; NID:g4154910; PIDN:AAD05964.1; PID:g415491
A;Experimental source: strain J99
C;Genetics:
A;Gene: flhA
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       A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residuse: 379-453 < BCS
A,Residuse: 379-453 < BCS
A;Cross-references: BMBL:X13060; NID:g52939; PIDN:CAA31458.1; PID:g899334
A;Cross-references: BMBL:X13060; NID:g52939; PIDN:CAA31458.1; PID:g899334
C;Superfamily: serum albumin; serum albumin repeat homology
C;Reywords: carrier protein; duplication; metal binding; plasma
F;1104-Domain: serum albumin repeat homology (fragment) <SA1>
F;123-296/Domain: serum albumin repeat homology (fragment) <SA3>
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Pred. No. 9.2;
5; Mismatches
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No. 13;
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C,Superfamily: regulatory protein lcrD
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Best Local Similarity 78.6
Matches 11; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Jarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A; Bescription: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: B90289
A; Accession: B90289
A; Accession: B90289
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-604 < KUR>
A; Crosex-references: GB: AE006641; NID: g13814539; PIDN: AAK41569.1; GSPDB: GN00155
C; Genetics:
A; Gene: SSO1331
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Search completed: April 19, 2004, 12:02:32 Job time: 2.70637 secs

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P02769
P14639
P49065
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                           141681 seqs, 52070155 residues
                                                                                                                                                                                               US-09-832-929-18_COPY_462_475
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ALBU CANPA
ALBU MACMU
ALBU DOVIN
ALBU SHEEP
ALBU SHEEP
ALBU SHEEP
ALBU RABIT
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Q911G6 cyanidium c Q9uhi6 homo sapien P30319 choristoneu Q80728 staphylococ P21976 neurospora P3146 bacillus su P36402 mus musculu P34080 rattus norv Q99ax5 staphylococ P7624 escherichia P57860 pasteurella	ALIGNMENTS  PRT; 609 AA.  1157; Q9P117; Q9UHS3; Q9UJZ0;  ed)  sequence update)  annotation update)	; Vertebrata; Euteleostomi; .ni; Hominidae; Homo.	g W.J., Dennison O.E., Hawkins J.W., albumin gene is revealed by of chromosome 4.";	nke A.E., Houck C.M.,	121. .:;   amino acide of human serum .7s(1982).	O1 Z.W., Yuan Z.Y.; DDBJ databases.) to the EMBL/GenBank/DDBJ databases. (PRC0903/PRO1708/PRO2044/PRO2619/PR02675). ang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,	121 new 1 liver bases.
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MEDLINE=78186630; PubMed=656055;
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SEQUENCE OF 222-229.
MEDLINE=76257808; PubMed=955075;
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TISSUE=Liver;
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MEDLINE=91316157; PubMed=1859851;
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        100.0%; Score 71; DB 1; Length 60 100.0%; Pred. No. 6.9e-05; ative 0; Mismatches 0; Indels
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Hilger C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                  ALBU CANFA STANDARD; PRT; 608 AA. P49822; 077705; Q9TS24; 101-0CT-1996 (Rel. 34, Created) 10-CCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Serum albumin precursor (Allergen Can f 3).
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MEDLINE=75011422; PubMed=4414013;
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Serum albumin precursor (Allergen Fel d 2).
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Best Local Similarity 92.9
Marches 13, Conservative
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206
349
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608 AA;
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MEDLINE 59211917, PubMed=8460152;

MEDLINE 59.211917, PubMed=8460152;

MEDLINE 59.211917, PubMed=8460152;

MEDLINE 5.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,

Davilet J., Putnam F.W.;

Davilet J., Putnam F.W.;

"cDMA and protein sequence of polymorphic macaque albumins that differ

in bilitubin binding.";

proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).

I. Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).

- !- FUNCTION: Serum albumin, the main protein of plasma, has a good

- i- FUNCTION: Serum and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

- SUBCELLULAR LOCATION: Secreted.

- ITSSUE SPECIFICITY: Plasma.

- ITSSUE SPECIFICITY: Belongs to the ALB/APF/VDB family.

- ISIMILARITY: Contains 3 albumin domains.
                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-REP-2003 (Rel. 41, Last annotation update)
Serum albumin precursor (Fragment).
                                                                              Macaca mulatta (Rhesus macaque)
                                                                                                                       Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                            SEQUENCE FROM N.A.
Q28522;
01-NOV-1997
01-NOV-1997
28-FEB-2003
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                                                    Hilger C., Grigioni F., Kohnen M., Hentges F.;
"Sequence of the gene encoding cat (Felis domesticus) serum albumin.";
"Sequence of the gene encoding cat (Felis domesticus) serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hordmones, blirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELBULAR LOCATION: Secreted.
-!- ALIBERGEN: Causes an allergic reaction in human.
-!- ALIBERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                        EMBL; X84842; CAA59279.1; -..
PIR; JC4660; S37632.
HISSP; P02768; IETB.
InterPro; IETB.
FAMIN PF00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
Prodom; PD002486; SERUM albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; P800212; ALBUMIN; 3.
PROFEP BY SIMILARITY.
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Pred. No. 0.00035;
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                             SEQUENCE FROM N.A.
MEDLINE=96194824; PubMed=8647469;
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                                                                                                                                                                          E45C871A670E740B CRC64;
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SERUM ALBUMIN 1
ALBUMIN 2
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY BY SIMILARITY BY SIMILARITY.
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1; Mismatches

1 VLHEKTPVSDRVTK 14 Conservative

486

à 용 600 AA

PRT;

STANDARD;

RESULT 4 ALBU MACMU ID ALBU MACMU

Gaps

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[5]
SEQUENCE OF 1-32.
MEDILINE-80024378; PubMed=488109;
McGillivray R.T.A., Chung D.W., Davie B.W.;
"Biosynthesis of bovine plasma proteins in a cell-free system. Amino-
terminal sequence of preproalbumin.";
Eur. J. Biochem. 98:477-485(1979).
                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F., Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            90.1%; Score 64; DB 1; Length 605; 85.7%; Pred. No. 0.0012; ive 2; Mismatches 0; Indels
                                                                                                                          -> D (IN REF. 1; AAA30988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT THR-214. Wu H.T., Huang M.C.; "The complete cDNA sequence of bovine serum albumin."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holowachuk E.W., Stoltenborg J.K., Reed R.G., Peters T. Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barry T., Power S., Gannon F.; Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214
                                                                                                                                                                                                                                                                                                       ALBU BOVIN STANDARD; PRT; 607 AA. P02769; 002787; 21-JUL-1986 (Rel. 01, Created) 10-PE-1996 (Rel. 33, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Serum albumin precursor (Allergen Bos d 6).
                    SIMILARITY
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Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANT THR-214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown J.R.;
"Structure of bovine serum albumin.";
Fed. Proc. 34:591-591(1975).
69410 MW;
                                                                                                                                                                                                                                483 VLHEKTPVSEKVTK 496
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 REVISIONS TO 190-195
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Best Local Similarity
Thes 12; Conserva
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                  MEDLINE=89016582; PubMed=3174440;
Baldwin G.S., Weinstock J.;
Baldwin G.S., Weinstock J.;
"Nuclectide Sequence of porcine liver albumin.";
Nucleic Acids Res. 16;9045-9045(1988).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. (a(2+1), Na++), K(+), fatty acids, binding capacity for water. (a(2+1), Na++), K(+), fatty acids, hormones, blintubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Delongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                          Gaps
                                                                                                                                                                                                                                                      Eukaryota, Macazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI TaxID=9823,
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0
             Score 64; DB 1; Length 600; Pred. No. 0.0012; 2; Mismatches 0; Indels
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EMBL; M36787; AAA30980.1; --
PIR; S01382; ABPGS.
HSSP; P02768; LETH.
InterPro; P02768; LTH.
InterPro; P02768; LTH.
Pfam; PF00273; LTHRSPORT PFOC; 3.
PRINTS; PR00802; SERUMALBUMIN.
PRODOM; P0002486; Serum albumin; 1.
SMART; SM0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
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SERUM ALBUMIN.

ALBUMIN 1.

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ALBUMIN 3.

COPPER (BY SIMILARITY).

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                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
08-PEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor (Fragment).
                                                                                                                                                         605 AA
                                                                                                                                                         PRT;
                Query Match 90.1%;
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                VLHEKTPVSEKVTK 491
                                                                  1 VLHEKTPVSDRVTK 14
                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                          Brown J.R.;

Brown J.R.;

"Structure of serum albumin: disulfide bridges.";

"Structure of serum albumin, the main protein of plasma, has a good pinding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Plasma.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the ALB/APP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                             SEQUENCE, AND REVISIONS TO 118-119 AND 180.
MEDLINE-91083649; PubMed=2260975;
Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";
Biochem. Biophys. Res. Commun. 173:639-646(1990).
                                                                                                                                                                                                                                SEQUENCE OF 25-41.

MEDLINES BR267456; PubMed=3389500;
Hsieb J.C., i.n. P.P., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical
"Electroblotting gel: a preparative method for isolating proteins
for N-terminal microsequencing.";
Anal. Blochem. 170:1-8(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR, 122...
InterPro; IPR, 122...
Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERUMALBIWIN.
Prodom: PD002486; SEM: albumin; 1.
SWART; SW00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
                                                                                  Patterson J.E., Geller D.M., "Bovine microsomal albumin: amino terminal sequence of bovine
            Reed R.G., Putnam F.W., Peters T. Jr.; "Sequence of residues 400-403 of bovine serum albumin."; Blochem. J. 191:867-868(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
                                                                                                                        Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERUM ALBUMIN.
                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998) to Swiss-Prot.
 MEDLINE=82023364; PubMed=7283978;
                                                         SEQUENCE OF 19-28.
MEDLINE=77134075; PubMed=843354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M73993; AAA51411.1; -.
EMBL; X5889; CAA41735.1; -.
EMBL; X17769; CAA76847.1; -.
EMBL; AF542069; AAN17824.1; -.
HSSP; P02766; 1E78.
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                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 1; Length 607;
Pred. No. 0.0012;
2; Mismatches 0; Indels
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C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

N -> D (IN REF. 6).

ST -> TS (IN REF. 6).

K -> R (IN REF. 6).

K -> B (IN REF. 6).

K -> B (IN REF. 6).
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01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                        69293 MW;
                                                                                                                                                                                                                                                                                                                                                  90.1%;
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1es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALBU SHEEP STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serum albumin precursor.
SEQUENCE FROM N.A.
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ALBU_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Pred. No. 0.0012;
2; Mismatches 0; Indels
## REMBL, X17055, CAA34903.1; -. ## HSPP, 206936, ABBHS.
## HSPP, 18702768, 18704.
## REMPTO, 18702768, 18704.
## REMPTO, 18702768, 18704.
## REMPTO, 1870373, transport prot; 3.
## PRINTS; PRO004286, Serumalbumin.
## PRO0773; transport prot; 3.
## PRO0773; transport prot; 3.
## PRO0773; transport prot; 3.
## PRO0773; ALBUMIN; 3.
## REMPT, SM00103; ALBUMIN; 3.
## REMPT, 25 604 ALBUMIN; 2.
## DOWAIN 25 604 ALBUMIN; 3.
## PRO07781 25 604 ALBUMIN; 3.
## PROMISED 25 204 ALBUMIN; 3.
## PROMISED 25
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01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 41, Last annotation update)
Serum albumin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 VLHEKTPVSEKVTK 498
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CC the Burgean Bioinformatics and the EMBL outstation of its use by non-profit institutions as long as its content is in no way to modified and this statement is not reserved. Usage by non-profit institutions as long as its content is in no way of modified and this statement is not removed. Usage by and for commercial continues a license agreement (See http://www.isb-sib.ch/announce/cor send an email to licensealsb-sib.ch).

BR HESP PO2768; INFN:

HESP PO2768; INFN:

HESP PO2713; INTNESCRIPTION OF SERUM Albumin.

BR HESP PO273; INTRESCRIPTION OF SERUM Albumin.

BR SMART; PRO0023; SERUM Albumin; 1.

BR SMART; SWOOD13; ALBUMIN; 1.

FT DOWALN 25 GOS SERUM Albumin.

FT DOWALN 26 GOS SERUM Albumin.

FT DOWALN 27 GOS SERUM Albumin.

FT DOWALN 26 GOS SERUM Albumin.

FT DOWALN 27 GOS SERUM Albumin.

FT DOWALN 27 GOS SERUM Albumin.

FT DOWALN 404 GOS SERUM Albumin.

FT DOWALN 500 SERUM Albumin.

FT DOWALN 500 SERUM Albumin.

FT DOWALN 600 SERUM 600 SERUM 600 SERUM 600 SERUM 600 SERUM 600 SER
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TIBURAT STANDARD; PRT; 608 AA.

ALBU RAT STANDARD; PRT; 608 AA.

POT70; PIT382;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].

GN ALB.

OS Rattus norvegicus (Rat).

OC Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TAXID=10116;
RN [1]
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223722; PubMed=7017712;
RA Sargent T.D., Yang M., Bonner J.;
RT "Nuclectide sequence of cloned rat serum albumin messenger RNA.";
RI "Nuclectide sequence of cloned rat serum albumin messenger RNA.";
RI "Puco. Natl. Acad. Sci. U.S.A. 78:243-246(1981).

v [2] p SEQUENCE OF 1-38, AND PROCESSING. K MEDLINE=77249657; PubMed=893447;

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608 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                    RESULT 10
ALBU HORSE
ID ALBU HORSE
AC P35747;
                                                                                                                                                                         VARIANT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                           MEDLINE=79001617; PubMed=80265;
A Acyagi Y., Ikenaka T., Ichida F.;
"Copper [II]-binding ability of human alpha-fetoprotein.";
"Copper [II]-binding ability of human alpha-fetoprotein.";
"Cancer Res. 38:3483-3486(1978)
C. !- FUNCTION: Sevum albumin, the main protein of plasma, has a good
binding capacity for water, CG(2+), Ma(+), K(+), fatty acids,
binding capacity for water, CG(2+), Ma(+), K(+), fatty acids,
confinence, bilirubin and drugs. Its main function is the regulation
of the colloidal osmotic pressure of blood.
C. !- FUNCTION: NPR regulates fat digestion, lipid absorption, and
blood flow (Potential).
C. !- SIMCELLULAR LOCATION: Secreted.
- ITSSUE SPECIFICITY: Plasma.
- ITSSUE SPECIFICITY: Plasma.
C. !- SIMLIARITY: Contains 3 albumin domains.
"Rat liver pre-proabbumin: Complete amino acid sequence of the pre-piece. Analysis of the direct translation product of albumin messenger RNA.";
J. Biol. Chem. 252:6846-6855(1977).
                                                                                                                                                               SEQUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.,
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                                                                                        MEDLINE-78109429; PubMed=564345;
Isemura S., Ikenaka T.;
"Amino acid sequences of fragments I and II obtained by cyanogen
bromide cleavage of rat serum albumin.";
                                                                                                                                                                                                                                                                                        Carraway R.B., Mitra S.P., Cochrane D.B.;
"Structure of a biologically active neurotensin-related peptide
"Structure of a biologically active neurotensin-related peptide
obtained (from pepsin-treated albumin(8).";
J. Biol. Chem. 262:5968-5973 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUROTENSIN-RELATED PEPTIDE.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INST. FOLLOW: TROOOZE4; Serum albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
SMART; SM00103; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
SMGAT-binding; Lipid-binding; Repeat; Signal; Copper.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERUM ALBUMIN.
                                                                                                                                                                                                                                                     SEQUENCE OF 166-174.
TISSUE=Plasma;
MEDLINE=87194805; PubMed=2437111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V01222; CAA24532.1; -.
                                                                                                                                            Biochem. 83:35-48(1978).
                                                                                SEQUENCE OF 25-222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02768; 1E7B
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TISSUB-LIVEY,

MEDLINE-9345459; PubMed-8344282;

MEDLINE-9454549; Medline Capalius)

MEDLINE-954549; Medline Capalius

MEDLINE-954549; Medline Capalius

MEDLINE-954549; Med
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Pred. No. 0.0012;
2; Mismatches 0; Indels
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01-UUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Equ c 3).
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BY SIMILARITY.
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PIR, S34053; ABHOS.
HSSP; P02766; 1E79.
InterPro; IPR00204; Serum_albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERUMALEUMIN.
ProDom; PD002486; Serum_albumin; 1.
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Best Local Similarity 85.7%; Pre
Matches 12; Conservative 2;
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RESULT 12
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                    g; Repeat; Signal; Copper; Allergen.
BY SIMILARITY.
BY SIMILARITY.
SERUM ALBUMIN.
ALBUMIN 2.
ALBUMIN 2.
ALBUMIN 2.
ALBUMIN 2.
COPPER (BY SIMILARITY).
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Pred. No. 0.0018;
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                  PROSITE: PSO0212; ALBUMIN; 3. Metal-binding; Residual binding; Res
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78.6%;
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                                                                  Query Match
Best Local Similarity
Thes 11; Conserve
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035090;
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    SMART;
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SEQUENCE FROM N.A.

STRAIN-STEPL/GJ; TISSUE-Tongue;

MEDLINE-21085660; Pubmed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 609
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                                                                                                         R RBL; AB006197; BAA21765.1; -. R PIR; AB006197; BAA21765.1; -. R PIR; AB006197; BAA21765.1; -. R RSP; PO2768; LETBER LET
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Pred. No. 0.0062;
3; Mismatches C
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ALBUMIN 2.
ALBUMIN 3.
COPPER.
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Best Local Similarity 78.6
Matches 11; Conservative
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van Reeth T., Gabant
Submitted (SEP-1998)
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609 AA;
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Aliawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., R. Saico T., Comanda Y., Sinch R., Saico T., Saico T., Saico T., Saico T., Saico T., Saico T., Saico G., Quadrona H., Saico T., Saico T., Saico G., Comanda T., Manio T., Saico T., Saico T., Saico G., Quadrona H., Manio T., Saico T., Saico T., Saico G., Quadrona H., Manio T., Saico T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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Pred. No. 0.0093;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> D (IN REF. 6).
-> D (IN REF. 6).
-> I (IN REF. 6).
292F7C7EED3A61B4 CRC64;
                                                                                                                                                                                                                                                                           Repeat; Signal; Copper.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (Rel. 40, Last annotation update)
Flagellar biosynthesis protein flhA.
FLHA OR FLBA OR UHP0383.
                                                                                                                                                                                                                                                                                                                                                             COPPER.
BY SIMILARITY
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ALBUMIN 2.
ALBUMIN 3.
                                                                                              EMBL; AJ011413; CAA05617.1; --
EMBL; AK010025; BAB26650.1; --
EMBL; BC049971; AAH49971.1; --
EMBL; M16111; AAA37190.1; --
EMBL; X13060; CAA31458.1; --
EMBL; X13060; CAA31458.1; --
EMBL; X13060; CAA31458.1; --
EMBL; A05139; A05139.1; --
EMBL; A05139; A07724; MOUSE.
MGD; MGI:87991; Alb1.
InterPro; IPR00204; Serum albumin.
PEm; PR00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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Best Local Similarity 78.6'
Matches 11, Conservative
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METAL
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SEQUENCE OF 93-733 FROM N.A.
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                         Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
TRANSMEM 28
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TRANSMEM
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                                                                                                                                                                pylori.
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                              SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R.; Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                           "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180 (1999).
-!- FUNCTION: INVOLVED IN THE EXPORT OF FLAGELLUM PROTEINS.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE PHIPEP (FLAGELLA/HR/INVASION PROTEINS EXPORT PORE) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILMA HELPY

O06759, O06759,

O1-NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

16-CCT-201 (Rel. 40, Last annotation update)

16-CCT-201 (Rel. 40, Last annotation update)

FLHA OR FLBA OR HP1041.

FLHA OR FLBA OR HP1041.

Helicobacter pylori (Campylobacter pylori).

Helicobacteria; Epchlobacteria; Epstlonproteobacteria; Campylobacterales;

Helicobacteriaceae; Helicobacter.
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                          48 POTENTIAL.
69 POTENTIAL.
145 POTENTIAL.
233 POTENTIAL.
266 POTENTIAL.
311 POTENTIAL.
333 POTENTIAL.
333 POTENTIAL.
334 POTENTIAL.
338 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BFP;
Schmitz A., Josenhans C., Suerbaum S.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00771; FHIPEP; 1.
PRINTS: PR00949; TYPEJIMAPROT.
TIGREPMS: TIGRO1994; FIDA; 1.
PROSITE; PS00994; FHIPEP; FALSE NEG.
Flagellum; Transport; Protein transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                     PIR; E71937; E71937.
InterPro; IPR001712; Bact FHIPEP.
InterPro; IPR006301; FlhA.
                Helicobacteraceae; Helicobacter.
NCBL_TaxID=85963;
                                                                                                                                                                                                                                                                                                                         EMBL; AE001473; AAD05964.1; -.
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53.8%;
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577 LLHEKIPIKDMLT 589
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733 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
TRANSMEM 28
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FLHA_HELPY
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN=26695 / ATCC 700392;
STAIN=26695 / ATCC 700392;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Xlenk H.-P., Gill S., Dougherty B.A.,
Nelson W., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                           The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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A - 8 (IN REF. 1).

LLL - 9 YC (IN REF. 1).

A - C (IN REF. 1).

T - A (IN REF. 1).

T - A (IN REF. 1).

L - I (IN REF. 1).

I - Y (IN REF. 1).

Y - A (IN REF. 3).

I - Y (IN REF. 3).

I - Y (IN REF. 3).

I - Y (IN REF. 3).
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PROSITE; PS00994; FHIPEP; FALSE NEG.
Flagellum; Transport; Protein transport; Transmembrane;
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53.8%; Pred. No. 7.7;
tive 3; Mismatches
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TIGR; HP1041; -.
InterPro; IPR006301; FlbA.
InterPro; IPR006301; FlbA.
Pfan; PP00771; FH1PEP; 1.
PRINTS; PR00949; TYPE31MAPROT.
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EMBL; Y13395; CAA73825.1; -.
EMBL; Y08762; CAA70007.1; -.
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A MEDIAINE_22834015; PubMed=12928499;

Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,

A Whin M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,

Andupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,

Andupu R., Daugherty S., Brinkac L., Beanan M.J., Yuan Q.,

RA Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q.,

RA Alfano J.R., Cartinhour T.V., D'Ascento M., Deng W.-L., Ramos A.R.,

A Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,

Antarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,

RA Hite O., Fraser C.M., Collmer A.A.,

White O., Fraser C.M., Collmer A.A.,

The complete genome sequence of the Arabidopsis and tomato pathogen

Breudomonas syringae pv. tomato DC3000.",

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).

Immediate electron acceptor for the enzyme in this species is

balieved to be ubiquinone. Couples the redox reaction to proton

translocation (for every two electrons transferred, four hydrogen

conserves the redox energy in a proton gradient (By similarity).

C. -: CORMANTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.

(P., Anderson P.)

C. -: CORMANTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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InterPro; IPROUGES; Complex175K.
InterPro; IPROUGES; Complex175K.
InterPro; IPROUGES; Complex175K.
InterPro; IPROUGES; Molybdopterin.
InterPro; IPROUGES; Molybdop_Fe484.
Pfam; PF00111; fer2; 10
Pfam; PF00181; Molybdop Fe484.
Pfam; PF004879; Molybdop Fe484; 1.
IGRFAMS; TIGR01973; NuGG; 1.
PROSITE; PS00641; COMPLEX175K_1; 1.
PROSITE; PS00642; COMPLEX175K_2; 1.
PROSITE; PS00643; COMPLEXI75K_2; 1.
PROSITE; PS00643; COMPLEXITE; PS00644; COMPLEXITE; PS0
                                                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
NADH-quinone oxidoreductase chain 3 (BC 1.6.99.5) (NADH dehydrogenase I, chain G) (NDH-1, chain G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity).
--- SUBURT: Composed of 13 different subunits. Subunits nuoCD, E, F, and G constitute the peripheral sector of the complex.
--- SIMILARITY: Belongs to the complex I 75 kDa subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
Pseudomonadaceae, Pseudomonas.
NCBI TaxID=323;
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34 IRON-SULFUR 1 (2FE-2S)
45 IRON-SULFUR 1 (2FE-2S)
                                                                                                                                       905 AA.
                                                                                                                                       PRT;
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     577 LLHEKIPIKDMLT 589
                                                                                                                                       STANDARD;
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METAL 34
METAL 45
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Q872Q4;
15-MAR-2004 (
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    (BY SIMILARITY).
(COTENTIAL).
(FOTENTIAL).
(FOTENTIAL).
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IRON-SULFUR 1 (2FE-25) (BY IRON-SULFUR 1 (2FE-25) (BY IRON-SULFUR 2 (4FE-45) (BY IRON-SULFUR 2 (4FE-45) (BY IRON-SULFUR 2 (4FE-45) (BY IRON-SULFUR 3 (4FE-45) (BY IRON-SULFUR 3 (4FE-45) (BY IRON-SULFUR 3 (4FE-45) (BY IRON-SULFUR 4 (4FE-45) (BY IRON-SULFUR 4 (4FE-45) (POTIRON-SULFUR 4 (4FE-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 1;
Pred. No. 14;
1; Mismatches
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ilarity 77.8%;
Conservative
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905 AA;
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P89201 sweet pocat
Q88915 rhizobium 1
Q884210 rhizobium 1
Q922k10 rhizobium 1
Q93047 mycobacteri
Q9nfa7 leishmania
G9637 mycobacteri
Q9nfa7 leishmania
G9637 mycobacteri
Q9nfa7 leishmania
G9611 leishmania
G9611 leishmania
Q9huz7 pseudomonas
Q8huz7 pseudomonas
Q8huz7 pseudomonas
Q8huz7 pseudomonas
Q8huz7 pseudomonas
Q8109 bacteroides
G8391 streptomyce
G9310 streptomyce
G9310 streptomyce
G97166 clostridium
Q84fp3 spirulina p
Q8760 streptomyce
Q9766 clostridium
Q84fp3 spirulina p
Q8760 streptomyce
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001545 caenorhabdi
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QBIUK8LE1: 23, Last sequence update)
Q1-OCT-2003 (TrEMBLre1: 25, Last senocation update)
Similar to serum albumin precursor.
Similar to serum albumin precursor.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Straubergy R.;
Straubergy R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EDGJ G010055615; C:extracellular space; IEA.
GO; G0:00056615; C:extracellular space; IEA.
GO; G0:0006810; P:transport; IEA.
InterPro; IPR0006810; P:transport; IEA.
FFAM; PFR013; Lransport prot; 2.
PRINTS; PR00802; SERUMALBIMIN.
SNART; SM00103; ALBUMIN; 2.
PROSITE; P800121; ALBUMIN; 2.
SEQUENCE 396 AA, 45159 MM; 756519C096463A9B CRC64;
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Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels
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Q82K00
Q7YSM9
Q870V1
Q8HXG0
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Q97H66
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Q9USA7
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Q97625
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Q933047
Q94M85
Q9CBE1
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07TVZ5
P72172
Q9NJ11
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Q8DTB0
Q8A079
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TISSUE=Liver;
              Q8IUK7
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Q8C7C7 mus musculu
Q8C7D3 mus musculu
Q9C7B3 pseudomonas
Q9SG99 helicobacte
Q87Zq4 pseudomonas
Q959A1 helicobacte
Q87B91 leptospira
Q7Viy5 helicobacte
Q8VIC7 burkholderi
Q97y10 sulfolobus
Q97y10 sulfolobus
Q95E07 arabidopsis
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Q86yg0 homo sapien
Q7ysg3 felis silve
Q95vb7 schistosoma
                                                                                                                                                                          April 19, 2004, 11:37:09 ; Search time 5.40351 Seconds (without alignments) 817.479 Million cell updates/sec
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                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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1 VLHEKTPVSDRVTK 14
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Listing first 45 summaries
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Q867G0
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Q8C7H3
Q8C7H3
Q8C8H6
Q917B3
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sp_inuman:*
sp_invertebrate:*
sp_organelle:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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STAIL—22354683; PubMed=12466851;

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And lysis of the mouse transcriptome based on functional annotation of the mouse transcriptome.

BL MACSOG44; BAC34360.1; -.

EMBL; AK050644; BAC34360.1; -.

BR MCO; GO:0005615; C:extracellular space; IEA.

GO; GO:0005615; C:extracellular space; IEA.

GO; GO:0006810; P:transport; IEA.

BR GO; GO:0006810; P:transport; IEA.

BR PROBO27; ENRUMALEMIN.

BR PROBO3; SERUMALEMIN.

BR PROBO3; ALBUMIN; 3.

R PROBUTE; PROBO3; ALBUMIN; 3.

FT NON TER

SEQÜENCE 576 AA; GS002 MW; F85733E99AE37F04 CRC64;
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                                                                                                                                                                                                                                           Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida,
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCTI_TaxID=6183;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%; Score 63; DB 5; Length 608;
85.7%; Pred. No. 0.0086;
iive 2; Mismatches 0; Indels
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Last sequence update)
Last annotation update)
                                               ol-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Albumin.
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608 AA.
PRT;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P., Rumpold H., Valenta R., Spitzauer S.; Buscherichia coli expression and purification of recombinant cat albumin:IgE recognition, induction of basophil activation and lymphoproliferative responses in atopic patients."; Submitted (MAY-2002) to the EMBL, GenBank/DDBJ databases. BMBL; AJ487677; CAD32275.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL) BC041789; AAH41789.1.
RGO; GO:0005615; C:extracellular space; IEA.
RGO; GO:0005816; F:carrier activity; IEA.
RGO; GO:0005810; P:transport; IEA.
R GO; GO:0005386; F:carrier activity; IEA.
R Interpro; IPR00264; Serum_albumin.
PROMO73; ERBUMALBUMIN.
PRODM; PR00802; SERUMALBUMIN.
PRODM; PR002486; Serum_albumin; 1.
R SMART; SMO0103; ALBUMIN; 2.
R SMART; SMO0123; ALBUMIN; 2.
R SEQUENCE 417 AA; 47360 MN; 16E764833EEF4E8D CRC64;
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94.4%; Score 67; DB 6; Length 584;
Best Local Similarity 92.9%; Pred. No. 0.0016;
Matches 13; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 584 AA; 65908 MW; B51002F12902C9CE CRC64;
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin (Fragment).
ALB.
                                                                           01-UTN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 AA
           417 AA
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                                                                                                                                                                                               Similar to alpha-fetoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 VLHEKTPVSERVTK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 VLHEKTPVSDRVTK 307
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1es 14; Conservative
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           PRELIMINARY;
                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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Q95VB7
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RESULT 3 Q7YSG3

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Gaps

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**Q8С7Н3** 

ò g RESULT 6
08C7H3
00C7H3
00C7H3
01-M
DT 01-M
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SEQUENCE FROW N.A.
STRAIN=ATC 15692 / PAO1;
STRAIN=ATC 15692 / PAO1;
STRAIN=ATC 15692 / PAO1;
Strover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Strover C.K., Pham X.-Q.T., Erwin A.L., Miragle W.O., Kowallik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M., Eroder K.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
A STRAIN=cv. Nipponbare;
A Staski T., Matemmoto T., Yamamoto K.;
A Clone: Po456C02 ";
Clone: P0456C02 ";
Discreted (NOV-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003833; BAC15482.1; -..
REMBL; AP003833; BAC15482.1; -..
REMBL; AP003833; BAC15482.1; -..
REMBL; SM002313 ank; 2.
REMBL; SM00248; ANK. 3.
REMBL; PS50027; ANK REPEAT; 2.
REMSTITE; PS50089; ANK REPEAT; 2.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

64.8%; Score 46; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 2; Indels
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Nature 406:959-964(2000).
Nature 406:959-964(2000).
EMBL; ARE004444; AAG03439.1; -.
EMBL; ARE0044419; P. 1970glutamyl-peptidase I activity; IEA.
GO; GO:0004219; P. 1970glutamyl-peptidase I activity; IEA.
GO; GO:0006508; P. 1970cellysis and peptidolygis; IEA.
InterPro; IRR000816; Peptidase CIS.
Hypothetical protein; Complete proteome.
SEQUENCE 553 AA; 60113 MW; BE9B75723D46FB3B CRC64;
Submitted (JUL-2001) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PA0049.
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Matches 6; Conservative
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113 HEKTPMDEAVTK 124
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Q91783;
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Q9S6G9
ID Q9S6C
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STRAIN=C57BL/60; TISSUB=Liver;

MEDLINE=22354683; PubMed=12466851;

A The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

Thanlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.;

IN Ature 420:563-573(2002).

REMBL; AKOSO248; BAC34145.1; ...

ROG; GO:0005515; C:extracellular space; IEA.

GO; GO:0005815; C:carriar activity; IEA.

ROG; GO:0006810; P:transport; IEA.

REMD: Pro; IPR000264; Serum_albumin.
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Q8GSH6;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
O1-JUN-2001.19 OR P0496C02.4
O1-JUN-2003 (Japonica cultivar-group).
O1-JUN-2003 (Japonica cultivar-group).
Spermatophyta, Viridplantea; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolicaphyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1477_F01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.6%; Pred. No. 0.046;
Matches 11; Conservative 2; Mismatches 1. .....
        Query Match 83.1%; Score 59; DB 11; Length 576; Best Local Similarity 78.6%; Pred. No. 0.043; Matches 11; Conservative 2; Mismatches 1; Indels
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PRINTS; PR00802; SERUMALBUMIN.

ProDom; PD002486; Serum albumin; 1.

SMART; SM00103; ALBUMIN; 3.

PROSITE; PS00212; ALBUMIN; 3.

SEQUENCE 608 AA; 68722 MW; 292P600EED3A61B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Albumin 1.
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486 LLHEKTPVSEHVTK 499
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454 LLHEKTPVSEHVTK 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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RESULT 7

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PROSITE; PS00641; COMPLEXI_75K_1; 1. PROSITE; PS00642; COMPLEXI_75K_2; 1. PROSITE; PS00643; COMPLEXI_75K_3; 1.
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es 7; Conservative
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                                                                                                                                                                                                                                                                                                                          592 HOKTPISDR 600
                                                                                                                                                                                                                                                                         3 HEKTPVSDR 11
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                                                                                  Complete proteome
SEQUENCE 905 AA
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SEQUENCE
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Q93EH4;
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Q8F9B1
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Buell R., Joardar V., Khouri H., Fedorcva N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorcva N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorcva N., Tran B., Russell D.,
Buell R., Joardar V., Salengut J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Salengut J., Nelson W., Davidsen T.,
A. Brinkac L., Beanan M., Haft D., Salengut J., Nelson W., Davidsen T.,
A. Complete sequence of Pseudomonas syringae.";
S. Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
ENBL; Abol6668; Abo56948.1; -.
ENBL; Abo16668; Abo16668; Abo16668; Abo16668; Abo16668; Abo16668; Abo16668; Abo16668; Abo16668; Abo166694; Abo166694; Abo166694; Abo166694; Abo166694; Abo166694; Abo166694; Abo166694; Abo166694; Abo166965; Molybdopterin, InterPro; IPR006965; Molybdopterin, InterPro; IPR00384; Molybdoperin; 1.
EFAm; PF004879; Molybdoperin; 1.
EFAm; PF04879; Molybdop_F6484; 1.
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                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
WCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINEATCC 43504;
MEDLINE=99214098; PubMed=10198012;
MCGED D.J., May C.A., Garner R.M., Himpsl J.M., Mobley H.L.T.;
"Isolation of Helicobacter pylori genes that modulate urease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.6%; Score 43; DB 2; Length 733; Best Local Similarity 53.8%; Pred. No. 43; Matches 7; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Descriol. 181:2477-2484(1999).

EMBL, AF125197; AAD27689.1; -...

EMBL, AF125197; AAD27689.1; -...

GO, GO:00160200; C:membrane; IEA.

GO, GO:000306; P:protein secretion; IEA.

InterPro; IPR001712; Bact FHIPEP.

InterPro; IPR006301; FlhA.

Pfam; PF00771; FHIPEP; I.

Pfam; PR00771; FHIPEP; I.

TIGREAMs; TTGR01399; FILM.

TIGREAMs; TTGR01399; FILM.

SEQUENCE 733 AA; 80883 MW; 6EB817AB4268128B CRC64;
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0972Q4,
001-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase I, G subunit.
           01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Flagellar biosynthesis/regulation protein FlbA.
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Helicobacteraceae, Helicobacter.
NCBI_TaxID=32025;
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
VCBI_TaxID=173;
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GEZ., From Y., Pox J.G.;

Med Z., Freng Y., Pox J.G.;

"Helicobacter hapaticus genome: construction of an ordered cosmid

library and sequence analysis of the selected genomic regions.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF356691; AAL16680.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:009306; P:protein secretion; IEA.

InterPro; IPR01712; Bant FHIPEP.

Pfam: PF00771; FHIPEP; 1.
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                  Query Match
59.2%; Score 42; DB 16; Length 905;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 1; Indels
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Pred. No. 13;
2; Mismatches 4; Indels
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EMBL, AE011216, AAN47483.1; -
Hypothetical protein, Complete proteome.
SEQUENCE 231 AA, 26471 MM, 15024FD58DE290D9 CRC64;
905 AA; 98333 MW; 53716244354E40DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 AA; 10789 MW; BED4A41B153EBA53 CRC64;
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01-MMR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Flagellar biosynthesis protein (Fragment).
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

RECALLIVER, and Skeletal muscle;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Expleton M., Soares M.B., Bonaldo M.F., Carainot P., Haieh F.,

RA Rapleton M., Soares M.B., Bonaldo M.F., Carainot P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McWany D.M., Sodergren E.J., Lu X., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully K.W.

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully K.R.,

RA Whiting M., Madan A., Young A.C., ShevChenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

RY Froc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002). Brown J.R., Shockley P., Behrens P.Q.; (In) Bing D.H. (eds.); The chemistry and physiology of the human plasma proteins, pp.23-40, Pergamon Press, New York (1979). TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
"Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. ņ SEQUENCE FROM N.A., AND VARIANT GLY-121.

\*\*\*RDINIFE-82105994; PubMed=6275391;

\*\*\*Dugaiczyk A., Law S.W. Wender S.W. C.E.;

\*\*\*\*Nucleotide sequence and the encoded amino acids of human serum "Nucleotide sequence and the encoded amino acids of human serum "Nucleotide sequence" SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675). Najarian R.C., Seeburg P.H., Wion K.L.; "The sequence of human serum albumin cDNA and its expression TISSUE=Liver; Yang S.Y., Qi Z.W., Yuan Z.Y.; Zhang R.A., Qi Z.W., Yuan Z.Y.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. SEQUENCE OF 25-609.
MEDLINE-76187907; PubMed=1225573;
Meloun B., Moravek L., Kostka V.;
"Complete amino acid sequence of human serum albumin.";
FEBS Lett. 58:134-137(1975). SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378. Huang M.C., Wu H.T., "The cDNA sequences of human serum albumin."; Submitted (40G-2002) to the EMBL/GenBark/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982) Nucleic Acids Res. 9:6103-6114(1981). SEQUENCE OF 1-455 FROM N.A. TISSUE-Liver; SEQUENCE OF 25-609 SEQUENCE FROM N.A. albumin mRNA." 

Menaya J., Parrilla R., Ayuso M.S.; Submitted (WAR-1995) to the EMBL/GenBank/DDBJ databases.

SEQUENCE OF 1-26 FROM N.A. MEDLINE=86140099; PubMed=2419329;

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NARIANTS TORINO LVS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
MEDLINE=91062352; PubMed=2247440;
Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
Markins S., Putnam F.W.;
"Muthtions in genetic variants of human serum albumin found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION OF VARIANT REDHILL.
MEDLINE=90115852; PubMed=2104980;
Bremans S.-O., Myles T., Peach R.J., Donaldson D., George P.M.;
Malbumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT CANTERBURY ASN-337.

MEDLINE=87157744; PubMed=3828358;

Brennan S.O., Herbert P.;

"Albumin Canterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin.";

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Urano Y., Watanabe K., Sakai M., Tamaoki T.;
"The human albumin gene. Characterization of the 5' and 3' flanking regions and the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
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Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAETANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
MEDLINE-90115905; PubMed-2404284;
Arai K., Madlason J., Shimuzu A., Putnam F.W.;
"Point substitutions in albumin genetic variants from Asia.";
Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
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Biochem. J. 171:453-459(1978).
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MEDLINE=88068523; PubMed=347977;
Takshashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M., Satoh C., Neel J.V., Neel J.V., "Mel J.V." Neel J.V." "Amino acid substitutions in inherited albumin variants from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
MEDLINE-89345611; PubMed=2762316;
Arai K., Madison J., Huse K., Ishioka N., Satoh C., Fujita l
Neel J.V., Sakurabayashi I., Putnam F.W.;
"Point substitutions in Japanese alloalbumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
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Saber M.A. Stockbauer P., Moravek L., Meloun B.;
Saber M.A. of Stockbauer P., Moravek L., Meloun B.;
Disulfide bonds in human serum albumin.";
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Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987)
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Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BILIRUBIN-BINDING SITE.
MEDLINE=78186630; PubMed=656055;
                                                                                 [12]
SEQUENCE OF 222-229.
MEDLINE-76257808; PubMed=955075;
                                                                                                                                                                                                                                     SEQUENCE OF 25-44 AND 480-499.
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Query Match
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.

STRAIN=MGS IDR; TISSUE=Liver;

KNEDIIRE=pain663; PubMed=455485,

XY Yoshida K., Seto-Ohshima A., Sinohara H.;

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin, the main protein of plasma, has a good

"I FUNCTION: Serum albumin, the main protein of plasma, has a good

"I FUNCTION: Serum albumin, the main protein of plasma, has a good

"I FUNCTION: Serum albumin, the main protein of plasma, has a good

"I FUNCTION: Serum albumin, the main protein of plasma, has a good

"I FUNCTION: Serum albumin of the regulation

"I SUMILARITY: Belongs to the ALB/AFP/VDB family.

"I SIMILARITY: Contains 3 albumin domains.
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Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.;
"Two alloalbumins with identical electrophoretic mobility are produced
                                                                                                                                                                                                                                                                                                                                               serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                 Variants IOWA CITY-2 VAL-25, IOWA CITY-1 VAL-389; KOWAGOME-3 HIS-23; KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.
MEDLINE=92052189; PubMed=1946412; Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsuda Y.-I., Amaki I., Putnam F.W.; "Genetic variants of serum albumin in Americans and Japanese."; Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
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Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                                                                                                   VARIANT CASEBROOK ASN-518.
MEDLINE=91316157; PubMed=1859851;
Peach R.J., Brennan S.O.; Structural characterization of a glycoprotein variant of human albumin: albumin Casebrook (494 Asp-->Asn).";
Biochim. Biophys. Acta 1097:49-54(1991).
                                                             MEDLINE=91296740, PubMed=2068071;
Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
Minchiotti L., Putnam R.W.;
"A donor splice mutation and a single-base deletion produce two
carboxyl-terminal variants of human serum albumin.";
Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels
        Italy.";
Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALBU MERUN STANDARD; PRT; 609 AA. 035030; 15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
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                                                    VARIANT VENEZIA
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified articement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  REMEN, ABOOGLOT, BAA21765.1; --
PIRE, JC5838; JC5838.
RISSP, PO2768; IE78.
RISSP, PO2768; IE78.
REMEN, PRO0273; TEANSONIC PICOL; 3.
REMAN, PRO0273; TEANSONIC PICOL; 3.
REMAN, PRO0273; TEANSONIC PICOL; 3.
REMAN, SMOOLOJ; ALBUMIN; 1.
REMAN, SMOOLOJ; ALBUMIN; 3.
REAL-binding; Lipid-binding; Repeat; Signal; Copper.
REAL-binding; Lipid-binding; Repeat; Signal; Copper.
REAL 1 1 18 BY SIMILARITY.
REAL 2 609 ALBUMIN; 1.
REAL 2 609 ALBUMIN; 1.
REAL 2 609 ALBUMIN; 1.
REAL 2 8 28 ALBUMIN; 1.
REAL 2 8 28 COPPER.
REAL 2 8 28 SIMILARITY.
DISULPID 193 202 BY SIMILARITY.
DISULPID 202 271 BY SIMILARITY.
DISULPID 303 304 BY SIMILARITY.
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DISULPID 466 473 BY SIMILARITY.
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DISULPID 509 500 BY SIMILARITY.
DISULPID 500 500 BY SIMILARITY.
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272 HGDLLE 277

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completed: April 19, 2004, 11:52:50 me : 0.437673 secs

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5 Q95VB7
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                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 HGDLLE 6
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q7tqm6 meriones un	Q8wmj3 macaca mula	Q8wmh8 macaca mula	019044 oryctolagus	Q9i612 pseudomonas	Q847i2 pseudomonas	Q9rbv8 pseudomonas	Q8n4i7 homo sapien	Q8c7z5 mus musculu	Q86yg0 homo sapien	Q7u5e3 synechococc	Q98975 oncorhynchu	Q9kyc4 streptomyce	Q8kq21 pseudomonas	Q88d23 pseudomonas	Q8c7c7 mus musculu
	07TQM6	28WMJ3	SWMHS	19044	Q916L2	712	BV8	Q8N4I7	08C7Z5	05864	USE3	8975	Q9KYC4	9KQ21	288D23	28C7C7
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RN SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

CATAIN-Japanese White;

A GACURACE T. Uchiyama Y., Kurachi Y.,

RA GACURACE, Uchiyama Y., Kurachi Y.,

RA GACURACE, Uchiyama Y., Kurachi Y.,

RA GACURACE, Their regulation of an inwardly rectifying potassium channel, KAB-2/Kir4.1, on mammalian retinal Muller cell

RT Detassium channel, KAB-2/Kir4.1, on mammalian retinal Muller cell

RT Submitted (ULL-1997) to the EMBL/GenBank/DDBU databases.

BR GO, GO:0005243; BAA21549.1; ---

CAG:0016020; Cimembrane; IEA.

CAG:0016020; Fineward rectifier potassium channel activity; IEA.

CAG:0016020; Fineward rectifier potassium channel activity; IEA.

CAG:0016020; Fineward rectifier potassium channel activity; IEA.

CAG:0016021; Fineward rectifier potassium channel activity; IEA.

CAG:0016021; Fineward rectifier potassium channel activity; IEA.

CAG:0016021; Fineward rectifier potassium channel pore.

CAG:0016021; K-channel Dore.

CAG:00100031; K-channel Dore.

CAG:00100031; K-channel LR; 2.

RT NON TER

SEQÜENCE 211 AA; 23279 MW; 1BC61D158AD09E3D CRC64;
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=1.D., Mizoguchi S.D., Warrener P.,
Stover C.K., Pam X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Kir4.1 (Fragment).
Obyctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadacee; Pseudomonas. NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels
100.0%; Score 33; DB 6; Length 194; 100.0%; Pred. No. 45;
                                                 0; Indels
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PA0278.
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    Query Match
Best Local Similarity 100.
Matches 6; Conservative
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O1-MAR-2002 (TTENBIrel. 20, Last sequence update)

O1-MAR-2002 (TTENBIrel. 20, Last sequence update)

O1-MAR-2003 (TTENBIrel. 25, Last annotation update)

Protocadherin alpha II (Fragment).

Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Mammaila; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi;

Cercopithecinae; Macaca.
    01-MAR.2002 (TrEMBLrel. 20, Created)
01-MAR.2002 (TrEMBLrel. 20, Last sequence update)
01-COT-2003 (TrEMBLrel. 20, Last sequence update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
Protocadherin alpha 8 (Fragment).
Macaca mulatta (Rhesus macaque).
Enkaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae, Macaca.
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TISSUB-medial basal hypothalamus;
Mungenast A.E., Ojeda S.R.;
Mungenast A.E., Ojeda S.R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF424842; AA140256.1;
GO, GO:0016020; F:canebrane; IEA.
GO, GO:0005199; F:call adhesion molecule activity; IEA.
GO, GO:0007155; P:call adhesion, IEA.
GO, GO:0007155; P:call adhesion, IEA.
GO, GO:0007156; P:homophilic cell adhesion; IEA.
InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 33; DB 6; Length 129; 100.0%; Pred. No. 29; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   TISSUE-Medial basal hypothalamus;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF424824; AAL40240.1;
RGJ; GO:0005509; F:calcium ion binding; IEA.
RGJ; GO:0007156; F:calcium ion binding; IEA.
RPRINTS; PR002012; Cadherin.
RPRINTS; PR002012; CADHERIN.
RPROSITE; PS50226; CADHERIN.1; 1.
RPROSITE; PS502268; CADHERIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERMYS, PRO0028, cadherin, 1.

PRINTS, PRO0205, CADHERIN.
SMART, SM00112, CA, Z.

PROSTIE; PS00228, CADHERIN 1; 1.

PROSTIE; PS50268, CADHERIN 2; 2.

Calcium, Calcium-binding; Cell adhesion, Glycoprotein.

NON TER 1 1 1

NON TER 194 AA; 21808 MW; FB93F0B6A454D747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AA; 14483 MW; 2D345B31CB6D0582 CRC64;
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Best Loc Matches

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RESULT 3

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100.0%; Score 33; DB 2; Length 283; 100.0%; Pred. No. 67; ive 0; Mismatches 0; Indels
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MEDLINE=20011227; PubMed=10543801;
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Best Local Similarity
Matches 6; Conserv
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Q8C7Z5;
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O8N417;
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  Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bedteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonas Norl TaxID=101164;
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                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 16; Length 250; 100.0%; Pred. No. 58; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zylstra G.J., Dennis J.J.;

"Complete nucleotide sequence of the NAH plasmid pDTG1 from morplete nucleotide sequences beaudomonas putida NCIB 9816-4 ";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF491307, AAG64290.1, -.

EMBL, AF491307, AAG64290.1, -.

InterPro; IPR006015; Usp.

PRINTS; PRO1438; UNYRSLGYRESS.

Hypotherical protein; Plasmid.

SEQUENCE 251 AA; 27295 MW; P9F4CEEFBB187FA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 33; DB 2; Length 251; 100.0%; Pred. No. 59; cive 0; Mismatches 0; Indels
                                                                                        opportunistic pathogen.";
Nature 406:359-964(2000).
BMBL; AB6094; F83609.
INTERPOS, IPR002781; DUF81.
IPTOS, IPR01925, DUF81.
HYDOCIDETIC protein; Complete proteome.
SEQUENCE 250 AA; 25773 MW; C5F5D079CEDA48A1 CRC64;
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Last annotation update)
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STRAIN=R9; TRANSPOSON=Tn1404;
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01-JUN-2003 (TERBLEL: 24, C;
01-JUN-2003 (TERBLEL: 24, L;
01-OCT-2003 (TERBLEL: 25, L;
Hypotherical protein.
Pseudomonas putida.
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Pseudomonadaceae; Pseudomonas
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Best Local Similarity luv...
6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  191 HGDLLE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NCIB 9816-4;
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Straubberg R;
Straubserg R;
Straubserg R;
Straubserg R;
Straubserg R;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034036; AAH34036.1; IBA.
GQ; GQ:0016020; Cimembrane; IBA.
GQ; GQ:0005247; F:inward rectifier potassium channel activity; IEA.
GQ; GQ:0005267; F:potassium channel activity; IEA.
GQ; GQ:0006813; F:potassium ion transport; IEA.
InterPro; IPR001632; K+channel_IR.
InterPro; IPR001622; K+channel_Dore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamailia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
01-JUM-2003 (TrEMBLrel. 24, Last annotation update)
Potossium inwardly-rectifying channel, subfamily J, member 10.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Local Similarity 100.0%; Pred. No. 90;
les 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01007; IRK; 1.
PRINTS; PR01320; KIRCHANNEL.
ProDom; PD001103; K+channel IR; 2.
SEQUENCE 379 AA; 42550 MM; 9D08E156BECEE4CDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Potassium inwardly-rectifying channel.
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à g us-09-832-929-18\_copy\_247\_252.rspt

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Authority 2. Miyashita T., Kubokawa K.;

Kubo Y., Miyashita T., Kubokawa K.;

The weakly inward rectifying potassium channel of the salmon brain:

The distance of the second transmembrane domain is insufficient for clutamate 179 in the second transmembrane domain is insufficient for the strong rectification.";

The distance of the second transmembrane domain is insufficient for clutamate 179. In the second transmembrane domain is insufficient for the second transmembrane in the second transmembrane domain channel activity; IEA.

The domain of the second transmembrane activity; IEA.

The domain domainel activity; IEA.

The second transmembrane domain domainel activity; IEA.

The second transmembrane domain domainel activity; IEA.

The second transmembrane domainel activity; IEA.
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MEDLINE=22825697. PubMed=12917641;

Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser D., Chain I Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,

Dufreene A., Partensky F., Webb E.A., Warerbury J.;

"The genome of a morile marine Synechococcus.";

Nature 424:1037-1042(2003).

Barbl: MSS5693, CAE08279.11 -

Hydrolase; Complete proteome.

SEQUENCE 419 AA, 44483 MW; DFF0860393F3298B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus masou (Cherry salmon) (Masu salmon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
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100.0%; Score 33; DB 13; Length 423;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                       Symechococcus sp. (atrain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Symechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, Greated)
01-OCT--2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Meakly inward rectifying potassium channel.
SWIRK.
                   01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative dihydroorotase (EC 3.5.2.3)
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PRINTS; PR01320; KIRCHANNEL.
ProDom; PD001103; K+channel_IR; 2.
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Matches 6; Conservative
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Q98975;
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Q98975
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RP SEQUENCE FROM N.A.

RX MEDLINE=22354683; PubMed=12466851;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOW Consortium,
RA THE RANTOW Consortium,
RA THE RIKEN Genome Exploration Research Group Phase I & II Team;
RATION Genome Exploration Research Group Phase I of II Team;
RATION Genome Exploration Research Group Phase I & II Team;
RATION GENOME Exploration Research Group Phase I & II Team;
RATION GENOME CONAS, "A CONTROL OF THE CONT
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01-JUN 2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to alpha-fetoprotein.
Homo sepiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Liver;
Straubberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041789; AAH41789.1;
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:00065015; C:extracellular space; IEA.
GO; GO:00065015; P:transport IEA.
RinterPro; IRR000264; Serum albumin.
Pfam; PP00273; transport DFC; 2.
RFRINTS; PR000815; Serum albumin; 1.
SPRINTS; PR000815; Serum albumin; 1.
SPRATI; SR00103; ALBUMIN; 2.
SRARI; SR001212; ALBUMIN; 2.
SEQUENCE 417 AA; 47360 MW; 16E764833EBF4E8D CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Created)
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Best Local Similarity 100.v
Local 6; Conservative
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Q7USE3 RESULT 11 Q7U5E3

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410 HGDLLE 415

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529 AA

PRT;

PRELIMINARY;

Q9KYC4

RESULT 13 Q9KYC4

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Search completed: April 19, 2004, 12:00:07
Job time : 4.31579 secs
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                                                                                                                                                     Q88D23
                                                                                               RESULT 15
Q88D23
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Like Y. H., Kim T.-K., Shin H.-D., Lee J.-N., Seo M.-C.;

Like Y. H., Kim T.-K., Shin H.-D., Lee J.-N., Seo M.-C.;

Like Y. H., Kim T.-K., Shin H.-D., Lee J.-N., Seo M.-C.;

Like Y. H., Kim T.-K., Shin H.-D., Lee J.-N., Seo M.-C.;

Buttida KT240 and its utilization for medium chain length

polyhydroxyalkanoate production.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY113181; AAM63409.1; -..

EMBL; AY113181; AAM63409.1; -..

InterPro; IPR000560; HisĀc_phsphtse.

InterPro; IPR000560; HisĀc_phsphtse.

Fram; PF00561; abhydrolase; I.

PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.

SRQUENCE 560 AA; 62640 MW; C0A768C17569B4D3 CRC64;
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MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Promson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=160488;
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                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SC06906 OR SC1B2.12C.
Streptomyces coelicolor.
Streptomycis coelicolor.
Streptomycineae; Streptomycetaceae; Streptomyces.
NCB1_TAXID=1902;
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Nature 417:141-147(2002).
EMBL, AJ939129; CAB92568.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 529 Aa; 57433 MW; 87075B0602262E11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PHA synthase 2.
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Matches 6; Conservative
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MEDLINES-2423060, PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes
Brinkac L., Beanann M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White C., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Klewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                              Pseudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-908(2002).

EMBL; AE016792; AAN70571.1; -
TIGR; PP5005; -
TOGO GO:0003993; Fracid phosphatase activity; IEA.

InterPro; IPR000560; HisAc_phsphtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560 AA; 62722 MW; 4BF0D75DB5874868 CRC64;
                                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
560 AA
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
Complete proteome.
SEQUENCE 560 AA; 62722 MM.
                                                                                                                                        Poly(3-hydroxyalkanoate) polymerase 2
PHAC OR PP5005.
                                                         (TrEMBLrel. 24, Created)
PRT;
                                                                                                                                                                                                                                                                 Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
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PRELIMINARY;
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April 19, 2004, 11:24:29; Search time 3.52909 Seconds (without alignments) 480.375 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		do	Human API	Human KRP	Alzheimer	Liver res	Human alb		Peptide #			Human bon	Human bra	Human liv	Human pep	Peptide #	Peptide #	Peptide #	Protein #	Human bon	Human bra	Human liv	Human pep	Human pro	Human pol	abcEST en	Human pol
		Description	Abb52153	_	8	Abr75499	Aab12469	φ		N	ω	Aam74619	-4	Abg56405	4	Aam18788	œ	S.	Abb23147	-	Aam58521	Abg52734	Abg40810	Aam25284	Aa00010B	98	Aao04435
<b>70</b>		1																									
SUMMARIES		ΩI.	ABB52153	ABP61551	œ	ABR75499	AAB12469	a	ABB40958	AAM34732	ABB25068	AAM74619	AAM61818	ABG56405	ABG44448	AAM18788	ABB37889	AAM31296	ABB23147	AAM71019	AAM58521	ABG52734	ABG40810	AAM25284	AA000108	86	AA004435
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de		Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	00	100.0	
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Abg01238 Novel hum Aa002571 Human pol Bay83948 Yeast cod Aay25672 Dog aller Ad34920 Dog aller Ad33082 Novel hum Aar131082 Novel hum Aar14178 Human Ser Abp51353 Human MDD App61357 Human Kid Aab47972 Human KiR Aab47972 Human KIR Aab47973 Human Ser Aap90390 N-termina	ALIGNMENTS AA.	#	ie #1. gene therapy; vaccine; jisease-Associated Feature; AF; tein Isoform; AFI; tryptic digest; orm; ERFI; proteolysis.		AC, Kimmel LH, Parekh B Stiger TR, Sunderland P'	e in a mammal, by making two-dimensional e abundance correlates with disease, and feature in samples of healthy persons.  for the screening, diagnosis and  The methods involve the detection of eatures (AFS) and Alzheimer's Disease- s) in cerebrospinal fluid, serum or and APIs is then normalised to an form (BRPI) in order to determine whether has a predisposition to, Alzheimer's
ABG01238 AA002571 AAX26326 AAX26326 AAX3082 AAU33082 AAP51353 AAP51353 AAP51353 AAP90387 AAP90389 AAP90389 AAP90399 AAP90399 AAP90399	ALIGN	  	Spic,		S UK LTD. erath HMAC, er BM, St: liams SA;	sease in the feature for the feature for feature f
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The relative abundance of the APs and APIs correlates with the of Alzheimer's Disease. The present sequence is a peptide from an API by proteolysis
                                                                                                                                                                                                                                                                                                                    Human; tryptic digest peptide; KRDI; kidney response; KR; nephroropic kidney response-associated protein isoform; gene therapy; antisense therapy; kidney function; tubular nephritis; renal failure; nephron cell metabolic pathway modulation; glomerular necrosis;
                                                                                                       Gaps
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                                                                            100.0%; Score 33; DB 4; Length 14; 100.0%; Pred. No. 5.5;
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                                                                                            red. No. 5.5
Mismatches
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                                                                                                                                                                                                                                                                                                Human KRPI tryptic digest peptide #46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 40; 168pp; English
                                                                                                                                                                                                                   ABP61551 standard; peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-2000; 2000US-0260392P
                                                                                                                                                                                                                                                                      (first entry)
                                                               Query Match
Best Local Similarity 100..
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kelly MD,
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                 severity or produced
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    Disease.
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DB 5; Length 14; 5.5;

Score 33; Pred. No.

100.0%; 100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods for screening or diagnosing Alzheimer's disease (AD) to determine the stage or severity of AD in a subject, to identify subject at risk of developing AD, or to monitor the effect of therapy administered. The methods comprise analyzing a test sample of body fluid by 2-dimensional electrophoresis to generate a 2-dimensional array of AD-associated features (AFs). The method alternatively comprises quantitatively detecting in a sample of body fluid from the subject, one or more AD-associated APIs; (APIs)
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Stiger TR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Noctropic, Neuroprotective, Alzheimer's disease, API; human, Alzheimer's Disease-associated protein isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC, Kimmel LH, Parekh
Snyder PJ, Soares HD,
WF, Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 33; DB 6; Length 14; 100.0%; Pred. No. 5.5; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durham LK, Friedman DL, Herath HWAC,
Potter DM, Rohlff C, Silber BM, Snyde
Sunderland PT, Townsend RR, White WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER PROD INC.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR75499 standard; peptide; 14 AA.
                                                                                                                                                                                                           ABR58983 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2, Page 43; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002; 2002WO-US031642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2001; 2001US-0326708P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-371957/35.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fluid from the suk
ABR58710-ABR59184)
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Amacher DE,

38-MAY-2003

Synthetic.

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The present invention describes hybridoma cells used for preparing an immunoglobulin G (1gG) monoclonal antibody capable of rapid reaction with human albumin. The hybridoma cells are prepared by fusion of mammal myeloma cells and spleen cells immunised with human serum albumin, and producing 1gG monoclonal antibody which rapidly react with human albumin. The monoclonal antibodies can be used in the diagnosis of diabetic nephropathy. The present sequence repersents a human albumin epitope peptide sequence which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                Hybridoma cells for preparation of IgG monoclonal antibody capable of rapid reaction with human albumin for diagnosis of diabetic nephropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Processing of protein or peptide samples used in mass spectrometer
                Monoclonal antibody, hybridoma cell, immunoglobulin, IgG, fusion;
human albumin; diabetic nephropathy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine serum albumin peptide, analysed by mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serum albumin; cattle; mass spectrometry; proteomics.
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100.0%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR62926 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                      (TOYW ) TOYOTA CHUO KENKYUSHO KK. (AISE ) AISIN SEIKI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example, Fig 1; 11pp; Japanese.
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                                                                                                                                                                                                                   98JP-00311677.
                                                                                                                                                                                                                                                              98JP-00311677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2001, 2001US-0343859P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MDSP-) MDS PROTEOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-433935/38.
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Best Local Similarity
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                                                                                                                               JP2000139460-A
                                                                                       Homo sapiens.
                                                                                                                                                                                                                      02-NOV-1998;
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                                                                                                                                                                         23-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duewel H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR62926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method (M1) for screening or diagnosing a liver response in a subject, determining the stage or severity of a liver response in a subject, dentifying a subject at tisk of developing liver response, or monitoring the effect of therapy administered to a subject having liver response, involving detecting liver response.

CC associated protein isoforms (LRRIS) (see the peptides given in ABR75395 cortening or diagnosing a liver response in a subject, or monitoring the effect of a drug or therapy administered to a subject, involves consecutive nucleotides complementary to a nucleotide sequence encoding an LPRI with RNA obtained from a biological sample from the subject or with only oppide from the RNA, where the contacting occurs under conditions that permit hybridisation of the probe to the nucleotide sequence, and comparing the hybridisation, if any, between the probe and the nucleotide sequence, and comparing the hybridisation, if any, detected in the above step, with the hybridisation detected in a control sample, or with a previously determined reference range. MI is useful for screening or diagnosing a liver response in a subject, identifying a subject at risk of developing liver response in a subject, identifying a subject at risk of developing liver response and monitoring the effect of therapy administered to a subject having liver response
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                       Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:84
                                                        Biomarker, liver response, liver response-associated protein isoform, LRPI, liver response-associated feature, LRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening, diagnosing, staging or identifying subject at risk of developing, liver response, or monitoring effect of therapy on liver response, by detecting Liver Response-Associated Protein Isoforms in
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                                                                                                                                                                                                                                                                                                                                                                                                                       Fasulo LM, Herath HMAC, Holt GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB
Pred. No. 5.5;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER PROD INC.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB12469 standard; peptide; 18 AA.
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100.0%; Pre
tive 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 55; 256pp; English
                                                                                                                                                                                                                                                                   31-OCT-2002; 2002WO-US034847.
                                                                                                                                                                                                                                                                                                           31-OCT-2001; 2001US-0335964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                         WO2003038444-A2.
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25-OCT-2000

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RESULT 5 AAB12469

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Length 18; 0; Indels

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The present sequence is a peptide fragment of bovine serum albumin (BSA). The peptide was produced by chemical reduction of cysteine residues with dithiothreitol, alkylation with iodoacetamide and enzymatic digestion with trypsin. This is an example of the protein processing method of the invention, which was designed for use in proteomics analysis by mass spectrometry (MS). The general method involves: reversibly immobilising protein or peptide samples onto a solid support, e.g. a cation-exchange resin, subjecting the immobilised protein or peptide to solid phase-based chemical and/or enzymatic modifications; eluting the resulting peptide or peptides in near-quantitative yields in a format suitable for identification by routine MS technologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe.
analysis, by reversibly immobilizing samples onto solid support, transforming to solid-phase chemical unit, eluting and recovering fragments from support.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #8464 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 33; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                           Example 4; Page 46; 66pp; English
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26-MAY-2000; 2000US-0207456P.
30-MUS-2000; 2000US-00608468.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023639P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483447/52
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                                                                                                                                                                                                                                                                                                                                       Sequence 21 AA;
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gene expression in human placenta.
present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                         Peptide #8769 encoded by probe for measuring placental gene expression.
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                              0; Indels
                                                                                                    4; Length
                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 35001; 654pp; English
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                                                                                                                                                                                                                                                           AAM34732 standard; protein; 58 AA.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                  17-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53
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                                                                           Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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expressed probe encoded protein SEQ ID NO: 34925.

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                            Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO 34925; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UIN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488900/53.
                     Human bone marrow
                                                                                                                                                                                           WO200157276-A2.
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                              39-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM61818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_sequences
                                                                                                                                                                                                                        Protein #7067 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                   Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Score 33; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; SEQ ID NO 26838; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                            ABB25068 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312F.

30-UNN-2000; 2000US-0207456F.

30-UNS-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

27-SEP-2000; 2000US-023468PP.

27-SEP-2000; 2000US-023468PP.

04-OCT-2000; 2000US-023459P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US000666
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                           23-JAN-2002
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                                                                                                                         ABB25068;
                             RESULT 9
ABB25068
ID ABB25068
XX
AC ABB2
XXX
DE Prot
XXX
XXX
Huma
XXX
Homo
XXX
PR Cong
XXX
PR 30-6
PR 21-6
PR 
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DR; Rank

Chen W,

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of such as lymphoma, lenkaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID NO: 33923.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                          ö
                                                                                                                                                                   Query Match
100.0%; Score 33; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            AAM61818 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                 34 HGDLLE 39
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                                                                                                                                                                                                                                                   1 HGDLLE
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                                                                                                                                          Sequence 58 AA;
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AAM74619 standard; protein; 58

(first entry)

06-NOV-2001

AAM74619

RESULT 10
AAM74619
ID AAM74
XX
AC AAM74
XX
DT 06-NO

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gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                            ABG44448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrania, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
brains.
                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                      Example 4; SEQ ID NO 33923; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                    100.0%; Score 33; DB 4; Length 58; 100.0%; Pred. No. 22; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                                                       Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human liver peptide, SEQ ID No 35053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank
                                                                                                                                                                                                                                                                                                                                                                             ABG56405 standard; peptide; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000US-0180312P.

30-UNY-2000; 2000US-0207456P.

30-AUG-2000; 2000US-00638468.

03-AUG-2000; 2000US-0033468P.

21-SEP-2000; 2000US-023468P.

27-SEP-2000; 2000US-023639P.

04-OCT-2000; 2000GB-00024263.
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    26-MAY-2000; 2000US-00608408.
30-UTV-2000; 2000US-00608408.
03-AUG-2000; 2000US-00542366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488898/53
                                                                                                         WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                             34 HGDLLE 39
                                                                                                                                                                                                                                                                                                          1 HGDLLE 6
                                                                                                                                                                                                                                                     Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification for complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis.

Involved in genetic liver diseases such as cirrhosis.

Involved with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at the printed specification fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human peptide encoded by genome-derived single exon probe SEQ ID 34113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicytosis; lumphangioleiomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cillary dysinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 33; DB
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches
Claim 27; SEQ ID NO 35053; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG44448 standard; peptide; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312F.
26-MX-2000; 2000US-0207456F.
30-UJN-2000; 2000US-00608450F.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687F.
27-SEP-2000; 2000US-0234687F.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1237 open reading frames derived from their 1261 probes. Also included are a microarray comprising the novel set of probes which publishes at high stringenty to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a call expressed in the human lung; measuring gene expression in a sample derived from human lung measuring (a) contacting the array with a call expressed in the human lung measuring (a) comprising (a) detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array identifying exons in a evaryatic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryore; and (b) detecting specific thy byridiatation of detectably labeled nucleic acids from entioned microarray, assigning exons to a single exon probe, having a fragment identical to the predicted exon probe in the above mentioned microarray; assigning exons to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene, a peptide comprising one probes/open reading frames (o) (RF). The probes are used for gene expression of the exons in a gene, a perficularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (IDD), interstitial lung disease (IDD), familial idiopathic pulmonary disease (IDD), interstitial lung cancer, chronic, surfaced pulmonary disease (IDD), interstitial lung probes are used for demined a disease, pulmonary disease (IDD), interstitial with pulmonary publication, but was obtained in e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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100.0%; Score 33; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels
measure gene expression in human lung samples.
                                                      Claim 27; SEQ ID NO 34113; 634pp; English.
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Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                 Peptide #5395 encoded by human foetal liver single exon probe.
                       ABB37889 standard; peptide; 85 AA.
                                                                                                                                                                                                                                                                           26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US000669
                                                                            04-FEB-2002 (first entry)
                                                                                                                                                                                   WO200157277-A2.
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                             09-AUG-2001
RESULT 15
ABB37889
                          Peptide #5222 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                            Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                       AAM18788 standard; protein; 85 AA.
                                                                                                                                                                                                                          (first entry)
                                                                                                    34 FGDLLE 39
                                                                                                                                                                                                                                                                                           cervical cancer
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                          12-OCT-2001
                                                                                                                                                                                                  AAM18788;
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AAM18788

ò g (MOLE-) MOLECULAR DYNAMICS INC

WO200157278-A2

X B X B X S X X X X B X B X B X X X X

09-AUG-2001

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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Heids cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Score 33; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 23614; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                       26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
2001WO-US000670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 HGDLLE 39
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    30-JAN-2001;
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NY WPI; 2001-483447/52.

XX WPI; 2001-483447/52.

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing proceed expression in human fetal liver.

XX Claim 27; SEQ ID NO 30524; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring considered exon nucleic acid probes may be used for predicting, measuring and claplaying gene expression in a sample derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe construction note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format construct in the printed specification, but was obtained in electronic format XX Sequence 85 AA;

Sequence 85 AA;
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O Sequence 85 AA;
Query Match
Best Local Similarity 100.0%; Score 33; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gape 0;

1 HGDLLE 6 |||||| 34 HGDLLE 39

8 8

Search completed: April 19, 2004, 11:51:19 Job time : 4.52909 secs

r B.

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April 19, 2004, 12:00:25; search time 2.52632 Seconds (without alignments) 654.724 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
| cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep./cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep./cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep.cgn2_6/ptodata/2/pubpaa/USIOC_PUBCOMB.pep.cgn2_6/ptodata/2/pubpaa/USIOC_PUBCOMB.pep.cgn2_6/ptodata/2/pubpaa/USIOC_PUBCOMB.pep./cgn2_6/ptodata/2/pubpaa/USIOC_PUBCOMB.pep./cgn2_6/ptodata/2/pubpaa/US6o_PUBCOMB.pep./cgn2_6/ptodata/2/pubpaa/US6o_PUBCOMB.pep.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1124875 seqs, 275673149 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-832-929-18_COPY_247_252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1 HGDLLE 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                Run on:
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					SUMMARIES		
		æ					
Result		Query					
No.	Score	Match	Match Length DB	DB	QH	Description	
П	33	100.0	44	o.	US-09-826-290-168	Sequence 168,	68, App
7	33	100.0	14	12	US-10-601-837-46	Sequence 46	_
m	33	100.0	14	15	US-10-285-394-84	Sequence 84	84, Appl
4	33	100.0	14	16	US-10-264-309-77	Sequence 77	
ເກ	33	100.0	58	σ	US-09-864-761-40366	Sequence 40366,	0366, A
φ	33	100.0	85	σ	US-09-864-761-38445	Sequence 38445,	8445, A
7	33	100.0		14	US-10-029-386-29821	Sequence 29821,	29821, A
<b>6</b> 0	33	100.0		14	US-10-029-386-29303	Sequence	29303, A
σ	33	100.0	111	14	US-10-029-386-29468	Sequence	29468, A
10	33	100.0	114	12	US-10-296-115-799	Sequence	799, App
11	33	100.0	114	14	US-10-029-386-29057	Sequence	29057, A
12	33	100.0	119	14	US-10-029-386-29571	Sequence	29571, A
13	33	100.0	126	14	US-10-029-386-29777	Sequence	29777, A
14	33	100.0	244	12	US-10-425-114-57360	Sequence	57360, A
15	33	100.0	379	15	US-10-353-690-88	Sequence	88, Appl

Sequence 2, Appli	Sequence 64794, A	Sequence 200, App	Sequence 2, Appli	e 445	e 26,	18,	a 18,	44	a 18,	18,	equence 18,	ij	equence 31,	34,	equence 5,	equence 5,	equence 1,	equence 2,	equence 1,	equence 2,	1,	equence 2,	L	equence 2,	equence 1,	'n	ij	equence 2	Sequence 7, Appli
-344-8	-10-425-114-	8-10-360-101-20	09-929-5	-09-932-613-4	-984-010-2	-09-833-041-1	-09-833-117-1	-09-932-322-4	-09-832-501-1	-09-833-118-1	19-833-245-1	-424-	10-425-	10-433-108-	10-153-064	10-15	10-319-263	10-319-	-414-46	10-414-46	10-413-83	10-413~8	10-413-832	10-413-83	-10-414-38	414-386	10-2	-10-462-262-	-98
15	12	15	σ	10	10	10	10	10	10	디	11	12	12	12	13	14	14	14	14	14	14	14	15	15	15	15	13	15	10
379	553	583	585	585	585	585	585	582	585	583	585	585	585	585	585	585	585	585	585	585	585	585	585	585	585	585	585	585	604
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
APPLICANT: Townsend, Robert Reid
APPLICANT: Townsend, Robert Reid
APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: White, Frost
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Alzheimer's Disease
TITLE OF INVENTION: Alzheimer's Disease
TITLE OF INVENTION: Alzheimer's Disease
FILE REPERENCE: 2572-1-010 NZ
CURRENT FILING DATE: 2001-04-30
CURRENT FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR FILING DATE: 2000-01-128
NUMBER OF SEQ ID NOS: 492
SOFTHARE: PSELSE for Windows Version 4.0
SEQ ID NO 168
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                               APPLICANT: Durham, L.Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
4.1;
                      Sequence 168, Application US/09826290 Patent No. US20020164668A1
                                                                                                                                                                                Kimmel, Lida H.
Parekh, Rajesh Bhikhu
Potter, David M.
Rohlff, Christian
Silber, B. Michael
Stider, Thomas K.
Sunderland, P. Trey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-168
                                                                        GENERAL INFORMATION:
-09-826-290-168
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Score 33; Pred. No. 4

100.08;

Query Match Best Local Similarity

Gaps

0

0; Indels

Mismatches

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6; Conservative

Matches

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HERERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David K.

APPLICANT: Rank, David K.

APPLICANT: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REPRENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-04

PRIOR PAPLICATION NUMBER: US 60/180,312

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR PELING DATE: 2000-09-05-6

PRIOR PELING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                Kidr APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLEY, RAJESTIAN
APPLICANT: SUNDER, PETTER J.
APPLICANT: WHITE, M. FROST R.
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION NUMBER: 60/326,708
PRIOR PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SEQ ID NO 77
LENGTH: 14
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Pred. No. 4.1:
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Patent No. US20020048763A1
                                            Application US/10264309
Io. US20040022794A1
                                                                             Publication NOTION GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KINMEL, LIDA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Best Local Similarity 100.
Matches 6; Conservative
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// ORGANISM: Homo sapiens
US-10-264-309-77
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                                                                                                                                                                                                                                                                       APPLICANT: Holt, Gordon D
APPLICANT: Kelly, Michael D
APPLICANT: Kelly, Michael D
APPLICANT: Kennedy, Sandra J
APPLICANT: Kennedy, Sandra J
APPLICANT: Moyese, Christopher
TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidr
TITLE OF INVENTION: Response
FILE OF INVENTION: Response
FILE SPERENCE: 2543-1-030
CURRENT APPLICATION NUMBER: US/10/601,837
PRIOR APPLICATION NUMBER: PCT/GB01/05777
PRIOR FILING DATE: 2001-12-24
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 272
SEQ TWARE: atentin version 3.1
SEQ ID NO 46

LENGTH: 14
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; Sequence 84, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INPORMATION:
APPLICANT: ARACHER, DAVID E.
APPLICANT: HEARTH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
APPLICANT: HEARTH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
APPLICANT: HOLT, GORDON DUANE
TILLE REFERENCE: POA-003.01
CURRENT APPLICATION NUMBER: US/10/285,394
CURRENT APPLICATION NUMBER: 000-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR PLING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SEQ ID NO 84
; LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; DB 12; Length 14; larity 100.0%; Pred. No. 4.1; Conservative 0; Mismatches n. Tall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Ratus No. US20040053309Alvegicus
                                                                                                                                                                                      Sequence 46, Application US/10601837
Publication No. US20040053309A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Homo sapiens US-10-285-394-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
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                                               4 HGDLLE 9
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1 HGDLLE 6
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US-10-029-386-29821
US-10-029-386-29821
US-10-029-386-29821
Sequence 29821, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharton G.
APPLICANT: Pank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: ADOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN STRAIL LIVER, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN BRAIL, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BRAIL, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEALA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEALA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.2

OTHER INFORMATION: STREASSED IN BORE MARROW, SIGNAL = 1.2

OTHER INFORMATION: STREASSED IN BORE MARROW, SIGNAL = 1.2

OTHER INFORMATION: STREASSED IN BORE MARROW, SIGNAL = 1.2

OTHER INFORMATION: STREASSED IN BORE MARROW, SIGNAL = 1.2

OTHER INFORMATION: STREASSED IN BORE MARROW, SIGNAL = 1.2

OTHER INFORMATION: STREASSED IN BORE MARROW, SIGNAL = 1.2
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PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
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ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Penn. Sharron G.

APPLICANT: Hancel, David R.

APPLICANT: Hancel, David R.

APPLICANT: Hancel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL.

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PAPLICATION NUMBER: US 69/632,366

PRIOR PILING DATE: 2000-06-03

PRIOR FILING DATE: 2000-06-03

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-04
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OTHER INFORMATION: MAP TO ACO08468.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: SET HUMAN HIT: A1969295.1, EVALUE 2.00e-25
US-09-864-761-40366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 33; DB 9; Length 58; 100.0%; Pred. No. 18;
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     PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION UNMER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PRIOR DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 HGDLLE 39
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US-09-864-761-38445
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Sequence 29057, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hansel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 799, Application US/10296115
; Sequence 799, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT HYPERION:
; TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
; TILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT PILING DATE: 2002-11-18
; PRIOR PILING DATE: 2000-01-21
; PRIOR FILING DATE: 2000-01-21
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; LANGTH: 114
TYPE: RRT
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FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(114)

OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3

US-10-296-115-799
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Similarity 100.0%; Score 33; DB 14; Length 111;
6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                 TYPE: PRT
ORGANISM: HOme sapiens
PEATURE:
OTHER INFORMATION: MAP TO CHR5.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66
OTHER INFORMATION: SWISSPROT HIT: Q9Y5H8, EVALUE 2.00e-57
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                           NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29468
LENGTH: 111
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CURRENT FILING DATE: 2001-12-20
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Best Local Similarity 100.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserva
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US-10-296-115-799
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Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HORSING GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INTELL OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILIOR DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 29303
LENGTH: 111
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APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: BXDRESSION ANALYSIS TWO
FILE DE INVENTION: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 33; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                  OTHER INFORMATION: MAP TO CHRS.1
OTHER INFORMATION: BYPRESSED IN ADULT LIVER, SIGNAL = 0.46
OTHER INFORMATION: BYPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: BYPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: BYPRESSED IN HELA, SIGNAL = 0.94
OTHER INFORMATION: BYPRESSED IN BRAIN, SIGNAL = 0.94
OTHER INFORMATION: BYPRESSED IN BONE MARROW, SIGNAL = 0.99
OTHER INFORMATION: BYPRESSED IN HEART, SIGNAL = 0.99
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.49

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.41

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.47

OTHER INFORMATION: SWISSPROT HIT: Q9UN75, EVALUE 1.00e-58
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ORGANISM: Homo sapiens
                           TYPE: PRT
ORGANISM: Homo sapiens
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US-10-029-386-29468
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US-10-029-386-29303
LENGTH: 99
                                                                                   FEATURE:
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US-10-45-114-57360
Sequence 57360, Application US/10425114
Sequence 57360, Application US/10425114
Sequence 57360, Application US/10425114
Sequence 57360, Sequence 57360, Sequence 57360
Publication No. US20040034888A1
GENERAL INFORMATION.
APPLICANT: Edou. Yihua
APPLICANT: Avair, David K.
APPLICANT: Tabaska, Jack E.
APPLICANT: Applicant Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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0
CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 2977

FIRML: 126

TYPE PRT

ORGANISM: Homo sapiens
FRAUTHS:
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER; SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: SERRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: SERRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: SERRESSED IN ADULT LIVER, SIGNAL = 1.1

US-10-029-386-29777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 14; Length 126; Pred. No. 39; 0; Mismatches 0; Indels
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US-10-425-114-57360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Miyoung
APPLICANT: Galvin, Katherine M.
APPLICANT: Healy, Aileen
APPLICANT: Accon, Susan L.
APPLICANT: Donoghue, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 HGDLLE 236
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ORGANISM: Zea mays
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Sequence 29571, Application US/10029386
Sequence 29571, Application US/20030194704A1
Sequence 29571, Application US/20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILLING DAFE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOUTHWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29571
LENGTH: 119
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 33; DB 14; Length 119; 100.0%; Pred. No. 37;
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.86

OTHER INFORMATION: SMISSPROT HIT: Q9YSI2, EVALUE 1.00e-58

US-10-029-386-29571
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COTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1

CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

COTHER INFORMATION: EXPRESSED IN UNG, SIGNAL = 0.75

COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.75

COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.78

COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

COTHER INFORMATION: SYMESSED IN ADULT LIVER, SIGNAL = 1.1

COTHER INFORMATION: SWISSPROT HIT: Q99511, EVALUE 6.00e-60
                      SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 29057
LENGTH: 114
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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US-10-029-386-29777
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APPLICANT: Secondin, Jacquelin APPLICANT: Percolin, Jacquelin APPLICANT: Percolin, Jacquelin APPLICANT: Recolin, Jacquelin APPLICANT: Recolin, Jacquelin APPLICANT: Recolin, Jacquelin APPLICANT: Rotting May Amelie TITLE OF INVENTIONS: Cardiovaccular disease using 1682, 51247, 2402, 7147, 11 TITLE OF INVENTIONS: 2910, 4375, 60991, 1371, 7077, 33207, 1419, 1835, 1826, 1810, 1815, 1810, 2856, 3234, 3448, 4484, 5827, 2402, 2157, 1711E OF INVENTION: 10932, 18610, 1857, 4448, 2448, 64634, 8431, 2825, 2815, 1711E OF INVENTION: 10932, 18610, 1857, 1759, 5686, 44848, 52135, 12268, 2917, 1711E OF INVENTION: 10932, 18610, 1852, 2868, 4488, 2484, 64634, 8431, 2831, 2831, 7711E OF INVENTION: 10932, 18610, 1852, 2917, 59590, 18992, 2094, 2252, 34711E OF INVENTION: 9792, 13840, 1452 or 6585 molecules 972, 1208, 2917, 59590, 18992, 2094, 2252, 34711E OF INVENTION: 9792, 13840, 1452 or 6585 molecules 972, 1208, 2917, 59590, 18992, 2094, 2252, 34711E OF INVENTION: 9792, 13840, 1452 or 6585 molecules 972, 2094, 2252, 34711E OF INVENTION: 9792, 13840, 1452 or 6585 molecules 972, 2094, 2252, 34711E OF INVENTION: 9792, 13840, 1452 or 6585 molecules 972, 2094, 2252, 34711E OF INVENTION: 9702, 13840, 1452 or 6585 molecules 972, 2094, 2252, 34711E OF INVENTION NUMBER: 60/386, 880 or 9720 or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HGDLLE 6
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Search completed: April 19, 2004, 12:54:58 Job time : 2.52632 secs

93 HGDLLE 98

1104, App 1127, App 1125, App 1125, App 127, App 101, App 116, App

Sequence 12:
Sequence 12:
Sequence 12:
Sequence 12:
Sequence 20:
Sequence 10:
Sequence 10:
Sequence 16:
Sequence 16:
Sequence 16:
Sequence 16:
Sequence 16:
Sequence 5:
Sequence 6:

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US-08-408-196A-7

US-08-408-196A-7

US-08-408-196A-7

US-08-408-196A-7

Detert No. 5705094

GENERAL INFORMATION:

GENERAL OF INFORMATION:

GENERAL MASHALL SPACE FLIGHT CENTER

STATE:

ADDRESSED:

ADDRESSED:

ADDRESSED:

GONDATER:

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Best Local Similarity 100.0%; Score 47; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels
US-10-153-064-104
US-10-153-064-127
US-10-153-064-125
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US-08-94-196A-4
US-08-94-196A-6
US-08-94-196A-6
US-08-94-196A-6
US-08-134-613-1
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     RESULT 1
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Sequence 14, Appli
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Sequence 110, Appli
Sequence 130, Appli
                                                                                                                             April 19, 2004, 11:40:29; Search time 1.3795 Seconds (without alignments) 336.813 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*

1: /cgn2_6/ptodaca/2/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodaca/2/iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-153-799-14
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US-08-9448-196A-3
US-08-94-176-1
US-08-702-572-2
US-10-153-064-5
US-08-937-956A-2
US-08-937-956A-2
US-09-976-96
US-09-976-96
US-09-984-186-2
US-09-984-186-2
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US-10-153-064-96
US-10-153-064-133
US-10-153-064-95
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                                                                                                                                                                                                                                                                                                                              389414 seqs, 51625971 residues
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                                                                                                                                                                                                 US-09-832-929-18_COPY_92_100
47
1 AKOEPERNE 9
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB &
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US-08-448-196A-3

JEGGUARDCA 1, APRILICANT 108-196A-196A

PATECRY NO. 5780584

PATECRY NO. 5780584

PATECRY NO. 5780584

PATECRY NO. 5780584

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN PRAGMENTS

TITLE OF INVENTION: CONTAINING SPECIFIC SINDING REGIONS OF SERUM ALBUMIN OR TITLE OF INVENTION: RELATED PROTEINS

TORRESPONDENCES: DASA

STRIE: ALABAMA

CONNETRY: HINTSVILLE

STRIE: ALABAMA

CONNETRY: BE FLORDY disk

CONFUTER: INP COMPANDALDS

SOFTWARE: Patentin Release #1.0, Version #1.30

CLASSIPICATION DATA:

APPLICATION NUMBER: US/08/448,196A

FILING DATE: 23-MAY-1995

CLASSIFATION: SOBERT I. B, 757

REFERENCE/DOCKET NUMBER: LB, 757

REFERENCE/DOCKET NUMBER: LB, 757

REFERENCE/DOCKET NUMBER: LB, 757

REFERENCE/DOCKET NUMBER: LB, 757

TELEPHONE: 205-544-0224

INFORMATION FOR SEG ID NO. 3

SEQUENCE THRACTERISTICS:

LENGTH: BEST STRIES

LENGTH: SSS amino acid

TYPE: Amino a
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Batent No. 5948609

GENERAL INFORMATION

APPLICANT: HO, JOSEPH X

APPLICANT: HO, JOSEPH X

APPLICANT: HO, JOSEPH X

APPLICANT: HO, JOSEPH X

APPLICANT: HO, TECNIAN

TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT

TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT

TITLE OF INVENTION: OXYGEN-TRANSPORTING EXPANDER

FILE REFERENCE: 08/984,176

CURRENT APPLICATION NUMBER: US/08/984,176

CURRENT FILING DATE: 1997-12-03

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FRAGMENT TYPE: N-terminal US-08-448-196A-3
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100.0%; Score 47; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.3%;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-08-153-799-14
US-08-153-799-14
US-08-153-799-14
US-08-153-799-14
US-08-153-799-14
US-08-153-799-14
Sequence 14, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
STREET: 100 Mountain Avenue
STREET: 100 Mountain Avenue
COUNTRY: USA
ZIP: 07974 Will
STATE: New Jersey
COUNTRY: USA
ZIP: 07974 Will
STATE: DADALE FORM:
MEDILUM TYPE: LibM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: IBM PC COMPATE:
APPLICATION NUMBER: US/08/153,799
FILING DATE: 29-ARR-1990
PRIOR APPLICATION NUMBER: OF MARR 1992
PRIOR APPLICATION NUMBER: BCT/GB90/00650
FILING DATE: 29-ARR-1990
PRIOR APPLICATION NUMBER: BCT/GB90/00650
FILING DATE: 29-CCT-1991
ATTORNEY APPLICATION NUMBER: 24864
REGISTRATION NUMBER: 24864
REGISTRATION NUMBER: 24864
REGISTRATION NUMBER: 2400
TELERPHONE: (908) 655 2400
TELERPHONE: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
   92 AKQEPERNE 100
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Gaps
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GENERAL INFORMATION:
APPLICANT: Sonnenschein, Carlos
APPLICANT: Sonnenschein, Carlos
APPLICANT: Sonnenschein, Carlos
APPLICANT: Sonnenschein, Carlos
TITLE OF INVENTON: Inhibiting Proliferation of Cancer Cells
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Madlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDPM FC compatible
OPERATING SYSTEM: DS/08/NS-DOS
COMPUTER: IDPM FC compatible
OPERATING SYSTEM: DS/08/769,746
FILING DATE: 19-DEC-1996
CLASSITCATION NUMBER: 13,837
REPERENCE/DOCKET NUMBER: 32,837
REPERENCE/DOCKET NUMBER: 32,837
REPERENCE/DOCKET NUMBER: 32,837
REPERENCE/DOCKET NUMBER: 32,837
REPERENCE/CATON INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 37-838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TTREE TIME AND ACTERISTICS:
LENGTH: 585 amino acids
TTREE TOWNERS: MINERAL ACTERISTICS:
LENGTH: 585 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 47; DB 3; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-769-746-2
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US-10-153-064-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKQEPERNE 9
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APPLICANT: Kerry-Williams, Sean M
APPLICANT: Gilbert, Sarah C
TITLE OF INVENTON: Yeast Strains and Modified Albumins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
CONTRY: USA
ZIP: 19406-1310
COMPUTER READABLE FORM:
MSPLIMM TYPE: POOPPY disk
COMPUTER: INP PC COMPATION
COMPUTER: NS-DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,572
FILING DATE: 11-MAR-1995
CLASSIFICATION NUMBER: GB 9404270.2
FILING DATE: 1-MAR-1995
APPLICATION NUMBER: GB 9404270.2
FILING DATE: 1-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nacmi Biswas
REGISTRATION NUMBER: GIO/878/4294
TELEPHONE: GIO/878/4294
TELEPHONE: GIO/878/4294
TELEPHONE: GIO/878/42294
TELEPHONE: GIO/878/42294
TELEPHONE: GIO/878/42294
TELEPHONE: HARACTERISTICS:
LENGTH: S85 annino acids
TTOPONE CHARACTERISTICS:
LENGTH: S85 annino acids
TTOPONE CHARACTERISTICS:
LENGTH: S85 annino acids
TOPONE CHARACTERISTICS:
TELEMENT: ADDRESSERIES TO ACIDS TO NOT ACIDS T
                                                                                                                                                                                                           100.0%; Score 47; DB 2; Length 585; 100.0%; Pred. No. 0.38; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-769-746-2
Sequence 2, Application US/08769746
; Patent No. 6274305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08702572
Patent No. 5965386
                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MOLECULE TYPE: protein US-08-702-572-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AKOEPERNE 100
                                                                                                                                                                                                                                                                                                                                                                                                             92 AKOEPERNE 100
                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-984-176-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKQEPERNE 9
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                 ; SEQ ID NO 1
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US-10-153-064-5

Sequence 5, Application US/10153064

Sequence 5, Application US/10153064

Patent No. 666346

GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING DATE: 2002-05-24

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: Patentin version 3.1

LENGTH: 585
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US/08/433,037

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 1; Length 609; 100.0%; Pred. No. 0.39;
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---- 0; Indels
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Patent No. 6663485;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PFS56
CURRENT FALING DATE: 2002-05-24;
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR APPLICATION NUMBER: 60/293,212
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOS-08-09-75-50-6.

JOS-08-09-75-50-6.

JOSEPHORE 2. Application US/08097956A

JOSEPHOR 2. Application US/08097956A

JOSEPHOR 2. Application US/08097956A

JOSEPHOR 2. Application Signature Applicant: Hermann Gram

JITLE OF INVENTION: Fusion Polypeptides

FILE REPERENCE: 600-7244/CPA

CURRENT APPLICATION NUMBER: US/08/08-7-21

PRIOR PELING DATE: 1997-07-21

PRIOR PELING DATE: 1996-07-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 609

TYPE: RAT

JORGANISM: Homo Sapiens

US-08-897-956A-2
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APPLICATION NUMBER: US/08/433, FILING DATE: 03-MAY-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: DIGIGILO, Frank S. REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 91082 REFERENCE/DOCKET NUMBER: 91082 TELEPHONE: (516) 742-4343 TELEPHONE: (516) 742-4346 TELEPK: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-433-037-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AKQEPERNE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-10-153-064-7
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Sequence 4, Application US/08433037

Patent No. 5707028

GENERAL INFORMATION:
APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Brierley, Russell A.
APPLICANT: Trinil, Gregory P.
APPLICANT: Trinil, Gregory P.
APPLICANT: TSChopp, Justy F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STATE: New York
COUTTY: Garden City Plaza
CITY: Garden City
STATE: New York
COUTTY: U. S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                        US-08-222-619-3
Sequence 3. Application US/08222619
Sequence 3. Application US/08222619
Fatent No. 565232
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
CORRESPONDENCE Anden Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
COTTY: Thousand Oaks
STRATE: California
COUNTRY: U.S.
ZIP: 31320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: RIORPY disk
COMPUTER: BARCHIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/222,619
FILING BATE:
CLASSIFICATION TOR SEQ ID NO: 3:
SERANDENESS: UNKNOWN
TOPOLOGY: UNKNOWN
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 1; Length 609; 100.0%; Pred. No. 0.39; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AKQEPERNE 124
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                                                  RESULT 8
US-08-222-619-3
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APPLICANT: Fournier, Alain
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Web, Patrice
APPLICANT: Yeb, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPREATION THEREOF AND PHARMACEDTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NOMBER OF SEQUENCES: 36
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                            Query Match 100.0%; Score 47; DB 5; Best Local Similarity 100.0%; Pred. No. 0.39; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMBUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
CURRENT APPLICATION DATA:
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
FILING DATE: 31-JAN-1997
CLASSIFICATION: 438
FRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
FRICANTON NUMBER: PCF,FR93/00085
FILING DATE: 31-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMICH Ph.D., JULIE K.
REGISTRATION NUMBER: P-38,619
REBERRENGE/DOCKET NUMBER: P38,619
REBERRENGE/DOCKET NUMBER: P38,619
REBERRENGE/DOCKET NUMBER: P38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CIIY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08797689
Patent No. 5876969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
                                   : 609 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
SEQUENCE CHARACTERISTICS LENGTH: 609 amino aci
                                                                       TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-04075-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AKOEPERNE 124
                                                                                                                                                                                                                                                                                                                                                                                                    1 AKQEPERNE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-08-797-689-2
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

RILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REPERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT PILING DATE: 2001-10-12

PRIOR FILING DATE: 2000-10-12

NUMBER: OF SEQ ID NOS: 1143

SEQ ID NO 977

SEQ ID NO 977
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TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STREET: U.S.
ZIP: 91320-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS MS-DOS
CORPUTER: PC-DOS MS-DOS MS-DOS
CORPUTER: PC-DOS MS-DOS MS-DOS
CORPUTER: PC-DOS MS-DOS MS-DOS
CORPUTER: PC-DOS MS-DOS MS-DOS MS-DOS
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                                                                                                                                                                                                Query Match
100.0%; Score 47; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9504075 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 977, Application US/09976594 Patent No. 6673549
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ORGANISM: Homo sapiens
   ; SEQ ID NO 7
; LENGTH: 609
: TYPE: PRT
; CRGANISM: HOMO Sapiens
US-10-153-064-7
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Matches 9; Conserv
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US-09-976-594-977
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1 AKQEPERNE 9

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Sequence 2, Application US/09984186
Patent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Guitcon, Jean-Dominique
Jung, Garard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
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100.0%; Score 47; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
GITY: Collegeville
STRATE: BA
COUNTRY: USA
STRATE: BA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READICATION NUMBER: US/09/984,186
FILING DATE: 29-OCC-2001
CURSEIFCATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1993
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-UUL-1997
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-UN-1993
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-UN-1993
APPLICATION NUMBER: P-38.619
REFERENCE/DOCKET NUMBER: ST92006-US
REGREENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3839
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERIFICS:
LENGTH: 610 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid

US-09-984-186-2
NOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2
NOLECULE TYPE: procein
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116 AKQEPERNE 124
116 AKQEPERNE 124
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Search completed: April 19, 2004, 12:05:19 Job time: 1.3795 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
April 19, 2004, 11:37:59; Search time 0.853186 Seconds

(without alignments)
789.208 Million cell updates/sec
Perfect score: 32
Sequence: 1 QAADKAA 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283366 segs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100\*

Listing first 45 summaries

Database: PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir2:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rum albumin pre	serum albumin prec		hypothetical cytos	ribosomal protein	ribosomal protein	2-hydroxyacid dehy			probable succinyl-	serum albumin prec	protein translocas	hypothetical prote	carbonic anhydrase		conserved hypothet		flagellar M-ring p	rotein		protein p		ne P4	dextranase - Strep		seomal prot		ribosomal	30S ribosomal chai
SUMMARIES	ū	A47391	ABPGS	ABHUS	AH3273	JC1273	T11792	AG3133	E98154	D95295	E70716	\$57632	AD3267	C83362	B87692	A43256	A86717	B38145	AD0223	A46312	A41971	A97887	T37062	D69799	T30291	H95354	R3EC8	S	G85995	00
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	ength	600	605	609	96	128	133	311	311	315	387	608	906	260	293	409	462	523	570	609	619	619	919	1001		60	130	130	130	130
a <b>ķ</b> e	Query	: 8	100.0	00	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5		v	84.4	4	4	4
	Score	32	32	32	29	53	29	29	29	29	29	29	29	28	28	28	28	28	28	28	28	28	28	28	28	27	27	27	27	27
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outer membrane pro	oncer memorane bro	histone-like prote	hypothetical prote	outer membrane pro	cationic 19 kDa ou	MHC cell surface a	hypothetical prote	hypothetical prote	sorbose-permease P	probable sorbose P	phosphotransferase	phosphotransferase	mannose-specific P	PTS enzyme IIC, ma	phosphotransferase
DNEC17	809104	D90651	D85502	AC0530	AD0129	I79640	AE1317	AE1689	H91253	D86094	WOECMP	850189	H90944	C85793	AG0726
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161	161	161	161	161	165	181	239	243	. 265	265	266	266	266	266	266
84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4
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## ALIGNMENTS

A47391  A47301  Serum albumin precursor - rheeus macaque  C;Species Macaca mallatta (rheeus macaque)  C;Species Macaca mallatta (rheeus macaque)  C;Species Macaca mallatta (rheeus macaque)  C;Accession: A47391  R;Warkins, S.; Saxamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.  Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993  A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in bilin.  A;Reference number: A47391  A;Accession: A47391  A;Accession: A47391  A;Accession: A47391  A;Besidues: Drelninhary  A;Molecule type: mRNA; protein  A;Residues: 1-600 «WAT.  A;Cross-references: G: Nor:  A;Cross-references: G: Nor:  A;Cross-references: G: Nor:  A;Cross-references: G: Nor:  A;Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIF:128281)  C;Superfamily: serum albumin repeat homology <sa1.>  F;21-194/Domain: serum albumin repeat homology <sa2.>  F;21-386/Domain: serum albumin repeat homology <sa3.>  F;21-386/Domain: serum albumin repeat homology <sa3.></sa3.></sa3.></sa2.></sa1.>	Query Match 100.0%; Score 32; DB 2; Length 600; Best Local Similarity 100.0%; Pred. No. 21; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 QAADKAA 7 Db 186 QAADKAA 192	RESULT 2 ABPGS serum albumin precursor - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Species: Sus scrofa domestica (domestic pig) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999 C;Accession: S01382; A61006 R;Weinserock, J; Baldwin, G.S. Nucleic Acids Res. 16, 9045, 1988 A;Title: Nucleotide sequence of porcine liver albumin. A;Reference number: S01382; MUID:89016582; PMID:3174440 A;Status: translation not shown	A; Molecule type: mknA A; Molecule type: mknA A; Residues: 1-605 <mei> A; Cross-references: EMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798 A; Cross-references: EMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798 B; Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M. J. Bone Miner: Res. 4, 235-241, 1989 A; Title: Serum albumin and its acid hydrolysis peptides dominate preparations of minera. A; Reference number: A61006; MUID:89269769; PMID:2728927 A; Accession: A61006</mei>
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A; Accession: 159313
A; Accession: 159313
A; Accession: Lanslated from GB/EMBL/DDBJ
A; Accession: Lanslated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 589-590, 'ALPRRVKNLLLGVKLP' < MAD>
A; Residues: 589-590, 'ALPRRVKNLLLGVKLP' < MAD>
A; Residues: 589-590, 'ALPRRVKNLLLGVKLP' < MAD>
A; Residues: 689-590, 'ALPRRVKNLLLGVKLP' < MAD>
A; Rosidues: this frame-shift variant is designated albumin Bazzano; four additional variant: R; Menaya, J.; Parrilla, R.; Ayuso, M.S.
A; Nocession: G01747
A; Reference number: G08292
A; Accession: G01747
A; Accession: G01747
A; Residues: L-120, 'G', 122-455 < MEN>
A; Residues: L-20, 'G', 1995
A; Title: Biodoproclosytic processing of recombinant proalbumin variants by the yeast Kex: A; A; Accession: 555314; WUID:95275251; PMID:7755581
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A, Residues: 25-48 < ROB5
R, Residues: 25-48 < ROB5
R, Princh, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
A, Accidues: 25-48 < Rob5
R, Princh, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
A, Rich and Spectrometric identification of modifications to human serum albumin treat
A, Reference number: $36882, MUID:93384321; PMID:8373198
A, Accession: $36882
A, Roceule type: protein
A, Robelle type: protein
A, Robelle type: protein
A, Robelle type: Spiteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A, Hele: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmo.
A, Reference number: $17599; MUID:92126241; PMID:1772598
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A;Molecule type: protein
A;Mesidues: 166-173 ccRs.
R;Mesidues: 166-173 ccRs.
R;Mogard, M.H; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; W.
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A;Atlle: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-transference number: A03239; MUID:86242180; PMID:3087352
A;Accession: A03239
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A,Residues: 25-54;354-357,431-447 <KAU>
A,Residues: 25-54;354-357,431-447 <KAU>
A,Residues: 25-54;354-357,431-447 <KAU>
A,Rote: 49-Leu was also found
A,Rote: 49-Leu was also found
Carraway, R.B.; Cochrane, D.B.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A,Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A,Reference number: A45800; MUID:89341406; PMID:2474609
A,Rocession: A45800
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A; Readdues: 166-173, 'L. cMOG>
A; Readdues: 166-173, 'L. cMOG>
A; Readdues: 166-173, 'L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, R:Galliano, M.; Minchiotti, L.; Porta, F.; 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 871-8725, 1990
A; Title: Mutations in genetic variants of human serum albumin found in Italy.
A; Reference number: A38255; MUID:91062352; PMID:2247440
A; Accession: C38255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 19-27 < LED>
R; Meloun, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A; Tille: Complete amino acid sequence of human serum albumin.
A; Reference number: A91420; MUID:76187907; PMID:1225573
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A Residues: 76-111 <GAL1>
A Accession: B38255
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NyAlternate names: preproalbumin
NyAlternate names: preproalbumin
NyAlternate names: preproalbumin
NyAlternate names: preproalbumin
CySpecies: Homo sapiens (man)
CyDate: 29-Jul-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000
CyDate: 29-Jul-1981 #sequence of Logania serum albumin CDNA and its expression in Escherichia coli AyTeile: The sequence of human serum albumin CDNA and its expression in Escherichia coli AyTeile: The sequence of human serum albumin Coli AyTeile: The sequence of human serum albumin Coli AyResidues: 1-419, KY, 421-609 cLAM>
AyTeile: The sequence Explain NO495; GB:JO0078; GB:LO0132; GB:LO0133; NID:G28591; PIDN:CAA23
AyDugaiczyk, A., Law, S.W.; Dennison, O.E.
AyTeile: Nucleotide sequence and the encoded anno acids of human serum albumin mRNA.
AyRecession: Ay3936; MyID:82105994; PMID:6275391
AyRocession: Ay3936
AyMolecule type: mRNA
AyResidues: 1-120, G'.122-609 cDUG>
AyCossion: AyBayasion Ay3936
AyMolecule type: mRNA
AyResidues: 1-120, G'.122-609 cDUG>
AyCossion: AyBayasion Ay3936
AyMolecule type: mRNA
AyResidues: Diol. Chem. 261, 3244-3251, 1986
AyMolecule type: MRNA
AyResidues: Diol. Chem. 261, 3244-3251, 1986
AyHile: The human albumin gene. Characterization of the 5' and 3' flanking regions and AyReserse connuber: Insalazion and encomparing the characterization of the 5' and 3' flanking regions and AyReserse translation.
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A;Rcteuseloum: 139944
A;Reteuser translation not shown
A;Rolecule type: DNA
A;Residues: 1-26 <URAN-3
A;Crose-references: GB:MI3075; NID:g178330; PIDN:AAA51688.1; PID:g553173
A;Crose-references: GB:MI3075; NID:g178330; PIDN:AAA51688.1; PID:g553173
B;Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.
B;Totle: A mucleotide insertion and frameshift cause analbuminemia in an Italian family.
A;Accession: 159286; MUID:94181575; PMID:8134387
A;Accession: 159286
A;Accession: 159286
A;Gatus: translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 282-290; KGRFDLQ, <WAFT.
A;Residues: 282-290; KGRFDLQ, <WAFT.
A;Residues: 282-290; KGRFDLQ, <WAFT.
A;Residues: GB:869192; NID:9546032; PIDN:AAB30282.1; PID:9546033
A;Roses-references: GB:869192; NID:9546032; PIDN:AAB30282.1; PID:9546033
A;Rote: this frame-shift variant, designated albumin Roma, leads to analbuminemia
B;Madison, J; Galliano, M; Watkins, S; Minchiotti, L; Porta, F; Rossi, A; Putnam, Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994
A;Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl-A;Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl-A;Title: Genetic variants A; Pull: PMID:8022807
                              A; Molecule type: protein

A; Residues: 23-51, X', 23-54; XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 < LIM>
A; Residues: 23-51, X', 23-54; XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 < LIM>
A; Experimental source: dental ename!

A; Note: albumin and other serum proteins are also found in bone

A; Note: albumin and other serum proteins are also found in bone

C; Comment: Serum albumin; serum albumin repeat homology

C; Superfamily: serum albumin; serum albumin repeat homology

C; Keywords: carriar protein; duplication; metal binding; plasma

F; 1-16, Domain: signal sequence (fragment) #status predicted < NRO-

F; 23-60; Product: serum albumin repeat homology < SA1-

F; 218-391/Domain: serum albumin repeat homology < SA2-

F; 218-391/Domain: serum albumin repeat homology < SA3-

F; 10-589, Domain: serum albumin repeat homology < SA3-

F; 10-589, Domain: serum albumin repeat homology < SA3-

F; 10-589, Domain: serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-589, Domain; serum albumin repeat homology < SA3-

F; 10-580, Main serum albumin repeat homology < SA3-

F; 10-580, Main serum albumin repeat homology < SA3-

F; 10-580, Main serum albumin repeat homology < SA3-

F; 10-580, Main serum albumin repeat homology < SA3-

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F; 10-580, Main serum albumin repeat homology < SA3-

F; 10-580, Main serum albumin r
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels
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hypothetical cytosolic protein BMEI0173 [imported] - Brucella melitensis (strain 16M) c; Species: Brucella melitensis
C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Accession: AH3273
R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A; Tritle: The genome sequence of the facultative intracellular pathogen Brucella meliten: A; Reference number: AD352; PMID:1175688
A; Accession: AH3273
A; Residues: DAA
A; Residues: 1-96 «KUR»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CyAccession: Journal meducation to sep-1999 (A)Accession: Journal M. A)Accession: JC1273 (A)Accession: JC1273 (A)A
             C; Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyrido:
                                                     F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-609/Product: serum albumin #status experimental <MPT>
F;25-002/Domain: serum albumin repeat homology <SA1>
F;166-174/Product: kinetenain #status experimental <KIP>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;43-925/Domain: serum albumin repeat homology <SA3>
F;73-Binding site: copper (His) #status predicted
F;77/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,F;71-86,99-115,114-125,148-193,192-201,289-170,269-277,289-303,302-313,340-385,384-393,F;214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE008917; PIDN:AAL51355.1; PID:g17982054; GSPDB:GN00190
A;Experimental source: strain 16M
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C;Species: Streptomyces antibioticus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
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A;Residues: 1-128 <PAR>
A;Residues: 1-128 <PAR>
A;Crose-references: GBNM99911; NID:g153436; PIDN:AAA26811.1; PID:g153438
C;Superfamily: Escherichia coli ribosomal protein L12
C;Keywords: protein biosynthesis; ribosome
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Pred. No. 18;
1; Mismatches 0; Indels
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Pred. No. 23;
1; Mismatches
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100.0%; Pred. No. 22;
ive 0; Mismatches
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Best Local Similarity 85...
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 QAADKAA 200
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Best Local Similarity
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Almosenule type: protein and action of the country 
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Cycomment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones
Cycomment: A large number of variants of human serum albumin have been described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4q11-4q13
C;Superfamily: serum albumin; serum albumin repeat homology
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probable succinyl-coa synthetase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 1.7-Ual-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70716
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable D-isomer specific 2-hydroxyacid [imported] - Sinorhizobium meliloti (strain 10 c)Species: Sinorhizobium meliloti (c)Species: Sinorhizobium meliloti (c)Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 (c)Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 (c)Date: 24-Aug-2001 #sequence_revision 25.5 #sequence_revision C: Abola, A.P.; Barloy-Hubler, F.; Bow ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Aritle: Nucleoride sequence and predicted functions of the entire Sinorhizobium melilor A,Reference number: A95262; MUD:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-315 cKUR.
A,Cross-references: GB:A.E006469; PIDN:AAK64926.1; PID:g14523348; GSPDB:GN00165
A,Experimental source: strain 1021, megaplasmid pSymA
A,Eathert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
A,Authors: Kahn, D.; Kahn, Worholter, F.J.; Weating, D.H.; Kiss, E.; Komp, C.; Lelaure
A,Authors: Rann D.; Andenbol, M.; Vorholter, F.J.; Weiner, S.; Wells, D.H.; Wong, K.; Yeh, K.A.; Reference number: A96039; MUID:21368234; PMID:11474104
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A;Reference number: A97359; MuID:21608551; PMID:11743194
A;Receasion: B98154
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <KUR>
A;AResidues: 1-311 <KUR>
C;Genetics:
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Pred. No. 55;
1; Mismatches 0; Indels
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90.6%; Score 29; DB
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches
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C,Superfamily: phosphoglycerate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                           A;Gene: AGR L 379
A;Map position: linear chromosome
C;Superfamily: phosphoglycerate dehydrogenase
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Best Local Similarity 85.7%;
Matches 6; Conservative
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C; Species: Agrobacterium tumefaciens
C; Date: 22.0ct-2011 #sequence_revision 22-0ct-2001 #text_change 18-Nov-2002
C; Accession: E98154
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
403133
2-hydroxyacid dehydrogenase Atu4691 [imported] - Agrobacterium tumefaciens (strain C58, 2-hydroxyacid dehydrogenase Atu4691 [imported] - Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 11.5an-2002
C; Date: 11.5an-2002
C; Date: 11.5an-2002
R; Mood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
F, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Accession: AG3133
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1:311 < KNR>
A; Residues: 1:311 < KNR>
A; Experimental source: strain C58 (Dupont)
A; Experimental source: strain C58 (Dupont)
A; Gonetics: Atu4691
A; Map position: linear chromosome
C; Superfamily: phosphoglycerate dehydrogenase
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0
                                                                                                                                                                                                                                         Tibosomal protein LI2 - Streptomyces virginiae
C;Species: Streptcmyces virginiae
C;Species: Streptcmyces virginiae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T11792
R;Yamada, Y.
Submitted to the EMBL Data Library, May 1995
A;Reference number: Z17345
A;Reference number: Z17345
A;Recession: T11792
A;Recession: T11792
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Residues: L133 <XAM>A;Residues: L133 <XAM>A;Residues: L133 <XAM>A;Residues: L133 <XAM>C;Coss-references: EMBL:D50624
C;Genetics:
A;Genetics:
C;Superfamily: Escherichia coli ribosomal protein L12
C;Keywords: ribosome
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85.7%; Pred. No. 24;
ive 1; Mismatches
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Best Local Similarity 85.7
Matches 6; Conservative
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114 EAADKAA 120
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EAADKAA 115
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A; Experimental source: strain 16M
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-260 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ORADKAA 7
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                                                    C;Genetics:
A;Gene: BMEI0121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PA2260
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(Species Brucella melitensis
C)Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C)Accession: AD3267
C)ACCESSION: AD3267
C)ACCESSION: AD3267
C)ACCESSION: AD3267
C)ACCESSION: AD3267
C)ACCESSION: AD3267
C) ACCESSION: B: ED STROWN E. F. ELSER B. C.; Mujer, C.; Los, T.; Ivanova, Mauur, M.; Goltsman, E.; Selkov, E.; Elser, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A.Accession: AD3267
A.Accession: AD3267
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUD:98295997; PMID:9634230
A;Accession: E70716
A;Accession: E70716
A;Accession: E70716
A;Accession: E70716
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Melecule type: DNA
A;Residues: 1-387 <COL>
A;Residues: 1-387 <COL>
A;Residues: 1-387 <COL>
A;COL>
A;C
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A,Molecule type: DMA
A,Residues: 1-906 «KUR»
A,Cross-references: GB:AE008917; PIDN:AAL51303.1; PID:g17981998; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serum albumin precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Decies: Felis silvestris catus (domestic cat)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
C;Accession: 074660; S5760; F.; Hentges, F.
Gene 169, 295-296, 1996
A;Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A;Reference number: 074660; MUID:96194824; PMID:8647469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A;Residues: 1-608 <HI2>
A;Cross-references: EMBL:X84842; NID:g886484; PIDN:CAAS9279.1; PID:g886485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 387; 66;
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C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain
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Best Local Similarity 85.7
Matches 6; Conservative
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 16-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Datesion: C83362
R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bu adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathx A;Reference number: A82950; MUID:20437337; PMID:10984043
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CiSpecies: Caulobacter crescentus
CiSpecies: Caulobacter crescentus
CiSpecies: Conjour-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
CiAccession: B87692
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, K.J.; Durkhin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N, J.; Ermclaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: Ag7249; MUID:21173698; PMID:11259647
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A,Experimental source: strain PA01
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A/Status: preliminary
A/Molecule type: DNA
A/Molecule type: DNA
A/Residues: 1-293 <STO>
A/Cross-references: GB:AE005673; NID:g13425312; PIDN:AAK25534.1; GSPDB:GN00148
C/Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PA2260 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                           Length 906;
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85.7%; Pred. No. 76;
ive 1; Mismatches 0; Indels
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85.7%; Pred. No. 86;
ive 0; Mismatches 1; Indels
                                                                                                   / Match 90.6%; Score 29; DB 2; Length 906 Local Similarity 85.7%; Pred. No. 1.5e+02; Pred. 6; Conservative 1; Mismatches 0; Indels
A, Map position: I
C, Superfamily: preprotein translocase secA
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Best Local Similarity 85.7
Matches 6; Conservative
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RESULT 15
A43256
mobilization protein mobA - Thiobacillus ferrooxidans plasmid pTF-FC2
C;Species: Thiobacillus ferrooxidans
C;Species: Thiobacillus ferrooxidans
C;Date: 10-Jun-1993 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
C;Accession: A43256; S27622
R;Rohrer, U; Rawlings, D.E.
J; Bacteriol: 174, 6230-6237, 1992
A;Title: Sequence analysis and characterization of the mobilization region of a broad-hc
A;Reference number: A43256; MUD:93015664; PMID:1400173
A;Accession: A4326
A;Status: pre-liminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-409 <ROH>
A;Residues: 1-409 <ROH>
A;Residues: 1-409 <ROH>
A;Rote: sequence extracted from NCBI backbone (NCBIP:115305)
C;Genetics:
A;Genetics:
A;Genetics: A;Geneme: plasmid
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87.5%; Score 28; DB 2; Length 409;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
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HSA prote Mature pr Amino aci Yeast cod Mature hu Human alb Human ser Mature fo B lymphoc Human ser Human

Aay84873 Aay83946 Aax83946 Aaax83946 Aae12417 Aae13129 Aae13131 Aae13399 Aae13339 Aae13339 Aae363321 Abg333847 Abg333847 Abg333847 Abg333847 Abg33585 Aae36935 Aae36935

Glycosyla Human alb Human alb

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The invention relates to human polymuclectides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodilatory activity and activity, tissue growth factor activity, immunomodilatory activity and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation, gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20, SEQ ID NO 16528; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                         AAY84873
AAY83946
AAM52567
AAE12417
AAE12403
AAE13129
                                                                                                                                         AAE13399
ABB79006
AAE08578
AAU75220
ABG70986
ABG33341
ABG71291
ABR55695
AAE30936
                                                                                                                                                                                                                                                                                                                                                                                               AA002636 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 16528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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N-PSDB; AAI82567.
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WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001.
 AA002636;
                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
 Aaco2636 Human pol
Aam25284 Human pro
Aaco4435 Human pro
Aaco4435 Human pol
Aau33082 Novel hum
Aar14178 Human ser
Aap90389 N-termina
Aap90389 N-termina
Aap90399 N-termina
Aap90391 N-termina
Aap90391 N-termina
Aaco3018 Human ser
Add22019 Heterolog
Aau22877 Human ser
Aaco318 Human ser
Aaco318 Human ser
Aar26318 Human ser
Aar26318 Human ser
Aar26318 Human ser
Aar2632 Synthetic
Aar2632 Synthetic
Aar2632 Human ser
Aar2632 Human ser
Aar2632 Synthetic
                                                                                                     April 19, 2004, 11:24:29 ; Search time 5.29363 Seconds (without alignments) 480.375 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                 1586107
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                               US-09-832-929-18_COPY_280_288
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Maximum Match 100%
Listing first 45 summaries
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AAP93344
AAP91388
AAR91422
AAR05318
AAR08457
AAR26207
AAR26207
AAR26302
AAR80301
                                                                            protein search, using sw model
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AAV00435
AAV33082
AAR133082
AAR178
AAP90387
AAP90390
AAP90390
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AAR90392
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Match
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Minimum DB seq Maximum DB seq

Database

Total number

Searched:

Scoring table:

Perfect score:

Sequence:

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OM protein

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Score

Result

gene therapy;

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antibacterial; endocrine; cardian; central nervous system; virucide;
antibacterial; endocrine; cardian; central nervous system; virucide;
antibacterial; endocrine; cardian; cardiavascular; antibacteria; anaemic; anaemic; antiagregant; hemostatic; vulnerary; antiulcer; osteopathic; eczema; we dermaclogical; antidalergic; antiasthmatic; antidiabetic; cytostatic; neuropscotective; antideperseant; nootropic; antidiabetic; cytostatic; meuropscotective; antideperseant; nootropic; antidiabetic; cytostatic; meuropscotective; antideperseant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antidianaphylactic; rheumatofid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropachology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabbetes; multiple sclerosis; depression; anaematorial disease; parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM5966 to AAM99904 encode the human proteins given in AAM25255 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory, antirheumatic; antiarthritic; immunosuppressive, antiinfacterial, endocrine, cardiant, central nervous system, virucide; anti-HIV, fungicide; antimutagen, cardiavosacular; antianematic, antiaggregant, haemostatic, vulnerary; antiulcer; osteopathic; dermatological; antialergic; antiabetic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
      part
                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
inflammation. Note: The sequence data for this patent did not form pof the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                       Query Match 100.0%; Score 47; DB 4; Length 112; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein sequence SEQ ID NO:799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 186; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                            AAM25284 standard; protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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EKPLLEKSH 11
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N-PSDB; AAH99225.
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                                                                                   Sequence 112
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                                                                                                                                                                                                                                                                                                                    RESULT 2
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UXAXHXBXBXBZBZBZBZBZBXX8X8XBXHXBXXXXXXBZBZBZBZBZBZBZX8XXBXB

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antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreaticis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat., horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forms in cinterest. They can be used in diagnostics, formsics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; BST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition.
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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
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Cao Y, Drmanac RA, Zhang J, Werhman T;
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17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-0063810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 114 AA;
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118 EKPLLEKSH 126

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Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                         Recombinant, human serum albumin; HSA; yeast codon bias; host cell; overlapping oligonucleotide; expression vector.
                                                                                                                                                                                                                                                                             Yeast codon-biased recombinant HSA protein fragment HSA-II.
                                                                                                                         AAY83948 standard; protein; 188 AA
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N-PSDB; AAA10093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis, tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      AAO04435 standard; protein; 126 AA.
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2000US-00577409
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protein of the invention
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N-PSDB; AAI84366.
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                                                 Sequence 123 AA;
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18-MAY-2000;
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AA0004435
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AA0004435
AA0004435
AA000435
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98CN-00102506 98CN-00102506

(first entry)

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The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonucleotide fragments that were extended. This sequence represents the sequence of the HSA fragment HSA-II encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression the process for producing human serum albumin in the yeast host cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 47; DB 3; Length 188; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vaccination; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #3573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU33082 standard; protein; 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 EKPLLEKSH 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EKPLLEKSH
                                                                                                                                                                                                                                                                                                                                 Sequence 188 AA;
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Gaps

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EKPLLEKSH 9

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us-09-832-929-18\_copy\_280\_288.rag

Human serum albumin fragment - where C-terminal of human serum albumin is lacking and which can be combined with various drugs.

89JP-00344701.

29-DEC-1989;

WPI; 1991-300976/41 (TOFU ) TONEN CORP.

Claim 1; Page 1; 23pp; Japanese.

This sequence corresponds to amino acids 1 to 303 of mature human serum albumin. The fragment lacking the C-terminal sequence can form part of a fusion protein, for example with drugs. (This sequence is taken from the full-length HSA sequence in EP-330451). See also AAR14179

Sequence 303 AA;

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the present of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberran expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or atimulation; as anti-inflammatory agents; and in treatment of leukaemias. AMU29310-AMU33304 represent the amino acid sequences of novel human expression and the invention.
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                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation; haematopolesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 705; 765pp; English
                                                                                                                                                                                                                                                   Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                        18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                        16-APR-2001; 2001WO-US008656
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Best Local Similarity 100.
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                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 293 AA;
                                                                          WO200179449-A2
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                                              Homo sapiens
                                                                                                           25-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as blood
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100.0%; Score 47; DB 2; Length 303; 100.0%; Pred. No. 0.32; atrive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New N-terminal fragments of human serum albumin - esp. plasma expanders.
                                                                                                                                                                                                                                                                                                                                                                                                                        Σ,
                                                                                                                                                                                                                                                       Human serum albumin polypeptide; plasma expanders.
                                                                                                                                                                                                                                                                                                                                                                                                                          Senior
                                                                                                                                                                                                                              N-terminal of human serum albumin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ballance DJ, Hinchliffe E, Geisow MJ,
                                                                                                                                   AAP90387 standard; protein; 373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  (DELZ ) DELTA BIOTECHNOLOGY LTD.
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                                                                                                                                                                                                                                                                                                                                                                           87GB-00025529.
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                                                                                                                                                                               (revised)
(revised)
(first entry)
  Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                        280 EKPLLEKSH 288
                                                                                                                                                                                                                                                                              Homo sapiens; (Human)
                                                 1 EKPLLEKSH 9
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25-MAR-2003
01-NOV-1989
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89JP-00344701

29-DEC-1989;

JP03201987-A

03-SEP-1991

RESULT

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N-terminal portion of human serum albumin. Used to make plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New N-terminal fragments of human serum albumin - esp. useful as blood
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                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                    Senior PJ
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ballance DJ, Hinchliffe E, Geisow MJ,
                                                                                                                                    Geisow MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90391 standard; protein; 390 AA.
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                                                                                                           (DELZ ) DELTA BIOTECHNOLOGY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal human serum albumin.
                                                                                                                                                                                                                                   Claim 2; Page 9; 20pp; English
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                                                                              87GB-00025529.
                                                                                                                                    Hinchliffe E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                            plasma expanders.
                                                                                                                                                                                                                                                                                                                                      Sequence 389 AA;
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25-MAR-2003
01-NOV-1989
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                                                     25-OCT-1988;
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                          28-JUN-1989
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EP322094-A
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AAP90391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - esp. useful as blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                    N-terminal human serum albumin polypeptide; plasma expanders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 47; DB 1; Length 388; 100.0%; Pred. No. 0.42; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Senior PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New N-terminal fragments of human serum albumin plasma expanders.
                                                                                                                                                                                                                         N-terminal human serum albumin polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90390 standard; protein; 389 AA.
                                                                                                            AAP90389 standard; protein; 388 AA.
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                                   EXPLIENSH 288
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Best Local Similarity
Matches 9; Conserv
                EKPLLEKSH
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                                                                                                                                                                                                                                                                                                                                                                                                                      (DELZ ) DELTA
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25-MAR-2003
01-NOV-1989
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25-MAR-2003
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This sequence corresponds to amino acids 123 to 585 of mature human serum albumin. The fragment lacking the N-terminal sequence can form part of a fusion protein, for example with drugs. (This sequence is taken from the full-length HSA sequence in EP-330451). See also AAR14178
                                                                                                                                                                                                                                                           Human serum albumin fragment - where C-terminal of human serum albumin is lacking and which can be combined with various drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New heterologous fusion proteins with granulocyte-colony stimulating factor activity, useful for increasing neutrophil levels and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heterologous fusion protein related protein sequence SEQ ID NO:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperglycosylated granulocyte-colony stimulating factor; G-CSF; human albumin, human albumin analogue; immunoglobulin; FC; immunoglobulin; FC; inmunoglobulin; FC; insufficient jrotein therapy; neutrophil level; chronic congenital neutrophil level;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 47; DB 2; Length 46
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD32019 standard; protein; 500 AA.
                                                                                                                                                                                                                                                                                                              Claim 6; Page 1; 23pp; Japanese
                                                                                                                                                                    89JP-00344701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAR-2002; 2002US-0361948P.
                                                                                                                                    89JP-00344701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heterologous fusion protein;
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             HSA; fusion protein; drug.
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                                                                                                                                                                                                    (TOFU ) TONEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 463 AA;
                                             Homo sapiens.
                                                                           JP03201987-A.
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                                                                                                                                                                                                                                                                                                                                                                                           Human serum albumin; mature protein; new polypeptides; plasma expanders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New N-terminal fragments of human serum albumin - esp. useful as blood plasma expanders.
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                                                          Score 47; DB 1; Length 390;
Pred. No. 0.43;
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                                                                                         0; Indels
field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human serum albumin lacking N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                         Mismatches
                                                                                                                                                                                                                                  AAP90392 standard; protein; 407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR14179 standard; protein; 463 AA
                                                          100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 9; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                             N-terminal human serum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87GB-00025529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DELZ ) DELTA BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                               (revised)
(revised)
(first entry)
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                                           Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens; (Human)
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                                                                                                                        1 EKPLLEKSH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-186464/26.
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                              Sequence 390 AA;
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01-NOV-1989
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                                                                                                                                                                                                                                                                  AAP90392;
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AAR14179
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Gaps

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The present invention describes a heterologous fusion protein (I)

Comprising a hyperglycosylated granulocyte-colony stimulating factor (G-
CSF) analogue fused to a polypeptide having human albumin, human albumin

analogues, or fragments of human albumin, or the Fc portion of an immunoglobulin, or

fragments of the Fc portion of an immunoglobulin. Also described: (I) a

heterologous fusion protein, which is the product of the expression in a

controlled an exogenous DNA sequence encoding (I); (2) an isolated

host cell of an exogenous DNA sequence encoding (I); (2) an isolated

comprising 1044 base pairs (see ADD32010), fused to the DNA

comprising 1044 base pairs (see ADD32010), fused to the DNA

comprising the administration of (I); (4) pharmaceutical formulations

comprising the administration of (I); (4) pharmaceutical formulations

adapted for the breatment of patients with insufficient neutrophil levels

comprising namy of (I); (5) a vector comprising the polynucleotide of (2);

(6) host cells comprising the vector of (5), or expressing at least one

heterologous protein; and (7) producing (I) are particularly useful in

activity, and can be used in protein therapy. (I) can be used for

medicaments for the treatment of patients with insufficient circulating

controlly levels or for the manufacture of a medicament for the

cutrophil levels or for the manufacture of a medicament for the

cutratable by stimulation of circulating neutrophils such as after

chemotherapy regimens or in chronic congenital neutrophila. The present

chemotherapy regimens or in chronic congenital neutrophila.

chemotherapy regimens or in chronic congenital neutrophila.
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patients with low circulating neutrophils, such as after chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 47; DB 7; Length 500; 100.0%; Pred. No. 0.56; tive 0; Mismatches 0; Indels
                                                       Disclosure, SEQ ID NO 25; 126pp; Egglish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU29877 standard; protein; 550 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #368.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-2001; 2001WO-US008656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 EKPLLEKSH 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 500 AA;
                      in neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200179449-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
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Matches
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Drmanac RT;

Liu C,

Tang YT,

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predsposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the conclination are also useful for producing the proteins are also useful for producing the proteins. The proteins of as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis, and in bone, cartilage, tendon and conclination; as anti-inflammatory agents; and in treatment of leukaemias. Conclination; as anti-inflammatory agents; and in treatment of leukaemias. Alugabilo-Abula3304 represent the amino acid sequences of novel human concerned.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 4; Length 550; Pred. No. 0.62; 0; Mismatches 0; Indels
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                                                                                                        Claim 20; Page 206; 765pp; English.
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100.0%;
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Best Local Similarity
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Sequence 11, Appl Sequence 26, Appl Sequence 7, Appli Sequence 370, App Sequence 12, Appli Sequence 7, Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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7, Appli 23, Appl 2, Appli

Sequence 7, A sequence 23, Sequence 2, Ap Sequence 2, A se

Sequence 2, Al Sequence 13, Al Sequence 16, Al

Sequence 14, A Sequence 15, A Sequence 17, A Sequence 13,

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Sequence 799, Application US/10296115
; General No. US20040053248A1
; GENERAL INFORMATION:
APPLICANT: Hyesq Inc
TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US99/488,725
; PRIOR APPLICATION NUMBER: US99/552,317
; PRIOR FILING DATE: 2000-01-21
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 799
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(114)

OTHER INFORMATION: Xaa = any amino acid or other as shown in Table US-10-296-115-799
                          US: 10-414-469-1
US: 10-414-469-1
US: 10-414-469-1
US: 10-413-831-1
US: 10-413-832-1
US: 10-413-832-1
US: 10-413-86-2
US: 10-414-386-2
US: 10-414-386-1
US: 10-414-386-1
US: 10-414-386-1
US: 10-414-386-1
US: 10-153-064-7
US: 10-153-064-7
US: 10-153-6048-7
US: 10-153-6048-7
US: 10-153-6048-7
US: 10-153-6048-7
US: 10-153-6048-7
US: 10-153-6048-7
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11arity 100.0%; Pred. No. 0.28;
Conservative 0; Mismatches n.
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US-10-237-708-2
US-10-237-866-2
US-10-237-871-2
US-10-433-108-13
US-10-433-108-14
US-10-433-108-14
US-10-433-108-14
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US-10-153-064-133
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US-09-929-552-2
Sequence 2, Application US/09929552
Patent No. US20020123080A1
  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKPLLEKSH 87
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les 9; Conser
US-10-296-115-799
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equence 2, Appli
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Appli
                                                                                                                        April 19, 2004, 12:00:25 ; Search time 3.78947 Seconds (without alignments) 654.724 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Sequence S
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Sequence
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| / Gan2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
| / Gan2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-934-010-26
US-09-933-117-18
US-09-932-322-445
US-09-832-501-18
US-09-833-118-18
US-09-833-245-18
US-09-833-245-18
US-09-833-245-18
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US-10-433-108-34
US-10-153-064-5
US-10-153-604A-5
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        1124875 segs, 275673149 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                          protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Gaps

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Length 114; Indels

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RESULT 12
US-10-425-000-31
US-10-425-000-31
Sequence 31, Application US/10425000
Publication No. US20040052777A1
GENERAL INVORMATION:
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Anglegenesis
FILE OF INVENTION: Anglegenesis
URRENT APPLICATION NUMBER: US/10/425,000
URRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2003-04-29
PRIOR FILING DATE: 2002-90-4
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
LENGTH: 585
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100.0%; Score 47; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Human derived fusion protein US-10-425-000-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-10-433-108-34
| US-10-433-108-34
| Sequence 34, Application US/10433108
| Publication No. US20040053370A1
| GENERAL INFORMATION:
| APPLICANT: Eli Lilly and Company
| TITLE OF INVENTION: GLP-1 FUSION PROTEINS
| FILE REFRENCE: K-13991
| CURRENT PEPLICATION NUMBER: US/10/433,108
| CURRENT PILING DATE: 2003-05-29
| RRIOR PILING DATE: 2000-06-12
| NUMBER OF SEQ ID NOS: 35
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 34
| LENGTH: 595
| TYPE: PRT
| CORRANISM: HOMO Sapiens
| US-10-433-108-34
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Sequence 5, Application US/10153064

Publication No. US2020142814A1

GENERAL INFORMATION:

APPLICANT: Bell et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
280 EKPLLEKSH 288
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Sequence 11, Application US/2040052810A1

Sequence 11, Application No. US20040052810A1

SEQUENCE 11, Application No. US20040052810A1

SEPLICANT: Neabit, Mark

APPLICANT: Cameron, Beatrice

APPLICANT: Blanche, Francis

TITLE OF INVENTION: Using Them to Inhibit Angiogenesis

TITLE OF INVENTION: Using Them to Inhibit Angiogenesis

TITLE OF INVENTION: Using Them to Inhibit Angiogenesis

CURRENT APPLICATION NUMBER: US/10/424,999

PRIOR APPLICATION NUMBER: 10/233,675

PRIOR APPLICATION NUMBER: 10/233,675

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin version 3.2

SEQ ID NO 11

LENGTH: 585
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              Query Match
100.0%; Score 47; DB 11; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                   VS-09-10-10
VS-09-33-245-18

Sequence 10, Application US/09833245

Publication No. US20040010134A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PF546PCT
CURRENT ETLING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/229, 388

PRIOR APPLICATION NUMBER: 60/226, 931

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SEQ ID NO 18

LENGTH. 585
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                   280 EKPLLEKSH 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-833-245-18
                                                                                                         1 EKPLLEKSH 9
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Matches 9; Conservat
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1 EKPLLEKSH 9

Search completed: April 19, 2004, 12:54:59 Job time : 3.78947 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model	April 19, 2004, 11:37:09 ; Search time 3.47368 Seconds (without alignments) 817.479 Million cell updates/sec
ch,	2007
sear	19,
protein	April
OM protein -	Run on:

Title: US-09-832-929-18\_COPY\_439\_447
Perfect score: 51
Sequence: 1 KHPEAKRMP 9

Sequence: 1 KHPEAKRMP 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL 25:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_mbc:\*
8: sp\_organelle:\*
9: sp\_organelle:\*
10: sp\_phage:\*
11: sp\_ordane:\*
12: sp\_virus:\*
13: sp\_virus:\*
14: sp\_unclassified:\*
15: sp\_virus:\*
15: sp\_virus:\*
16: sp\_archeis:\*
17: sp\_archeis:\*
17: sp\_archeis:\*

17: sp\_archeap:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	OBiuk7 homo sapien	OB6vg0 homo sapien	Osfdrl escherichia	Osfbys escherichia	Ogrics pseudomonas	091618 pseudomonas	088ax2 pseudomonas	088a98 pseudomonas	098286 streptomyce	Oggyge caenorhabdi	Q84vx7 arabidopsis	Q89kx8 bradyrhizob	O9c8k6 arabidopsis	094ms7 bacteriopha	OBa5v9 bacteroides	067673 aquifex aeo
di.	QBIUK7	Q86YG0	5 QBFDR1	5 QBFBY8	Q9RLC5	5 Q91618		6 Q88A98	5 Q98286	O9GYG6	0 Q84VX7	6 Q89KX8	0 Q9C8K6	Q94MS7	6 Q8A5V9	6 067673
* Query Watch Length DB	396 4	417 4	125 16	125 16	254 2	352 16	352 16	352 16	55 16	98 5	415 10	765 16	1036 10	122 9	224 16	267 16
% Query Match I	100.0	100.0	76.5	76.5	76.5	76.5	76.5	76.5	74.5	74.5	72.5	72.5	72.5	70.6	9.04	9.07
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0 10 10 10 10 10 10 10 10 10 10 10 10 10	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	4 4 4 4 4 1 5 6 4 5

### ALIGNMENTS

RESULT 2 Q86YG0

250 KHPEAKRMP 258

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22 SEQUENCE FROM N.A.
32 SEQUENCE PROM N.A.
33 Welch R.A., Burland V., Plunkett G. III, Redford P., Rosech P.,
34 Welch R.A., Burland V., Plunkett G. III, Redford P., Rosech P.,
35 Rasko D., Buckles E.L., Lidou S.R., Boutin A., Hackett J., Stroud D.,
36 Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
37 Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
38 Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
39 "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
31 "Extensive mosaic structure revealed by the Complete genome sequence of uropathogenic Escherichia coli.";
32 "Extensive mosaic complete proteome.
33 EMBL; ARO16769; AAN83010.1;
34 Mypothetical protein; Complete proteome.
35 SEQUENCE 125 AA; 13964 MW; 473BED42C8398644 CRC64; Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia. NCBI TaxID=217992; Query Match 76.5%; Score 39; DB 16; Length 125; Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches 0; Indels 01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein yeeV. 119 KHPEAKR 125 Escherichia coli 06. 1 KHPEAKR 7 QSRLC5 QSFBY8; QBFBY8 RESULT 5 Q9RLC5 28FBY8 a à SEQUENCE FROM N.A.
STRAIN-06:41/ (CTTOT3 / ATCC 700928;
STRAIN-06:41/ (CTTOT3 / ATCC 700928;
WEDLINE-23388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL, ADUIGFG; AANS212E.1;
BMPL, ADUIGFG; AANS212E.1;
SEQUENCE 125 AA; 14014 WW; 26AB67E398121996 CRC64; Gaps 01-070/2003 (TrEMBLrel. 24, Created)
01-070/2003 (TrEMBLrel. 24, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Similar to alpha-fetoprotein.
Similar to alpha-fetoprotein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia. NCBI\_TaxID=217992; 0 STRUMBERG R.;
STRUMBERG R.;
STRUMBERG R.;
SCHA1189.13 -- SELL/GenBank/DDBJ databases.
RMBL; BC041789.3 AAH41789.1; -- SECTION ROOFS R. GO; GO:0005386; F:carrier activity; IEA.
R GO; GO:0005386; F:carrier activity; IEA.
R GO; GO:000610; F:transport; IEA.
R InterPro; IPR000264; Serum albumin.
R PROMO; PO0273; transport proct; R.
R PRINTS; PR00802; SERUMALBUMIN; R.
R PROJET; PS00212; ALBUMIN; 2.
R PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 417 AA; 47360 MW; 16E764833EF94E8D CRC64; Query Match 100.0%; Score 51; DB 4; Length 417; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 9; Conservative 0; Mismatches 0; Indels 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein yeeV. PRELIMINARY; 271 KHPEAKRMP 279 1 KHPEAKRMP 9 Escherichia coli 06. SEQUENCE FROM N.A. NCBI\_TaxID=9606; TISSUE=Liver; Query Match Q8FDR1; Q8FDR1 RESULT 3 Q8FDR1

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Gaps

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125 AA.

PRT;

PRELIMINARY;

417 AA.

PRT;

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Gaps
                                                                                                                                                                                                 Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Grauphers, 20, Wackernagel W.; Grauphers, S.; Wackernagel W.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; A29742; CABS6476.1; -. GO; GO:0004076; F:biotin synthase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. InterPro; IPR006638; Elb3.
InterPro; IPR006638; Elb3.
InterPro; IPR007197; Radical SAM. Firm; FP04055; Radical SAM. Firm; FP04055; Radical SAM. T. SMO7729; Elp3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 76.5%; Score 39; DB 2; Length 254; Best Local Similarity 77.8%; Fred. No. 24; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 254 2771 MW; F512DF0FEEC12F67 CRC64;
                          Q9RLC5,
01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Biotin synthetase (SC 2.8.1.6) (Fragment).
PRT; 254 AA
PRELIMINARY;
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76.5%; Score 39; DB 16; Length 125; 100.0%; Pred. No. 12; tive 0; Mismatches 0; IndelB

Local Similarity 100.

Best Loca Matches

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Query Match

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SEQUENCE FROM N.A. STRAIN=DC3000;
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BIOB OR PSPTO0494
                                                                                                                                                                                    Query Match
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Q88A98;
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Q9S2S6
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                                                                                                                                                                                                                                STRAIN=ATCC 15692 / PAO1;
STRAIN=20437337; PAO1;
STRAIN=2043737; PAO1;
STRAIN=20437337; PAO1;
STORT C.K., Pham X.D.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folter K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Mature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nation & Santos V.A.P., Fours D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                             Biotin synthase.
BIOB OR PAGS00.
Pseudomonas aeruginosa.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.5%; Score 39; DB 16; Length 352; 77.8%; Pred. No. 34; 2; Indels tive 0; Mismatches 2; Indels
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SEQUENCE 352 AA; 39113 MW; E46491B67DDF369A CRC64;
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Last sequence update)
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                                                                                                                         Last sequence update)
Last annotation update)
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PIR; F83582; F83582.
GO:0004076; F. Enictin synthase activity; IEA.
GO:0009102; F. Enictin synthesis; IEA.
InterPro; IPR002684; Biotin synth.
InterPro; IPR007197; Radical SAN.
Pfan; PF04055; Radical SAN; I.
SMO0729; Elp3; I.
                                                                                                             Created)
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 77.8
                                                                                    PRELIMINARY;
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                      KHPSAKDMP 117
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1 KHPEAKRMP 9
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BIOB OR PP0362.
                                                                                                                                                                                                             NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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10 0880
AC 08802
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DT 01-JI
DT 01-JI
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DE Biot:
Biot:
CO Pacult
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"Complete sequence of Pseudomonas syringae.";

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, ARO16857; AAO54038.1; -.
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Laiber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraeer C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pred. No. 34;
0; Mismatches 2; Indels
                                                                                                                                          "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Embriton. Wicrobiol. 4:799-808(2002). EMBL; AR06775; AAN65993.1; -. TIGR; PP0362; --
                                                                                                                                                                                                                                                                                        Interproj IPR007197; Radical_SAM.
Pfam. PF04055; Radical_SAM; I.
Complete protecme.
SEQUENCE 352 AA; 38950 MW; 7EAC944861D3553F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA; 38610 MW; B2AB050D00F03F50 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Putative small hydrophilic protein.
SCO2063 OR SC496.32.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro, IPRO07197; Radical SAM.
PERM, PF04055; Radical SAM; I.
Complete proteome.
SEQUENCE 352 AA; 38610 MW; B2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas.
NCBI TaxID=323;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 77.8
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Gaps

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Pred. No. 15; 1; Mismatches

75.0%;

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Conservative
Best Local Similarity
Matches 6; Conserv
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BLR4770.
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Matches
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Q84VX7
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                 MEDLINE-2196410; PubMed=12000953; MEDLINE-2196410; PubMed=12000953; MEDLINE-2196410; PubMed=12000953; MEDLINE-2196410; Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford, K., Rutter S., Seeger K., Saunders D., Sharp S., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
BMBL: A339111; CAB51455.1;
PIR; 735022; 735092.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 16; Length 55;
Pred. No. 8.2;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U41508; A6000023.1;
- PR; T26046; T26046.
WormPep; W01C8.1; CE05029.
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D65B2FFFBF9FBB59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AA; 6247 MW; 2F34EDC4E906354F CRC64;
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Last annotation update)
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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11 KHPQAERSP 19
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                                                                                                   SEQUENCE FROM N.A.
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Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Bristol N2;
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Waterston R.;
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Length 98;

DB S;

Score 38;

74.5%;

Query Match

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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                         Cheuk R., Chen H., Kim C.J., Shinn P., Bowser D., Carninci P., Chan M.M.; Cheng C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Nemann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Ondera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Saki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

ENEL, BTOGGGS2, AAO42878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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46747 MW; 2024DEEC55F82E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                01-0TN-2003 (TrEMBLrel. 24, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                   415 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR006652; Kelch rep.
InterPro; IPR001005; Myb_DNA_binding.
PROSITE; PS01344; Kelch; 4.
                                                                                                                                                                          084VX7;
01-JUN-2003 (TrEMBLrel. 24, Created)
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                                                                                                                                                   PRELIMINARY;
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                                       13 HPEEKRLP 20
2 HPEAKRMP 9
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Best Local Similarity
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122

PRT;

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P42.
Bacteriophage Mx8.
Viruses, dsDNA viruses, no RNA stage; Caudovirales; Podoviridae; P22-like viruses.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Youderian P., Walthers D., Salmi D., Magrini V., Hartzell P.L.;

Youderian P., Walthers D., Salmi D., Magrini V., Hartzell P.L.;

"Genome organization of temperate Myxococcus phage Mx8.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF396866; AAK94377.1;

SEQUENCE 122 AA; 12811 MW; 6F3E8978D3ADB17A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
70.6%; Score 36; DB
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches
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Q8A5V9
                 RESULT 14
294MS7
AC 094MS
AC 094MS
DT 01-DE
DT 0
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SEQUENCE FROM N.A.

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SEQUENCE TO N.A.

STRAIN-CV. Columbia;

A Theologis A. Ecker J.R., Falm C.J., Federspiel N.A., Kaul S.,

Theologis A. Ecker J.R., Falm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Falm C.J., Federspiel N.A., Kaul S.,

A Theologis A., Ecker J.R., Falm C.J., Craway A.R., Creasy T.H.,

A Chung M.K., Conn L., Conway A.B., Craway A.R., Creasy T.H.,

A Chung M.K., Conn L., Conway A.B., Craway A.R., Creasy T.H.,

A Lin J.B., Goldsmith A.D., Hass B., Hansen N.F., Haghes B., Fujii C.Y.,

A Lin J.L., Jenkins J., Johnson-Hopson C., Khan S., Kwan A., Lam B.,

A Lin J.L., Jenkins J., Johnson-Hopson C., Khan S., Kwan A., Lam B.,

A Lin J.L., Jenkins J., Johnson-Hopson C., Khan S., Kwan A., Lam B.,

A Lin X., Liu S.X., Liu Z.A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Lucros J.S., Maiti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Schwartz J.R., Shinn P., Southwick A.M.,

RA G., Ecterson J., Schwartz J.R., Shinn P., Southwick A.M.,

RA G., Ecterson J., Schwartz J.R., Shinn P., Southwick A.M.,

RA Jan, G., Peterson J., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

BA J. Sequence and analysis of chromosome 1 of the plant Arabidopsis

R. Haliana...,

RE MBL, ACO24261, AAG52629.1; -.

BR FIR 196553. 196553.

RINE PROS17E; PRO10055 Welch rep.

BR ROS17E; PRO10055 Welch rep.

BR ROS17E; PRO10052 Welch rep.

BR PROS17E; PSO0334; WMB_DIA binding.

REM PROS17E; PSO0334; WMB_DIA binding.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                               72.5%; Score 37; DB 16; Length 765; 77.8%; Pred. No. 1.7e+02; Ative 0; Mismatches 2; Indels
DNA Reg. 9:189-197(2002).

BMBL; AP005925; BACS0035.1; -.

InterPro; IPR0089258; SLT dom.

InterPro; IPR008941; TPR-like.

Pfam; PF01464; SLT; 1.

Complete proteome.

SEQUENCE 765 AA; 84473 MW; BF26CB2DEB360326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1036 AA.
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                        Query Match
Best Local Similarity 77...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                94 KHABAKKKP 102
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Q9C8K6
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0; Indels

||||||: 53 HPEAKRL 59 2 HPEAKRM 8

9; Length 122;

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STRAIN=VPL-5482 / ATCC 29148;
STRAIN=VPL-5482 / ATCC 29148;
STRAIN=VPL-5482 / ATCC 29148;
A. Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
A. Chiang H.C., Hooper L.V., Gordon J.I.;
A. Chiang H.C., Hooper L.V., Gordon J.I.;
I. Agnomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
R. Embl., AE016-5934, AA077234.1;
R. GO, GO:0006152, Findralase activity; IEA.
GO, GO:0006152, Finetabolism, IEA.
R. InterPro; IPR00683; Higholase, Nydrlase.
R. InterPro; IPR00583; Higholase, Nydrlase.
R. Princh Pro; IPR005834; Hydrolase.
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0
                                                                                                                                                          Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCSI_TAXID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 224;
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TIGREAMS, TIGRO1509, HAD-SF-IA-v3; 1.
Complete proteome. 224 AA; 24939 MW; DF4ECF1911D09538 CRC64;
                              Q8ASV9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative beta-phosphoglucomutase.
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70.6%; Score 36; DB 16;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 2; Mismatches 0;
224 AA
PRT;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | : | | | 86 YPEAERMP 93
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   Q8A5V9
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Search completed: April 19, 2004, 12:00:13

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959 KHPETKKM 966

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1 KHPEAKRM

Job time : 5.47368 secs

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AAE08578
AAU75220
ABG00986
ABG3321
ABG33847
ABG71291
ABG71291
ABG71291
ABG71291
ABG71291
ABG71291
ABG71291
        April 19, 2004, 11:24:29; Search time 5.29363 Seconds (without alignments) 480.375 Million cell updates/sec
    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                 US-09-832-929-18_COPY_439_447
51
1 KHPEAKRMP 9
                       protein - protein search, using sw model
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Mature hu
Human alb
Human alb
Human alb
Human alb
Human alb
Human mat
Human met
Human ser
Mature fo
B lymphoc
Human ser
Human B i
Glycosyla
Mature hu
Human alb

Aae13115 Aae13311 Abb79006 Abb79006 Abd78278 Abd78278 Abd7828 Abd72321 Abg71291 Abg71291

#### ALIGNMENTS

Human, cytokine, cell proliferation, cell differentiation, gene the vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomodulatory, cancer, leukaemia, nervous system disorders; arthritis; inflammation. AA004431 standard; protein; 106 AA Human polypeptide SEQ ID NO 18323 06-NOV-2001 (first entry) AAO04431;

26-FEB-2001; 2001WO-US004927. WO200164835-A2 Homo sapiens. 07-SEP-2001. 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2002s:\*
6: geneseqp2003as:\*
7: geneseqp2003bs:\*
8: geneseqp2004s:\*

SUMMARIES

Query Match Length DB

Result

rang YT, Liu C, Drmanac RT; WPI; 2001-514838/56. N-PSDB; AAI84362.

Claim 20; SEQ ID NO 18323; 1399pp + Sequence Listing; English.

Human con Yeast cod Novel hum Novel hum Novel hum Novel hum Novel hum Novel hum Mature hu Mature hu Human ser Human

Aau27873 F Aay83949 Aay83949 Aau38949 Aau33074 Aau32896 Aau32896 Aau32896 Aau32896 Aau32897 Aau32897 Aau3289 Aar2655 A

ABG72381 AAP93344 AAP90388

AAO03606 AAU33085 AAV33089 AAU33081 AAU33081 AAU39876 AAU39876 AAU39876 AAU39876

AAR05318 AAR08457 AAR26207

AAR26362 AAR20029 AAR80301 AAO20111 AAW59841 AAY84873

RESULT 1

Total number of hits satisfying chosen parameters:

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000

A\_Geneseq\_29Jan04:\*

Database :

geneseqp1980s:\* geneseqp1990s:\*

1586107 segs, 282547505 residues

BLCSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

score:

о п

Run δ

Sequence:

therapy;

28-FEB-2000; 2000US-00515126. 18-MAY-2000; 2000US-00577409.

(HYSE-) HYSEQ INC.

Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.

The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and

1 KHPEAKRMP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                    Query Match
100.0%; Score 51; DB 4; Length 106;
Best Local Similarity 100.0%; Pred No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         AAO02645 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 16537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                      65 KHPEAKRMP 73
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N-PSDB; AAI82576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 119 AA;
                                                                               Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                AAO02645;
                                                                                                                                                                                                                                                                                                  RESULT 2
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide cherapy, stem cell growth factor; haematopoiesis, tiseue growth factor; immunomodulatory, cancer, leukaemia, nervous system disorders; arthritis; inflammation.
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                                                                                               AA003606 standard; protein; 133 AA.
                                                                                                                                                                                                           Human polypeptide SEQ ID NO 17498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Drmanac RT;
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                                                                                                                                                                      (first entry)
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Best Local Similarity 100...
9, Conservative
    46 KHPEAKRMP 54
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N-PSDB; AAI83537.
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                    AA003606;
                                                          RESULT 3
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AAU33085 standard; protein; 151 AA

AAU33085,

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Gaps

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Query Match 100.0%; Score 51; DB 4; Length 119; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 9; Conservative 0; Mismatches 0; Indels

KHPEAKRMP 86

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nervous system disorder; inflammatory disorder; cell differentiation; anapidogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroporotective; osteopathic; antidiabetic; antiasthmatic; antiallergic; immunostimulant; analgesic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F
Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-2000; 2000US-00577409.
17-JUN-2000; 2000US-00597707.
19-JUN-2000; 2000US-00516807.
19-SEP-2000; 2000US-00664641.
                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US004926.
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                                                                                                                                                                                                                         Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimulation; as anti-inflammatory agents; and in treatment of leukaemias. AUC29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                       Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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                                                                     Novel human secreted protein #3576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 705; 765pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT;
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                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                     WO200179449-A2.
                                                                                                                                                                                                                       Homo sapiens
                         18-DEC-2001
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2000US-00515126.

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Sequences AAU27676-AAU28019 represent full-length polypeptides and contignolypeptides of the invention. The proteins and their associated DNA control of the invention. The proteins and their associated DNA control of the invention. The protein as an analysis of disorder in a mammalian subject such as a human, dog, warious types of disorder in a mammalian subject such as a human, dog, control of the search and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, disorders such as Parkinson's disorders such as Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and disorder, amyotrophic lateral sclerosis, spinal muscular atrophy and wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to anglogenesis, cell proliferation, cell differentiation, stem cell growth factor. Control of over itself the tone control of one control of caugment or replace cells damaged by illness, accidental damage of enetic cartilage, tendons and ligaments and in tissue repair and burn healing. Control of the printed specification, but were obtained in electronic format directly from WIPO control of the printed printe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for detection.
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                                                                                                                                                                                                                                                  Claim 10; Page 127; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.0%;
9; Conservative C
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Best Local Similarity
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the full feature of or predisposition to a disease associated determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the mucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used to express them are also useful for producing the proteins are useful in genetic vaccination, testing and therapy, and can be used to surfacesse stem cell or proliferation, to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or attiluation; as anti-inflammatory agents; and in treatment of leukaemias. AM109510-AM033304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 4; Length 245; 100.0%; Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 705; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU33074 standard; protein; 386 AA.
                                                                                        16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                            Liu C, Drmanac RT;
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                                                                                                                       18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 245 AA;
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                      WO200179449-A2
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                                                       25-OCT-2001.
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AAU33074
       %XCCCCCCCCCCX&X44X8X54X4X4X4X4XAXAXAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonuclectide fragments that were extended. This sequence represents the sequence of the HSA fragment HSA-III encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression vector, yeast host cells carrying the recombinant expression vector and the process for producing human serum albumin in the yeast host cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                       Recombinant; human serum albumin; HSA; yeast codon bias; host cell; overlapping oligonucleotide; expression vector.
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0
                                                                                                                         Yeast codon-biased recombinant HSA protein fragment HSA-III.
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                                                                                                                                                                                                                                                                                                                                                                                                   (HAIJ-) HAIJI BIOENGINEERING CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #3572.
                  AAY83949 standard; protein; 228 AA.
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                                                                                                                                                                                                                                                                                                                                                                  98CN-00102506.
                                                                                                                                                                                                                                                                                                                                   98CN-00102506
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the process for producing hur
especially in secretory mode
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                                                                                      (first entry)
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N-PSDB; AAA10094.
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                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                 17-JUN-1998;
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                                                   AAY83949;
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AAU33081
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for useful an pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to requirate hemantopolessis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias.

AAUZ9510 AAU3101 for the mine acid sequences of novel human
                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #367.
                                                                                                                                                                                               Claim 20; Page 704; 765pp; English
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                                                                    Tang YT, Liu C, Drmanac
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                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 386 AA;
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acide encoding the polypeptides and cells genetically engineers nucleic acide encoding the polypeptides and cells genetically engineers to express them are also useful for producing the proteins. The proteins of a unitational supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AMI29510-AAU33304 represent the amino acid sequences of novel human construction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #3777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU33286 standard; protein; 507 AA.
                                                            Claim 20; Page 206; 765pp; English
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26-JAN-2001; 2001US-00770160.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 401 AA;
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with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide wectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU25510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
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Sequence 507 AA;

Gaps .; 0 100.0%; Score 51; DB 4; Length 507; 100.0%; Pred. No. 0.66; 1. Indels 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative 1 KHPEAKRMP 9 à

215 KHPEAKRMP 223

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AAU32994 ID AAU

AAU32994 standard; protein; 507 AA.

AAU32994;

(first entry) 18-DEC-2001 Novel human secreted protein #3485.

Human, vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia. 

Homo sapiens.

WO200179449-A2

25-OCT-2001

16-APR-2001; 2001WO-US008656

18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160.

(HYSE-) HYSEQ INC

Drmanac Liu C, YT, Tang

RT

WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

Claim 20; Page 696; 765pp; English

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the motelic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used

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as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis; and in bone, cartilage, tendon stand/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU25510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
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Sequence 507 AA;

Gaps ö 4; Length 507; 100.0%; Score 51; DB 4; Length 50 100.0%; Pred. No. 0.66; iive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.v.

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215 KHPEAKRMP 223 σ 1 KHPEAKRMP

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AAU29877 standard; protein; 550 AA.

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AAU29877;

entry) (first 18-DEC-2001 Novel human secreted protein #368.

Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration; immune suppression, immune stimulation, anti-inflammatory, leukaemia.

Homo

WO200179449-A2.

25-OCT-2001

16-APR-2001; 2001WO-US008656.

18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160.

(HYSE-) HYSEQ INC

Liu C, Drmanac RT; Lang YT,

WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

Claim 20; Page 206; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used a nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopodesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimate and relations as anti-inflammatory agents; and in treatment of leukaemias.

Secreted proteins of the invention 

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The synthetic gene was constructed by designing a nucleotide sequence in which the codons which are most frequently used by the chosen non-human host were selected. In this case, it is yeast cells (LL20; Leu2-3; 112, His 3-11, 15). The synthetic HSA gene was assembled from 24 coligonucleotide blocks. HSA is used in therapy for the treatment of hypovolaemia, shock and hypoalbuminaemia. It is also used as an additive in perfusion liq. for extracorporeal circulation and as an experimental antigen. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Artificial gene coding for authentic human serum albumin - constructed on
the basis of codons most frequently used by chosen non-human host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human serum albumin; mature protein; new polypeptides; plasma expanders.
                                                                            mature human serum albumin (HSA) as encoded by artificial
                                                                                                                              Mature human serum albumin; artificial gene; oligonucleotide block;
hypobolaemia; shock; hypoalbuminaemia.
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100.0%; Score 51; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; pp. 11-16; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                          (SKAN-) SKANDIGEN AB.
(WAGY ) MTA SZEGEDI BIOLOG KOEZPONTI.
(VEPE-) VEPEX CONTRACTOR LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90388 standard; protein; 585 AA.
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(first entry)
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N-PSDB; AAN90997.
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25-MAR-2003
01-NOV-1989
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                                                                                   Sequence of
                                 25-MAR-2003
23-JUN-1990
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AAP93344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to testing human cancer cells, comprising obtaining cancer cells from the patient and contacting the cell ex vivo with an antibody to the receptor for human albumin. The method is useful for testing human cancer cells in particular breast and prostate cancer cells. The present sequence is mature human serum albumin, HSA. The antipoliferative effect of HSA was assayed in an experiment included in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Testing human cancer cells, especially breast and prostate cancer cells, by contacting cancer cells obtained from biopsy of a patient ex vivo with antibody specific to human albumin receptor.
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prostate cancer; anti-proliferative.
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100.0%; Score 51; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels
                100.0%; Score 51; DB 4; Length 550; 100.0%; Pred. No. 0.72; ive 0; Mismatches 0; Indels
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Misc-difference 241. 242
/note= "Encoded by GTCCACGG"
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                                                                                                                                                                                                                ABG72381 standard; protein; 584 AA.
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                                                                                                                                                                                                                                                                                                                       Mature human serum albumin #2
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                                                       Conservative
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                                                                                                                         404 KHPEAKRMP 412
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N-PSDB; ABX13582.
                                                                                         1 KHPEAKRMP 9
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                      Query Match
Best Local Similarity
Matches 9; Conserv
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19-DEC-1996;

RESULT 14
AAP93344
ID AAP93

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05-SEP-2002

Homo sapiens

10-FEB-2003

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us-Uy-654-729-Io COpy 159 141/ . rag

88EP-00310000. 28-JUN-1989.

WOII WEL TA T2:7:7:77 7004

Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ; (DELZ ) DELTA BIOTECHNOLOGY LTD. 87GB-00025529. WPI; 1989-186464/26. N-PSDB; AAN90128. 30-OCT-1987; 

New N-terminal fragments of human serum albumin - esp. useful as blood plasma expanders.

Disclosure, Fig 2; 20pp; English.

Mature protein of human serum albumin (see corresp. AAN90128). Used to make new N-terminal fragments which are used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

Sequence 585 AA;

0; Gaps Query Match
100.0%; Score 51; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels

; 0

à qq Search completed: April 19, 2004, 11:51:21 Job time : 6.29363 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

COPY 439

78-07-977-777-78

1011 Apr 13 13:2/:21 2004

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 12:00:25 ; Search time 3.78947 Seconds (without alignments)

654.724 Million cell updates/sec

Title: US-09-832-929-18\_COPY\_439\_447

Sequence: 1 KHPEAKRMP 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1124875 seqs, 275673149 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/Deny PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_TRW PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/USO6\_NEW PUB.pep:\*

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18: /cgn2\_6/ptodata/2/pubpaa/USO0B\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 2, Appli	Sequence 445, App	Sequence 26, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 445, App	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 11, Appl	31,	Sequence 34, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli
SUMMARIES		OI.	US-09-929-552-2	US-09-932-613-445	US-09-984-010-26	US-09-833-041-18	US-09-833-117-18	US-09-932-322-445	US-09-832-501-18	US-09-833-118-18	US-09-833-245-18	US-10-424-999-11	US-10-425-000-31	US-10-433-108-34	US-10-153-064-5	US-10-153-604A-5	US-10-319-263-1
		DB	9	10	10	10	10	10	10	11	11	12	12	12	13	14	74
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	av ;	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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-10-319-26	US-10-414-4	US-10-4	US-10-413-8	0-413-83	US-10-413-83		US-10-414-38	US-10-414-386	US-10-233-6	US-10-462-2	US-09-984-01	US-09-919-03	US-10-609-34	US-10-153-064	US-10-153-60	US-10-365-	US-09-984-186-2	US-10-237-667	US-10-	US-10-237-866	US-10-	US-10-237-62	US-10-433-108-1	US-10-433-108-1	US-10-433-1	US-10-433-108-1	US-10-433-108-1	US-10-153-	
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1
US-09-929-552-2
i Sequence 2, Application US/09929552
j Sequence 2, Application US/09929552
j Sequence 2, Application US/09929552
j Patent No. US20020123080A1
gENERAL INFORMATION:
GENERAL INFORMATION:
ITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF ENCURENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Median & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
GITY: San Francisco
GITY: San Fra

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Gaps

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/ Match 100.0%; Score 51; DB 10; Length 585; Local Similarity 100.0%; Pred. No. 0.98; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 0.98;
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Publication No. US20030171267A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Radeghi, Homa
APPLICANT: Padeghi, Homa
TITLE OF INVENTION: Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF 43.
CURRENT APPLICATION NUMBER: US/09/833,117
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR PLING DATE: 2000-04-12
PRIOR PLING DATE: 2000-04-12
PRIOR PLING DATE: 2005-04-12
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US-09-33-041-18

Sequence 18, Application US/09833041

Sequence 18, Application US/09833041

GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, William A.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF545

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/229,358

PRIOR APPLICATION NUMBER: 60/226,931

PRIOR APPLICATION NUMBER: 60/226,931

PRIOR PLING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/199,384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PRECENTIN OF THE SES

LENGTHE: 585
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APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 19-DEC-1996
INFORMATION FOR SEG ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 aning acids
                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
WOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: Homo Sapiens
US-09-833-041-18
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Best Local S:
Matches 9
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: IBM PC COMPathle
COMPUTER: IBM PC COMPathle
COMPUTER: PERM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPathle
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR PERLICATION NUMBER: US/09/984,010
FILING DATE: 25-UUN-1998
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Publication No. US20030104578A1
GENERAL INPORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
                                                                                                                                                                                                                                                                                                                                                                Sequence 445, Application US/09932613

Sequence 445, Application US/09932613

Publication No. US20030091565A1

GENERAL INFORMATION:

APPLICANT: Hanan Genome Sciences, Inc.

APPLICANT: Petter, M. Daniel

APPLICANT: Petter, M. Daniel

APPLICANT: Pieming, Tony J.

APPLICANT: Pieming, Tony J.

APPLICANT: BIEMING POLYPEPTIDES AND METHODS BASED THEREON

FILE REFRENCE: Dyx-025.1 PCT; DYX-025.1 US

CURRENT APPLICATION NUMBER: US/09/932,613

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: PatentIn version 3.1

SEQ ID NO 445

LIENGTH: 585
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Pred. No.
                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                TYPE: amino acid
                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: HomoSapiens
US-09-932-613-445
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US-09-932-613-445
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US-09-984-010-26
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Sequence 18, Application US/0983245

Publication No. US2C040010134A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT

CURRENT FILING DATE: 2001-04-12

PRIOR PILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/259, 358

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PALENT NOW SECOND OF SECOND NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PALENT NOW SECOND OF SECOND NOS: 2267

SEQ ID NO 18

LENGTH: 585

TYPE: RRT

ORGANISM: Homo Sapiens
US-09-833-245-18
                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/09833118
Publication No. US20030219875A1
GENERAL INFORMATION
APPLICANT: Haseltine, William A.
ITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF644
CURRENT FLING DATE: 2001-04-12
PRIOR APPLICATION UNMERR: US/09/833,118
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION UNMERR: 60/229,388
PRIOR APPLICATION UNMERR: 60/226,931
PRIOR APPLICATION UNMERR: 60/199,384
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
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  ; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-832-501-18
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ORGANISM: Homo Sapiens
US-09-833-118-18
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US-09-833-118-18
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Publication No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Delter, James P.
APPLICANT: Delter, M. Daniel
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Potter, M. Daniel
APPLICANT: Planing, Tony J.
APPLICANT: Planing, Tony J.
APPLICANT: Planing, Tony J.
APPLICANT: Potter, M. Daniel
APPLICANT: Potter, M. Daniel
APPLICANT: Potter, M. Daniel
APPLICANT: Potter, M. Daniel
APPLICANT: Planing, Tony J.
APPLICANT: Planing, Tony J.
APPLICANT: Story D. NUMBER: US/09/932,322
CURRENT PILING DATE: 109/09/932,322
CURRENT PILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
LENGTH: 585
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100.0%; Score 51; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels (
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PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 18
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo Sapiens
US-09-833-117-18
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ORGANISM: HomoSapiens
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100.0%; Score 51; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels C
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| Publication No. US20020142814A1
| GENERAL INFORMATION:
| APPLICANT: Bell et al.
| TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
| FILE REPERENCE: PFS56
| CURRENT APPLICATION NUMBER: US/10/153,064
| CURRENT PLING DATE: 2002-05-24
| PRIOR PRILICATION NUMBER: 60/293,212
| PRIOR PRILICATION NUMBER: 60/293,212
| PRIOR PRILICATION NUMBER: 00/105-25
| NUMBER OF SEQ ID NOS: 137
| SEQ ID NO 5
| LENGTH: 585
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Publication No. US20030143191A1
GENERAL INFORMATION:
APPLICATION SAPPLICATION:
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION UNMBER: US/10/153,604A
CURRENT APPLICATION NUMBER: 60/293,212
                                                                                             RESULT 12
US-10-433-108-34
Sequence 34, Application US/10433108
Publication No. US20040053370A1
GENERAL INFORMATION:
APPLICATE III Lilly and Company
ITLE OF INVENTION: GLP-1 FUSION PROTEINS
FILE REFERENCE: X-13391
CURRENT PILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-29
NUMBER OF SEQ ID NOS: 35
SOFURARE: Patentin version 3.1
SEQ ID NO 34
ILENGTH: 585
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US-10-433-108-34
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US-10-153-064-5
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nesbit, Mark
APPLICANT: Nesbit, Mark
APPLICANT: Nesbit, Mark
APPLICANT: Sameron, Beatrice
APPLICANT: Salanche, Francis
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REREAGNES: STO1027-A
CURRENT PRILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR APPLICATION NUMBER: 10/233,675
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.2
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APPLICANT: Neebit, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Clanch, Beatrice
APPLICANT: Clanch, Francis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
TITLE OF INVENTION: Argiogenesis
TITLE OF INVENTION: Argiogenesis
TITLE OF INVENTION: Argiogenesis
TITLE OF INVENTION: Argiogenesis
CURRENT APPLICATION NUMBER: US/10/425,000
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
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100.0%; Score 51; DB 11; Length 585; 100.0%; Pred. No. 0.98; tive 0; Mismatches 0; Indels
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100.0%; Score 51; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                       RESULT 10
US-10-424-999-11
Squence 11, Application US/10424999
Publication No. US20040052810A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/10425000 Publication No. US20040052777A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                      Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                  439 KHPEAKRMP 447
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ID NO 11
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US-10-425-000-31
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LENGTH: 585
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  Query Match
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1 KHPEAKRMP 9

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PRIOR PITION DATE: 2001-05-25

WUNDER OF SECTION ONS: 13.7

SECTION ON USECONOMY.

RESULT 15

DD 439 KHPBAKEMP 447

RESULT 15

SEQUENCE 1. APPLICANT: LAW DAY.

APPLICANT: L
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Db 439 KHPEAKRMP 447

1 KHPEAKRMP 9

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Search completed: April 19, 2004, 12:54:59 Job time : 3.78947 secs

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TELEFAX: (908) 771 6159
TELEX: 2194844
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-153-799-14
                                                                                                           April 19, 2004, 11:40:29 , Search time 1.3795 Seconds (without alignments) 336.813 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    389414 segs, 51625971 residues
                                                                                                                                                                                     US-09-832-929-18_COPY_280_288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                                                   1 EKPLLEKSH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
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Sequence 127, App Sequence 129, App Sequence 125, App Sequence 121, App Sequence 101, App Sequence 4, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5132, Appli
                                                                  US-10-153-064-129

US-10-153-064-129

US-10-153-064-129

US-10-153-064-101

US-10-153-064-101

US-08-256-938-2

US-08-256-938-4

US-08-97-689-16

US-09-984-186-16

US-08-97-956A-3

US-08-87-956A-3

US-08-88-196A-1

US-08-48-196A-1

US-08-48-196A-1

US-08-48-196A-1

US-08-48-196A-1

US-08-48-196A-1

US-08-48-196A-1
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US-08-448-196A-6
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#### ALIGNMENTS

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COMPUTER READABLE FORM:

MODIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SPECIAL CANDER: IBM COMPATER
COMPUTER: IBM COMPATER
COMPUTER: SPECIAL CANDER: 
Sequence 19, Application US/08153799
Fatent No. 5766883
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
```

```
RESULT 3

US-09-984-176-1

US-09-984-176-1

Sequence 1, Application US/08984176

Patent No. 5948609

GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C

APPLICANT: HOLOSEH X

TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

TITLE OF INVENTION: UNDER: US/08/984,176

CURRENT FILING DATE: 1997-12-03

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 1

LENGTH: 585

TENGTH: 585

TENGTH: 585

TENE ORGANISM: Home sapiens
US-08-984-176-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS-08-702-572-2

Sequence 2, Application US/08702572

Sequence 2, Application US/08702572

Sequence 3, Application Sequence

APPLICANT: Rerry Williams, Sean M
APPLICANT: Gibbert, Sarah C

TITLE OF INVENTION: Yeast Strains and Modified Albumins

NUMBER OF SEQUENCES: 16

NUMBER OF SEQUENCES: 16

STREET: 1020 First Avenue

CITY: King Of Prussia

STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 47; DB 2; Length 585; 100.0%; Pred. No. 0.33; ative 0; Mismatches 0; Indels
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COUNTRY: 19406-1310
COMPUTER: READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: READABLE F10ppy disk
COMPUTER: MCIOSOft Word 6.0
CURRENT APPLICATION NUMBER: US/08/702,572
FILING DATE: 1-MAR-1996
REPLICATION NUMBER: WO 95/23857
FILING DATE: 1-MAR-1994
APPLICATION NUMBER: GB 9404270.2
FILING DATE: 5-MAR-1994
APPLICATION NUMBER: GB 384
RESTRATION NUMBER: GB 384
RESTRATION NUMBER: 38,384
RESTRATION NUMBER: CE0114 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                     1 EKPLLEKSH 9
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US-08-448-196A-3
US-08-448-196A-3
Sequence 3, Application US/08448196A
Patent No. 5780594
TITLE OF INVENTION: CARTER, DANIEL C.
TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR TITLE OF INVENTION: RELATED PROTEINS
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASA
STREET: MARSHALL SPACE FLIGHT CENTER
STATE: ALABAMA
COUNTRY: ALABAMA
COUNTRY: USA
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100.0%; Score 47; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                              NAME/KEY: Region
LOCATION: 369..419
OTHER INFORMATION: /note= "Alternative C-termini of OTHER INFORMATION: HSA(1-n)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MODIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
LOCATION: 1..585
OTHER INFORMATION: /note= "Amino acid sequence of
OTHER INFORMATION: natural HSA"
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NAME: BROAD UR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEPAX: 205-544-0021
TELEPAX: 205-544-0021
TELEPAX: 205-544-0021
TELEPAX: 205-544-0021
TELEPAX: 205-544-0021
TELEPAX: 205-644-0021
TELEPAX: 205-644-0021
TELEPAX: 205-644-0021
TELEPAX: 105-621
TELEPAX: 205-644-0021
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FRAGMENT TYPE: N-terminal
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 EKPLLEKSH 288
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CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 585
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MOLECULE TYPE: protein
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                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapiens
US-10-153-064-5
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08769746

Patent No. 6274305

GENERAL INFORMATION:
APPLICANT: Somenschein, Carlos
APPLICANT: Socion Ana M.
TITLE OF INVENTON: Inhibiting Proliferation of Cancer Cells
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
STREET: San Francisco
STREET: California
COUNTRY: United States of America
COUNTRY: United States of America
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100.0%; Score 47; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY COUNTY CONTROLL CONTROLL CONTROLL COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Beatin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,746
FILING DATE: 19-DEC-1996
CLASSIFICATION NUMBER: 32,837
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE CONTUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: S88 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-10-153-064-5
Sequence 5, Application US/10153064
; Patent No. 665485
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; FILLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 3;
Pred. No. 0.33;
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Best Local Similarity 100.0%;
Matches 9; Conservative 0;
         SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , TOPOLOGY: linear, MOLECULE TYPE: protein US-08-769-746-2
                                                    TYPE: amino acid
TOPOLOGY: linear
MULECULE TYPE: protein
US-08-702-572-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 EKPLLEKSH 288
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US-08-769-746-2
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Sequence 3, Application US/08222619
Patent No. 5662352
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STREET: 1840 DeHavilland Drive
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICANTON DATA:
FILMAC DAMPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels
Query Match
100.0%; Score 47; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels
                           0.33; 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sreekrishna, Kotikanyadan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/08433037; Patent No. 5707828; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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PCT-US95-04075-3; Sequence 3, Application PC/TUS9504075; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 EKPLLEKSH 312
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                                                                                                                  304 EKPLLEKSH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
US-10-153-064-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EKPLLEKSH 9
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                                                                                                                                                                                                        RESULT 10
US-10-153-064-7
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APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Tachopp, Uterg F.
APPLICANT: Tachopp, Uterg F.
TITLE OF INVENTION: EXPESSION OF HUMAN SERUM ALBUMIN IN TITLE OF INVENTION: EXPESSION OF HUMAN SERUM ALBUMIN IN TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDEDS ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STATE: New York
COUNTY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTY: US.A.
ZIP: 11530-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
COMPUTER: BM FO Compatible
COMPUTER: BM FO Compatible
COMPUTER: BM FO Compatible
COMPUTER: BM FO Compatible
COMPUTER: BM FO COMPATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MA-1995
CLASSIFICATION NUMBER: 31,346
REPRENCE/DOCKET NUMBER: 31,346
REP
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100.0%; Score 47; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.34;
Mismatches 0; Indele
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100.0%; Pred. No. v...
0; Mismatches
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Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Philip Lake
TILE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR APPLICATION NUMBER: 60/022,689
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 609
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
US-08-433-037-4
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US-08-897-956A-2
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Sequence 977, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Burness, Michael
APPLICANT: Burness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPRESENT APPLICATION NUMBER: US/09/976,594
CURRENT APPLICATION NUMBER: 60/240,409
PRIOR PLILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
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Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.34;
tive 0; Mismatches 0; Indels
Sequence 7, Application US/10153064

Patent No. 6663485

GENERAL INFORMATION:
APPLICANT: Ball et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REPERENCE: PFS56
CURRENT APPLICATION WUMBER: US/10/153,064

CURRENT APPLICATION WUMBER: 60/293,212

PRIOR APPLICATION WUMBER: 60/293,212

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SEQ ID NO 7

LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
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RESULT 14
US-09-984-186-2
Sequence 2, Application US/09984186
Sequence 2, Application US/09984186
Sequence 2, Application US/09984186
Sequence 2, Application US/09984186
Sequence 2, Application:
Batanier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Seh, Patrice 1 NOWEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 47; DB 2; Length 610; 100.0%; Pred. No. 0.35;
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
COREATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-0ct-2001
CLASSIFICATION: cunknown.
PRIOR APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 32-UTL-1994
APPLICATION NUMBER: PCTFR93/00085
FILING DATE: 28-UTL-1994
APPLICATION NUMBER: PCTFR93/00085
FILING DATE: 28-UTL-1994
APPLICATION NUMBER: PCTFR93/00085
FILING DATE: 28-UTL-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMICH Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: P-38,619
REFERENCE/CATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: SB-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REGISTRATION NUMBER: GT92006-US
FELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3899
TELEPHONE: (610) 454-3899
TELEPHONE: (610) 454-3898
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACATERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid

COPOLOGY: Linear

MOLECULE TYPE: protein
US-08-797-689-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9, Conservative
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Sequence 2, Application US/08797689

Patent No. 5876599

GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Veh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: REPERRATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegaville
STRATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 47; DB 5; Length 609; Best Local Similarity 100.0%; Pred. No. 0.34; Matches 9; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSES: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
CONTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Batentin Release #1.0, Version #1.25
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acids
STRANDENESS: unknown
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Mord 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIPFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
FRICK APPLICATION NUMBER: BR 92/01064
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
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us-09-832-929-18_copy_280_288.rai
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SEQUENCE CHARACTERISTICS:

LINGTH: 610 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: procesin
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-984-186-2

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No: 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy ERLLEXSH 312

RESULT 15

US General 13, Application US/10153064

DD 30.4 EKLLEXSH 312

RESULT 15

US General INVORMATION:
TITLE OF IN
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Search completed: April 19, 2004, 12:05:20 Job time : 1.3795 secs

346 EKPLLEKSH 354

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1 EKPLLEKSH 9

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April 19, 2004, 11:37:59; Search time 0.853186 Seconds (without alignments) 789.208 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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38
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Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                               1 AAADPHE 7
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1: pir1:*
2: pir2:*
3: pir3:*
                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                               Scoring table:
                                                            OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                               Searched:
                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	ption	central of micros	erum albumin pre	ical p	щ	38e ex		hypothetical prote	ISS family transpo	hypothetical prote	probable hexosyltr	probable transfera	X-pro aminopeptida	hydroxypyruvate re	hypothetical prote	ribulose-5-phospha	probable pyrroline	hypothetical prote	hypothetical prote	~		al			subur	ted 1	probable rpoC prot	raria		probable PPE prote
SUMMARIES	ΩI	A47391	ABHUS	D71311	78	2	H75392	4	AH3101	B98185	C70859	E87123	A69504	AH3200	C72631	872623	D71281	T32969	T34213	725863	<b>A96601</b>	T49415	A28706	A84210	D87145	S31146	G70535	A58881	C75544	G70738
	DB	2	Н																											
	Length	009	609	177	575	740	238	308	345	351	414	438	363	421	105	238	263	272	300	345	418	634	713	883	ന	1316	ന	Ф	152	232
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	Score	1 60	38	34	34	34	33	e e	33	93	33	e e	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	30	30
	Result No.	:	2	m	4	Ŋ	φ	7	00	σι	10	디	12	13	14	15	16	17	18.	19	20	21	22	23	24	25	26	27	28	29

RESULT 2

serum albumin precursor [validated] - human
NyAlternate names: preproalbumin
NyAlternate names: preproalbumin
NyAlternate names: preproalbumin
NyAlternate names: preproalbumin
NyContains: Kinetensin
C;Species: Homo sapiens (man)
C;Date: 29-Jul:1981 #sequence\_revision 31-Jan-1997 #text\_change 17-Mar-2000
C;Accession: A93743; A93936; I36427; IS9286; IS9313; G01747; S55314; A93420; S06422; S3:
R;Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seebu:
Nucleic Acids Res. 9, 6103-6114, 1981
A;Rithe: The sequence of human serum albumin cDNA and its expression in Escherichia col:
A;Reference number: A93743; MUD:82081882; PMID:6171778
A;Residues: 1-419, KK, 421-609 <LAM>
A;Residues: 1-419, KK, 421-609 <LAM>
A;Residues: 1-419, KK, 421-609 <LAM>
A;Residues: RMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:CAA2:
R;Dugaiczyk, A.; Law, S.W.; Dennison, O.E.
Proc. Natl. Acad. SGI. U.S.A. 79, 71-75, 1982
A;Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.
A;Reference number: A93936; MUID:82105994; PMID:6275391

RESULT 1 AAAN CONTENT NATION AAN	30         78.9         280         2         T29200         hypothetical prote           30         78.9         308         2         T29754         hypothetical prote           30         78.9         308         2         T36029         hypothetical prote           30         78.9         449         2         T08309         conserved hypothet           30         78.9         538         2         F69215         adenine deaminase           30         78.9         556         2         H69279         ferradoxin-nitrite           30         78.9         556         2         H83729         pyruvate carboxyla           30         78.9         557         2         H83729         pyruvate carboxyla           30         78.9         556         2         H81654 <th>RESULT 1  A47391  Serum albumin precursor - rhesus macaque C;Deccession malatta (rhesus macaque) C;Deccession A47391  C;Deccession A47391  C;Deccession A47391  C;Deccession A47391  C;Deccession A47391  Droven A5 Sakanoto, V; Madison, U; Davis, E; Smith, D.G.; Dwulet, J.; Putnam, A7Title: CDNA and protein sequence of polymorphic macaque albumins that differ in bill A7Title: CDNA and protein sequence of polymorphic macaque albumins that differ in bill A; Reference number: A47391; MUID:93211971; PMID:8460152  A; Constitus: B/B homozygote A; Accession A47391  A; Mocession A</th> <th>378 AAADPHE 384</th>	RESULT 1  A47391  Serum albumin precursor - rhesus macaque C;Deccession malatta (rhesus macaque) C;Deccession A47391  C;Deccession A47391  C;Deccession A47391  C;Deccession A47391  C;Deccession A47391  Droven A5 Sakanoto, V; Madison, U; Davis, E; Smith, D.G.; Dwulet, J.; Putnam, A7Title: CDNA and protein sequence of polymorphic macaque albumins that differ in bill A7Title: CDNA and protein sequence of polymorphic macaque albumins that differ in bill A; Reference number: A47391; MUID:93211971; PMID:8460152  A; Constitus: B/B homozygote A; Accession A47391  A; Mocession A	378 AAADPHE 384
	о п п п п п п п п п ч ч ч ч ч ч ч ч ч ч	RESULT 1 A47391 Serum albumin prec C;Species: Macaca C;Species: Macaca C;Accession: A4739 R;Watkins; S.; Sak Proc. Natl. Acad. A;Reference number A;Contents: BLB hA;Contents: Drelimin A;Residues: prelimin A;Residues: prelimin A;Residues: 1-600 A;Cross_reference A;Residues: 1-600 A;Cross_reference A;Residues: 1-600 A;Cross_reference A;Residues: 1-600 A;Cross_reference C;Superfamily: sex F;11-194/Domain: F;105-584/Lomain: F;105-584/Lomain: F;105-584/Lomain: B;113-386/Lomain: F;105-584/Lomain: Antches A3AAI AAAI	

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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; W;
B;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; W;
B;Jochen B;Jophys. Res. Commun. 136, 983-988, 1986
A;Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A;Reference number: A03239; MUD:86242180; PMID:3087352
A;Accession: A03239
A;Molecule type: protein
A;Residues: 166-173, 'L' <AMOS-
A;Title: Mutations in genetic variants of human serum albumin found in Italy.
A;Reference number: A38255; MUD:91062352; PMID:2247440
A;Residues: 76-111 <AML>
A;Accession: C38255
A;Molecule type: protein
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A;Residues: B2-105,'K', 107-110
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A;Accession: A38255
A;Molecule type: protein
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A;Rolecule type: protein
B;Rolecule type: protein
A;Tile: Atomic structure and chemistry of human serum albumin.
A;Tile: Atomic structure and chemistry of human serum albumin.
A;Reference number: A46756; WUID:9234427; PMID:1630489
A;Contents: annotation; X-ray crystallography, 2.8 angstroms
B;Rorwi, J.R.; Shocklay, P.; Behrens, P.Q.
B;The Chamistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-40,
B;The Chamistry and Physiology of the Human structure and disulfide bonds
B;Contents: annotation; Aree-dimensional structure and disulfide bonds
B;Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect Czech Chem. Commun. 42, 564-579, 1977
A;Tile: Disulfide bonds in human serum albumin.
A;Reference number: A90330
A;Contents: annotation; disulfide bonds
A;Tile: Lysine residue 240 of human serum albumin is involved in high-affinity binding
A;Reference number: A90299; WUID:731866055
A;Contents: annotation; bilirubin-binding site
B;Peters, T.; Reed, R.G.
in Albumin: Structure, Biosynthesis, Punction, Peters, J., and Sjoholm, I., eds., 11-20,
A;Reference number: A94408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Title: The Structural characterization and bilirubin-binding properties of a A, Reference number: 833298; MUID: 93292504; PMID: 8513793
A, Accession: 833298; MUID: 93292504; PMID: 8513793
A, Accession: 833298
A, Molecule type: protein
A, Residues: 255-263, "E', 266-281 < MINI>
A, Residues: 255-263, "E', 266-281 < MINI>
A, Note: this variant is designated albumin Herborn
R, Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, Blichim. Biophys. Acta 1119, 212-218, 1992
A, Title: Two alloalbumins with identical electrophoretic mobility are produced A, Reference number: 821078; MUID: 92190239; PMID: 1347703
                                                                                                                                                                                                                                                                                         by the
                                               A;Accession: S17599
A;Molecule type: protein
A;Reaidues: 25-54;334-357;431-447 <KAU>
A;Reaidues: 25-54;334-357;431-447 <KAU>
A;Reaidues: 25-54;334-357;431-447 <KAU>
A;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol: 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed B;Reference number: 445800; MUID:89341406; PMID:2474609
A;Accession: A45800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 76-83, 7K', 85-106 <GAL3>
A; Note: this variant is designated albumin Torino
R; Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. V Biochem. 214, 437-444, 1993
A; Title: The structural characterization and bilirubin-bi
        A;Reference number: S17599; MUID:92126241; PMID:1772598
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Annocession: A33356
Annocession: A35357
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Annoce
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A;Molecule type: protein
A;Residues: 45-67;141-160;311-337;469-490;570-581 <FIN>
R;Kausler, E.; Spiteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A;Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
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He

albumin

produced by

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probable fprB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: C70781
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Mamlin, N.; Holroyd, S; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Stetus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-575 <COL>A;Residues: 1-575 <COL>A;Residues: 1-575 <COL>A;Residues: 1-576 <COL>A;Residues:
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C;Species: Archaeoglobus R.B.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso: FixIenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso: FixIenk, H.P.; Clayton, L.; Coverbeek, R.; Gocayne, J.D.; Weidman, W.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaer A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69420
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-740 cKLE>
A;Residues: 1-740 cKLE>
A;Residues: 1-740 cKLE>
A;Cross-references: GB:AR001009; GB:AR000782; NID:g2689332; PIDN:AAB89876.1; PID:g264921
C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation faci
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 575;
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100.0%; Pred. No. 27;
iive 0; Mismatches 0
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Pred. No. 36;
1; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative 1
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Best Local Similarity 100.
Matches 6; Conservative
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606 AAREPHE 612
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                                                                                                                                 85 AAVDPHE
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E69420
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A; Contents: annotation; binding sites

R; Asarper, M. B.; Duggiczyk, A.

Am. J. Hun. Genet. 35, 565-57, 1983

A; Rtla: Lingago of the evolutionarily-related serum albumin and alpha-fetoprotein genes
A; Reference number: A90029; Multio:8329982; PMID:6192711

R; Malker, J.E.
FBSS lett. 66, 173-175; Multio:8329982; PMID:955075

A; Mote: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicyclic acid
A; Contents: annotation of Lyg(190) as the primary binding site for pyridoxal S·phospha
A; Mitte: Login mumber: A56294; Multi:918081; PMID:955075

A; Mote: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicyclic acid
R; Nohmey, J.P.; Rona, M.L.; Feldhoff, R.C.
RSB lett. 663, 193-77

A; Mote: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; A; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; A; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; D; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; D; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; D; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; D; Note: the nonenzymatic binding of pyridoxal phosphate (Sidentics: Alarge number of variants of human serum albumin, acrea bunding predicted 4315
C; Comment: Serum albumin, a prediction; metal binding; phosphoprotein; plasma; pyridox
C; Moters-references: Garma albumin separa homology 4313-
F; 21-34/Domain: serum albumin separa homology 432-
F; 21-34/Domain: serum albumin separa homology 433-
F; 21-34/Domain: serum albumin serum albumin
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D71311
hypothetical protein TP0552 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: 24-Vul.1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: D71311
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwir rson, J.; Khalak, H.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: D71311
A;Aolecule type: DNA
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;COL>
A;Residues: 1-177 <COL>
A;Residues: 1-177 <COL>
A;Genetics:
A;Genetics:
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100.0%; Score 38; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels
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89.5%; Score 34; DB 2; Length 177;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 1; Indels
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A; Gene: AGR L 863gl
A; Map positIon: linear chromosome
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7%;
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-351 <KUR>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Datces: Arabidopsis thaliana (mouse-ear cress)
C;Datcession: F8647
C;Accession: F8647
C;Accession: F8647
C;Accession: F8648
C;A
C: Accession: H75392
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shon, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Vanter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;ittle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75392
A;Accession: H7
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1S5 family transposage tnp [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH3101
C;Accession: A
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A,Residues: 1-308 <STO>
A,Gendidues: 1-308 <STO>
A,Cross-references: GB:AE005172; NID:g8671835; PIDN:AAF78398.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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86.8%; Score 33; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
Matches 6; Conserv
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C;Accession: B98185
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 23, 2328, 2028, 2021
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tw A;Reference number: A97359; MUID:21608551; PMID:11743194
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A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AGR L 863g1 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
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                      A;Accession: AH3101
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45230.1; PID:g17742912; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: tnp
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE007870; PIDN:AAK89004.1; PID:g15158792; GSPDB:GN00170
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Pred. No. 26;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                Length 345,
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A; Reference number: AB2577; MUID:21608550; PMID:11743193
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Pred. No. 25;
0; Mismatches
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ribulose-5-phosphate-epimerase (EC 5.1....) - yeast (Saccharomyces cerevisiae)
NyAlternate names: PoS18 protein; protein J0731; protein YJ121c
C)Species Saccharomyces crevisiae
C;Species Saccharomyces crevisiae
C;Date: 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: S72623; S51587; $56902
Mol. Gen. Genet. 252, 456-464, 1996
A;Title: Mutant that show increased sensitivity to hydrogen peroxide reveal an importan A;Reference number: S72623; MUID:97033550; PMID:8879247
A;Reference Number: S72623
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein APE1506 - Aeropyrum pernix (strain K1)
C.Species: Aeropyrum pernix
C.Species: Aeropyrum pernix
C.Species: Aeropyrum pernix
C.SACCESSION: C72631
S.RAWATABAYASI, Y. Y. HIND. Y.; HORIKAWA, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A.Fitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A.Reference number: A72450; MUID:99310339; PMID:10382966
                                                            C;Accession: AH3200
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, R;Wood, D.W.; Setubal, J.C.; Gant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80505.1; PID:d1044291; PID:g51
A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                        ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Aefestence number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AH3200
                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <KUNA
A;Residues: 1-421 <KUNA
A;Cross-references: GB:AE008687; PIDN:AAL46022.1; PID:g17743779; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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Pred. No. 18;
1; Mismatches 0; Indels
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C,Superfamily: Pyrococcus abyssi hypothetical protein PAB1021
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51;
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Pred. No. 51;
1; Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 85.7%;
Matches 6; Conservative
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A,Molecule type: DNA
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: O'-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C;Accession: B87123
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutherford, K.M.
A;Title: Massive gene decay in the leprosy bacillus.
A;Authors: Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-438 <STO>
A;Crossion: E8123
A;Residues: 1-438 <STO>
A;Crossion: GB:AL450380; NID:G13093472; PIDN:CAC30668.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1715
C;Superfamily: probable hexosyltransferase ytxN
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C;Species: Archaeoglobus fulgidus
C;Accession: A69504
R;Klenk, H.D.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
F;Klenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.
Clodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Ritle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Residues preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-363 -KLE>
A;Residues: 1-363 -KLE>
A;Residues: 1-363 -KLE>
A;Cross-references: GB:AE000962; GB:AE000782; NID:g2689285; PIDN:AAB89220.1; PID:g26485G
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hydroxypyruvate reductase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
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R;Cubmitted to the EMEL Data Library, December 1994
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Run on:

141681 seqs, 52070155 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

141681 Total number of hits satisfying chosen parameters:

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SwissProt\_42:\* Database :

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SUMMARIES

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Migherti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,

Migherti W.G., Dugaiczyk A.;

"Molecular structure of the human albumin gene is revealed by

"Molecular structure of the human albumin gene is revealed by

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"Molecular structure of human serum albumin cDNA and its expression in E.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=82105994; PubMed=6275391;
Dugaiczyk A., Law S.W., Dennison O.E.;
"Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.";
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).
                                                                                                                                                                                           Query Match 100.0%; Score 38; DB 1; Length 600; Best Local Similarity 100.0%; Pred. No. 2.6; Matches 7; Conservative 0; Mismatches 0; Indels
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Q9P157; Q9P117; Q9UHS3; Q9UJZ0;
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1-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Serum albumin precursor.
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        BILIRUBIN (POTE
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Homo sapiens (Human).
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MEDLINE=90115852; PubMed=2104980;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
Brennan S.O., Wyles T., Peach R.J., Donaldson D., George P.M.;
Albumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of
human serum albumin whose precursor has an aberrant signal peptidase
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KOMAGOME-2 ARG-152 AND KOMAGOOME-1 GLU-396.

Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsica Y.-I., Amaki I., Putnam F.W.;

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MEDLINE=817744; PubMed=3828358;
Brennan S.O., Herbert P.;
Brennan Ganterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin."; 191-197 (1987).
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MEDLINE=89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M.,
Neel J.V., Sakurabayashi I., Putnam F.W.;
"Point substitutions in Japanese alloalbumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
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MEDLINE=88068523; PubMed=3479777;
Takshashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M., Satoh C., Neel J.V., Lisobe T., Putnam F.W., Fujita M., "Amino acid substitutions in inherited albumin variants from Amerindian and Japanese populations.";
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Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990)
Electrophoresis 15:1459-1465(1994)
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MEDLINE=78186630; PubMed=656055;
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WEDLINE=91316157; PubMed=1859851;
Peach R.J., Brennan S.O.;
Blochim. Blophys. Acta 1097;49-54(1991).
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WEDLIME SONDRIO LYS-357 AND PARIS-2 ASN-587.
WEDLINE=92190239; PubMed=1347703;
Winchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.;
"Two alloalbumins with identical electrophoretic mobility are produced
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MEDLINE-88332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Venter J.C.;
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VCBI_TaxID=160;
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Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%; Score 34; DB 1; Length 177;
85.7%; Pred. No. 4.9;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGN: TPO552; -. Hypothetical proteome. Hypothetical protein; Complete proteome. SECUENCE 177 Aa; 20172 MW; 59AOFOB815D006EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
HVPOChbetical protein TP0552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001230; AAC65538.1; -. PIR; D71311; D71311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AAADPHE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAADPHE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAADPHE
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85 AAVDPHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
Y552_TREP
AC 083563;
DT 16-0CT-20
DE HYPOCHECT
DE HYPOCHECT
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                                                                                                                                                                                                                                                                                                      SPECISS=M.tuberculosis, STRAIN=H137Rv;
MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia P.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-M.tuberculosis; STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Risen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Risen J.A., Exmolaeva M., Salzberg E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SPECIES=M.bovis; STRAIN=AF2122/97;
MDDLINE=22709107; PubMed=12788972;
MDDLINE=22709107; PubMed=12788972;
MDDLINE=22709107; PubMed=12788972;
MDLINE=2709107; PubMed=12788972;
MDLIDS S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                           01-0CT-1996 (Rel. 34, Created)
1-0CT-2096 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable ferredoxin/ferredoxin-NADP reductase (EC 1.18.1.2) (FNR).
PREB OR WY0886 OR WT0909 OR WTCY31.14 OR MB0910.
Mycobacterium tuberculosis, and
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ferredoxin + NADPH.
-! -CORACTOR: FAD; probably binds one or two 4Fe-4S clusters.
-! SIMILARITY: In the N-terminal, belongs to the bacterial-type ferredoxin family.
-! SIMILARITY: IN THE C-TERMINAL, TO OTHER FERREDOXIN NADP
                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaes; Mycobacterium.
                      575 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE006978; AAK45151.1; -. EMBL; BX248336; CAD93771.1; -. PIR; C70781; C70781. HSSP; Q45560; LBD6. TIGR; MT0909; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z73101; CAA97393.1; -.
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             SEOUENCE FROM N.A.
                    MYCTU
                      FPRB MY
Q10547;
FPRB_MYCTU
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0; Indels

Score 34; DB 1; Length 575;

6; Conservative

Matches

Query Match Best Local Similarity

METAL SEQUENCE

FEREDOXIN--NADP REDUCTASE.

1 IRON-SULFUR 1 (BY SIMILARITY).

15 IRON-SULFUR 2 (4FE-45) (BY SIMILARITY).

46 IRON-SULFUR 2 (4FE-45) (BY SIMILARITY).

49 IRON-SULFUR 2 (4FE-45) (BY SIMILARITY).

52 IRON-SULFUR 2 (4FE-45) (BY SIMILARITY).

54 IRON-SULFUR 2 (4FE-45) (BY SIMILARITY).

56 IRON-SULFUR 2 (4FE-45) (BY SIMILARITY).

57 IRON-SULFUR 1 (BY SIMILARITY).

58 IRON-SULFUR 1 (BY SIMILARITY).

59 IRON-SULFUR 1 (BY SIMILARITY).

115 9 15 19 46 49 52 56 575 AA;

PROSITE; PS00198, 4FE4S FERREDOXIN, 1. Oxidoreductase; Flavoprotein; NADP; FAD; Electron transport;

Iron-sulfur, 4Fe-48; Complete proteome. DOMAIN 1 83

83 575

InterPro; IPR001450; 4Fe45 ferredoxin.
InterPro; IPR000813; 7Fe ferredoxin.
InterPro; IPR000132; Adridx reductase.
InterPro; IPR001327; FAD\_Dyr\_redox.
Pfam; PF000137; fer4; 2.
Prints; PR00134; 7FB8SRRDOXIN.
PRINTS; PR00134; ADXRDTASE.
PRINTS; PR001369; FADPNR.

Tuberculist, Rv0886;

```
    -!- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
    -!- SIMILARITY: Belongs to the ribulose-phosphate 3-epimerase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                  STEALN-S288C / FY1679;
MEDLINE-97103775; PubMed-8948101;
MEDLINE-97103775; PubMed-8948101;
MEDLINE-97103775; PubMed-8948101;
MEDLINE-97103775; PubMed-8948101;
Caspelluch C., Kordes E., PubOld A., Jauniaux J.-C.;

reveals 19 open reading frames including URA2 [5' end), TRK1, PBS2, SPT10, GC014, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon.";
                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 39, Last annotation update)
Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Pentose-5-phosphate 3-epimerase) (PPE) (RPE)
RPEI OR POSIS OR VIII2C OR VO731.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97074231; PubMed=8929392; Miosga T., Zimmermann F.K.; "Cloning and characterization of the first two genes of the non-oxidative part of the Saccharomyces cerevistae pentose-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Genet. 30:404-409(1996).
-!- CATALYTIC ACTIVITY: D-ribulose 5-phosphate = D-xylulose 5-
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        PRT; 238 AA.
                                                                                                                        STANDARD;
                                  270 AADPHE 275
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
2 AADPHE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate.
                                                                                                                        RPE YEAST
P46969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway.";
                                                                                                                                                                                                                                                                                                                                                                           Juhnke H
                                                                                       RESULT 5
RPE_YEAST
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Gaps . 0 81.6%; Score 31; DB 1; Length 238; 83.3%; Pred. No. 28; 0; Indels ive 1; Mismatches 0; Indels Query Match Best Local Similarity 83... Si Conservative

g

8

PROC\_TREPA STANDARD; PRT; 263 AA.
P2771; 083775;
01-AUG-1992 [Rel. 23, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pyrroline-5-carboxylate reductase (BC 1.5.1.2) (PSCR) (PSC reductase).
PROC OR TP0797;
Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBL\_TaxID=160; TREPA RESULT PROC\_TR

SEQUENCE FROM N.A.
STRAIN=Nichols;
MEDLINE=90264287; PubMed=2188947;
Gherardini F.C., Hobbs M.M., Stamm L.V., Bassford P.J. Jr.;
"Complementation of an Escherichia coli proc mutation by a gene cloned from Treponema pallidum.";
J. Bacteriol. 172:2996-3002(1990). 

SEQUENCE FROM N.A.

STRAIN=Nichols,
MEDLINE=9833270; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,

spirochete.";

"Complete genome sequence of Treponema pallidum, the syphilis

Science 281:375-388(1998).
-!- CATALYTIC ACTIVITY: L-proline + NAD(P)(+) = 1-pyrroline-5-catboxylate + NAD(P)H.
-!- PATHWAY: Proline + NAD(P)H.
-!- PATHWAY: Proline + NAD(P)H.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

DR TIGRY TROUGH, PSCR.

DR TIGRY TROUGH, PSCR.

DR TIGRAMS, TROUGH, PSCR.

DR TIGRAMS, TIGROULLS, proc; 1.

DR TIGRAMS, TIGROULLS, proc; 1.

DR PROSTIE, PSOCRA, 1.

KW Oxidoreductase, Proline biosynthesis, NADP, Complete proteome.

KW OXIGOREDUCT 1 65 MWGRWTOPERCRESSYRICATSGRENGER.

FT CONFLICT 77 93 VLRDROGFGRVLISLA -> GTARSPIFQESAISC (IN FT SPT CONFLICT 77 93 VLRDROGFGRVLISLA -> GTARSPIFQESAISC (IN FT CONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT CONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

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FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1).

FT TONFLICT 256 260 VRAAL -> CRMLS (IN REF 1). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMED custation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL, M73825, AAA27478.1, -EMBL, AE001250, AAC65760.1, -. PIR, D71281, D71281. .
Best Local Similarity 83.30, 

106 AADPHQ 111 7 2 AADPHE g

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Gaps

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Score 31; DB 1; Length 263; Pred. No. 31; 1; Mismatches 0; Indels

SEQUENCE FROM N.A.

SETAIN=AV19 / DSM 6324 / JCM 9639;
STRAIN=AV19 / DSM 6324 / JCM 9639;
X MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Wararova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
A Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
A Malykh A.G., Koonin E.V., Kozyavkin S.A.;
The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
I.P. Toralli AV19 archaeal elyde 449 (2002)
C.-I. CATALITC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NAD(P)(+) = 3-phospho-D-glyceroyl phosphate + NAD(P)(-)
C.-I. SUBUNIT: Homotetramer (By similarity).
C.-I. SUBUNITY: Belongs to the glyceraldehyde 3-phosphate Methanopyrus kandleri. Archaea, Buryarchaeota, Methanopyri, Methanopyrales, Methanopyraceae, 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.59) (GAPDH)
(NAD(P) -dependent glyceraldehyde-3-phosphate dehydrogenase).
GAP OR GAPA OR MK0618. 350 AA PRT; STANDARD; NCBI\_TaxID=2320; Methanopyrus G3P METKA P58839; RESULT 7
G3P\_METKA 

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ICAL PIG STANDARD; PRT, 713 AA.

ID ICAL PIG STANDARD; PRT, 713 AA.

DT 01-0CT-1989 (Rel. 12, Created)

DT 01-0CT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

GR CAST.
                                                                                                SOUTH THE TERM TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (UUN-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (UUN-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (UUN-2000) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: Contains 1 SET domain.

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                                                                                         EMBL; AE010355; AAMO1833.1; -.
HAWAP; MF_00559; -; 1
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR000436; GAPDH-II_archae.
Pfam; PF00144; gpdh; 2:
Pfam; PF00146; gpdh; 2:
IGRFAMS; TIGRO1546; GAPDH-II_archae; 1.
TIGRFAMS; TIGRO1546; GAPDH-II_archae; 1.
PROSITE; PS00071; GAPDH; 1.
PROSITE; PS00071; GAPDH; 1.
GINCLARADEHYDE 3-PHOSPHATE (BY GINCLARADEHYDE 3-PHOSPHATE (BY SIMILARITY).
SEQUENCE 350 AA; 38367 MW; F9BCB72702E22E02 GRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. Yang X.-H., Huang S., Yang X.-H., Genes as candidate tumor "A family of novel PR-domain (PRDM) genes as candidate tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
81.6%; Score 31; DB 1; Length 504;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF591094CCF45515 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
PRDM11 OR PFM8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SET.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||:
177 AADPHQ 182
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|:|||| 426 ASDPHE 431

2 AADPHE 7

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REQUENCE OF 304-554 FROM N.A.

REDALINE=87054580; PubMed=3780962;

A Takano E., Maki M., Hatanaka M., Mori H., Zenita K., Sakihama T.,

A Kanadi R., Mariti T., Titani K., Marchi T.;

Takano E., Maki M., Hatanaka M., Mori H., Zenita K., Sakihama T.,

A Kanadi R., Mariti T., Titani K., Marchi T.;

Evidence for the repetitive domain structure of pig calpastatin as demonstrated by cloning of complementary DNA.";

TENDIATION: Specific inhibition of calpain (calcium-dependent cysteine protease). Plays a key role in postmortem tenderization of meat and have been proposed to be involved in muscle protein degradation in living tissue.

C -- DOMAIN: Has four inhibitory domains.

C -- SIMILARITY: Belongs to the calpastatin family.
Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NOCEL_TaxID=9823,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Heart;
MEDINE=88241021; PubMed=2837276;
ATAKANO E., MAKIN, MORI H., HALANAKA M., MARLI T., Titani K. Kannagi R., Ooi T., Mirachi T.;
"Pig heart calpastatin: identification of repetitive domain structures and anomalous behavior in polyacrylamide gel electrophoresis."

Biochemistry 27:1964-1972(1988).
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81.6%; Score 31; DB 1; Length 713;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 1; Indels
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PKWA THECU
ID PKWA_THECU
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1316 AA

STANDARD;

MYCLE

RPOC\_MYC P30761; RPOC\_MYCLE

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                                                                                                                                                                                                                                                                                                                                                       STRAIN=CCM 3352;

STRAIN=CCM 3352;

MEDLINE=950201225;

Danda L., Tichy P., Spizek J., Petricek M.;

"A deduced Thermononospora curvata protein containing

"A deduced Thermonone protein kinase and WD-repeat domains.";

"Bacteriol. 178:1489-1489(1996).

-: FUNCTION: MAY PLAY A REGULATORY ROLE DURING THE COMPLEX GROWTH
OYCLE AND IN SECONDARY METABOLITE PRODUCTION.

-: CATALYTIC ACTIVITY: ATP 4 a protein = ADP + a phosphoprotein.

-: SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

-: SIMILARITY: Contains 7 WD repeats.
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable serine/threonine-protein kinase pkwA (EC 2.7.1.37).
PKWA OR PKW1.
Thermomonospora curvata.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Thermomonospora.
NCB1_TaxID-2020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.6%; Score 31; DB 1; Length 742;
83.3%; Pred. No. 92;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PRO/GLU/ASP-RICH (SPACER).
WD 1.
WD 2.
WD 3.
WD 4.
WD 4.
WD 5.
WD 5.
WD 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Overy Match
Best Local Similarity 83.2
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22
444
1138
3301
3301
3301
362
572
566
666
742 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD repeat.
DOMAIN
ND BIND
BINDING
BINDING
ACT SITE
DOMAIN
REPEAT
REPEAT
REPEAT
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REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene, decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21128732; PubMed=11234002; James K.D., Thomson N.R., Cole S.T., Eglameier K., Parkhill J., James K.D., Thomson N.R., Siglameier K., Parkhill J., Churcher C., Harris D., Muheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruthers S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {RNA}(N).
-!- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
    01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain)
RPOC OR Mil890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substrates.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta' chain.
-!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                                                                                                                                                  MEDLINE=9118701; PubMed=8446028; MEDLINE=9118701; PubMed=8446028; Honore N.T., Bergh S., Chanteau S., Doucet-Populaire F., Elglmeier K., Garnier T., Georges C., Launois P., Limpaiboon T., Newton S., Niang K., del Portillo P., Ramesh G.X., Reddi P., Ridel P.R., Sittisombut N., Wu-Hunter S., Cole S.T., Reddi P., "Nucleotide sequence of the first cosmid from the Mycobacterium "nucleotide sequence of the first cosmid from the Mycobacterium leprae genome project: structure and function of the Rif-Str
                                                                                                                                              Mycobacterium leprae.
Batteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z14314; CAA78669.1; --
EMBL; AL583923; CAC30844.1; --
ERRIC; AL583923; CAC30844.1; --
FIR; D87145; D87145.
FIR; S31146; S31146.
HSSP; Q9KWU6; 1HQM.
Leproma; ML1890; --
INCEPPO; IPR007080; RNA_DOl_Rpbl_1.
INCEPPO; IPR007080; RNA_DOl_Rpbl_3.
INCEPPO; IPR007081; RNA_DOl_Rpbl_4.
INCEPPO; IPR007081; RNA_DOl_Rpbl_4.
INCEPPO; IPR007081; RNA_DOl_Rpbl_7.
INCEPPO; IPR00592; RNA_DOl_Rpbl_7.
Ffam; PF04997; RNA_DOl_Rpbl_1.
Pfam; PF049983; RNA_DOl_Rpbl_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 7:207-214(1993).
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SEQUENCE FROM N.A.
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RPOC_MYCTU

ID RPOC_MYCTU

RPOC_MYCTU

RPOC_MYCTU

AC P47769; O06771;

DT 01-FEB-1996 (Rel. 33, Created)

DT 15-DEC_1998 (Rel. 37, Last sequence update)

DT 15-DEC_1003 (Rel. 42, Last annotation update)

DF 10-CGT-2003 (Rel. 42, Last annotation update)

DF DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).

GN RPOC OR RV0668 OR MT0596 or MTC1376.07C OR MB0687.

OS Mycobacterium tuberculosis, and OS Mycobacterium bovis.

OS Mycobacterium bovis.

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98295987; PubMed=9634230;
MEDLINE-98295987; PubMed=9634230;
A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elglmeier K., Barkhill J., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsy T., Osborne J., Krogh A., Mcrean J., Moule S., Murphy L., A. Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T. "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Il Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES=M.bovis; STRAIN=AF2122/97;
MEDIJNE=22709107; PubMed=12788972;
MEDIJNE=22709107; PubMed=12788972;
MEDIJNE=22709107; Promiseler K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating J., Wheeler P.R.
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                               81.6%; Score 31; DB 1; Length 1316; 83.3%; Pred. No. 1.7e+02; tive 1; Mismatches 0; Indels
Pfam; PF05000; RNA_pol_Rpbl_4; 1. Pfam; PF04999; RNA_pol_Rbbl_5; 1. SMART; SMO663; RPGLA_N; 1. Transferase; DNA-directed RNA polymerase; Transcription; Complete proteome. S98 A -> R (IN REF. 1). SEQUENCE 1316 AA; 146895 MW; 7131AE63E53F6EGF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-148 FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37Rv;
MEDLINE=94304130; PubMed=8031050;
Miller L.P., Crawford J.T., Shinnick T.M.;
"The Trobs gene of Mycobacterium tuberculosis.";
Antimicrob. Agents Chemother. 38:805-811(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                               Local Similarity 83.3
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Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-:- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                      {RNA}(N).
-!- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1 beta' chain.
-!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                                                                                                                                                                       substrates.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT ARG-1775.
MINEY Y., SWENSEN J., Shattuck-Eidens D., Futreal P.A., Harshman K., Martigy Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harshman K., Tavtigian S., Liu Q., Cochran C., Bennett L.M., Ding W., Bell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR007022; RNA_pol_Rpbl_1.
InterPro; IPR007080; RNA_pol_Rpbl_1.
InterPro; IPR007083; RNA_pol_Rpbl_3.
InterPro; IPR007083; RNA_pol_Rpbl_4.
InterPro; IPR007083; RNA_pol_Rpbl_5.
InterPro; IPR06592; RNA_pol_Rpbl_1.
InterPro; IPR06593; RNA_pol_Rpbl_1.
IPfam; PF04993; RNA_pol_Rpbl_3; 1.
IPfam; PF04993; RNA_pol_Rpbl_4; 1.
IPfam; PF04998; RNA_pol_Rpbl_4; 1.
IPfam; PF04998; RNA_pol_Rpbl_4; 1.
IPransfererase; DNA-directed RNA_polymerase; Transcription; ITRNSFERERSE; DNA-directed RNA_polymerase; Transcr
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EMBL; AR065864; AAK44922-1; -
EMBL; L27989; AAA21417-1; -
EMBL; BX248336; CAD93549-1; -
EMBL; BX248336; CAD93549-1; -
EMSP; Q9KWU6; 1HQM.
TIGR; MT0696; -
Tuberculist; Ry0668; -
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BRC1_HUMAN
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Rosenthal J., Hassey C., Tran T., WcClure M., Prp C., Battler T., A hadgen Stranc A., Ratcher H., Yakhuno K. Gholani Z., A hadgen Stranc A., Ratcher H., Yakhuno K. Gholani Z., A hadgen Stranc A., Ratcher H., Yakhuno K. Gholani Z., A hadgen Stranc A., Sacoba S., Bayes G., Ward C., Bodgen R., Daybanath P., L., A cannon-Abright L., Goodag. D., Wissen N., Kan A., Skollik W. H., Schollik M. H., Scholani S., Barter S., Ratcher H., Skollik M., Scholani S., Ratcher S., Skollik M., Scholani S., Scholani S., Skollik M., Skolli

VARIANTS ARG-239; TRP-841 AND ILE-1512.
VARIANT BC GLY-61, AND VARIANTS ARG-239; TRP-841 AND ILE-1512.
VARIANT BC GLY-61, AND VARIANTS,
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RY Ovarian cancer: no evidence for other ovarian cancer-susceptibility ponder B.A.J.;

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

RESULT 14

BRC1 PANTR

1D Q9GXG9.

AC Q9GXG9.

DT 15-WAR-2004 (Rel. 43, Created)

DT 15-WAR-2004 (Rel. 43, Last sequence update)

CN RECAL.

OS Pan troglodytes (Chimpanzee).

OC Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OC NCEL TaxID=9598;

RN [1]

RP GIU-1100.

RP GIU-1100.

RP GIU-1100.

RA Takeda R., Hink R.L., Jogodka C., Walter N.A.R., Messier W.;

RT TROSSUENE ROW N.A., AND VARIANTS GIU-309; GLV-731 AND RP GIU-1100.

RA Takeda R., Hink R.L., Jogodka C., Walter N.A.R., Messier W.;

RT "Positive selection on the human BRCA1 gene may have resulted from pressure for prolonged care for infants.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DDBU databases.

RA KOUPEINE FROM N.A.

RA KOUPFINE N.;

RT "Pan troglodytes BRCA1 genomic sequences.";

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Bacteria, Actinobacteria, Actinobacteria, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.

NCBI_TaxID=1773;
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Tuberculist; Rv3426; -.
Interpro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPF: 1.
Hypothetical protein; Complete proteome.
SEQUENCE 232 AA; 25872 MW; D76512D49EB272C6 CRC64;
83.3%; Pred. No. 2.5e+02;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HV3yochetical PPE-family protein Rv3426.
RV3426 OR MTCY78.03C.
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78.9%; Score 30; DB 1; Length 232; 85.7%; Pred. No. 43; ive 0; Mismatches 1; Indels

Query Match
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 198 117	DR GO DR INT DR PE	Query Ma Best Loc Matches

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PRT;
InterPro; IPR008938; ARM.
InterPro; IPR000569; HECT domain.
InterPro; IPR000449; UBA_Gomain.
Ffam; PP00632; HECT; 1.
Ffam; PF00627; UBA; 1.
SMART; SM00119; HECTC; 1.
SMART; SM00119; HECTC; 1.
PROSITE; PS50337; HECT; 1.
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Q7Z3Y1
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QBNF55
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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STRAIR=Bristol N2;
STRAIR=Bristol N2;
Edwards J., Du H., Lamar B., Kemp K., Wohldmann P., Walker C.;
"The sequence of C. elegans cosmid Y67D8C.";
Submitted (MAR-2000) to the BMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 38; DB 4; Length 417; ilarity 100.0%; Pred. No. 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                EMBL; AC025724; AAG23375.2; -..., WormPep; Y67D8C.5; CB31665. GO; GO:0005622; C:intracellular; IEA. GO; GO:000542; F:ubiquitin-protein ligase activity; IEA. GO; GO:0006512; P:ubiquitin cycle; IEA.
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Waterston R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Hypothetical protein Y67D8C.5.
                                  01-070-2003 (TrEMBLrel. 24, Created)
01-070-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to alpha-fetoprotein.
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        417 AA
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STRAIN=BAISECOL NZ;
MEDLINE=99069613; PubMed=9851916;
Waterston R.;
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        PRELIMINARY;
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                                                                                                      Homo sapiens (Human).
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Matches 7; Conserva
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TISSUE=PERIPHERAL Nervous System;
TISSUE=22380257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Spleen;
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                    100.0%; Score 38; DB 5; Length 4177; 100.0%; Pred. No. 1.5e+02; cive 0; Mismatches 0; Indels (
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85.7%; Pred. No. 35;
1:ve 1; Mismatches 0; Indels
Hypothetical protein.
SEQUENCE 4177 AA; 465401 MW; 9C32EF90ABB7FD58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK090424; BAC03405.1; -.
InterPro; IPR000949; ELM2.
Pfam; PF01448; ELM2; 1.
NON TER 1
SEQÜENCE 157 AA; 17936 MW; BDFB8C792B17D1BE CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 100.
Matches 6; Conservative
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          6; Conservative
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NCBI TaxID=7955;
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TISSUE=Body
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Q7ZUE6
          Matches
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Q8XZ00
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Rometein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKennan K.J., Abramson R.D., Mullahy S.J.,
Richards S. Worlley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Richards D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Antilon S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences."
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Bibb M.J., Sherman D.H., Omura S., Hopwood D.A.;
"Cloning, sequencing and deduced functions of a cluster of
Streptomyces genes probably encoding biosynthesis of the polyketide
antibiotic frenolicin.";
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Reeves C.D., Soliday C.L.;

Reeves C.D., Soliday C.L.;

"Analysis of a 27 kb region of Streptomyces roseofulvus containing genes for frenolicin biosynthesis.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

BMBL, ARC18030;

GO: COLOS020;

CO: COMESSA21;

Firansporter activity; IEA.

GO; GO: ORG810;

Firansporter activity; IEA.

Interpre: IPRO00515;

Pfam;

PFO0528;

PFAM;

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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33902;
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85.7%; Pred. No. 70;
ive 1; Mismatches 0; Indels
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Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; EC052976; AAH52976.1; -.
HYPOCHACICAL protein.
SEQUENCE 310 AA; 35335 MW; 0B07FDE180821E44 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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7 AAADPHK 13
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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Brachydanio remio (Zebrafish) (Danio remio).
Brachydanio remio (Zebrafish) (Danio remio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
similar to guanine nucleotide-releasing factor 2 (Specific for crk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnad S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Wassenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.5%; Score 34; DB 13; Length 691; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.5%; Score 34; DB 16; Length 323;
85.7%; Pred. No. 73;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC49305; AAH49305.1; -
SEQUENCE 691 AA; 76263 MM; 90CC6764E6DB9EE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, ALG46065, CAD15308.1; -.
InterPro, IPR000286, His deacetylse.
Pfam; PF00850; Hist deacetyl; 1.
PRINTS; PR012-0; HDÄSUPER.
Hypothetial protein; Complete proteome.
SEQUENCE 323 AA; 34637 MW; 304513B9155416DB CRC64;
                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
Hypothetical (TrEMBLrel. 23, Last annotation update)
Hypothetical protein RSc1606.
RSC1606 OR RS03969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        691 AA.
                                     Q8XZ00;
01-MAR-2002 (TrEMBLrel. 20, Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
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RA SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-306 (ATCC 13902 / XV 101);

MEDLINE-22022145; PubMed=12024217;

RA Ga Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C. Camargo L.B.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Clapina L.P.,

Carelli R.M.B., Coutinho L.L., Cureino-Santos J.R., El-Dorry H.,

RA Camarotte G., Cannavan F., Ferreira R.C.C., Gruber A.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.D., Greggio C.C., Gruber A.,

RA Fariand B.C., Machado M.A., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.A., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Preira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Schubal J.C., Kitajima J.P.,

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RL Martin A.D. A.D., Shadishid, Complete proteome.

RM Hypotherical protein; Plasnid; Complete proteome.

KW Hypotherical protein; Plasnid; Complete proteome.

KW Hypotherical protein; Plasnid; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20036896; PubMed=1056726;
MEDLINE=20036896; PubMed=10567266;
Mahte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Mamathevan J.J., Lam P., MoDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Plasmid pXAC64.
Bacteria; Protecobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.8%; Score 33; DB 16; Length 180;
85.7%; Pred. No. 64;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 protein; Complete protecme.
238 AA; 25113 MW; 489BBC792C11E7AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DR1454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008941; TPR-like.
Hypothetical protein; Complete
SEQUENCE 238 AA; 25113 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001990; AAF11027.1; -. PIR; H75392; H75392.
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Science 286:1571-1577(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 ARADPHE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAADPHE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                         NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rIGR; DR1454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framer C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9RUD4
Q9RUD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR1454
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098UD4
AC 098UD4
DT 01-MAD
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   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mason M. D. Springs T. Artiach P. Kaine D., Nelson K.E., Ketchum K.A., Dodson R.J., Tomb M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Pietschaman R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S. Reich C.I., Morsil L.K., Badger J.H., Glodek A., Zhou L. Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea K.P., Bowman C., Kuili C., Garland S.R., Wasson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Neater J.C., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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85.7%; Pred. No. 1.7e+02;
ive 1; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-1998 (TREMBLrel. 24, Last annotation update)
Hydrogenase expression/formation regulatory protein (HYPF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein XACD0006.
XACB0006.
Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0003999; F:acylphosphatase activity; IEA.
InterPro; IPR004721; Acylphosphatase.
InterPro; IPR004421; Hyp?
InterPro; IPR006071; SUAS/ycio/yrdC.
InterPro; IPR006070; SuaS/ycio/yrdC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 180 AA
                                                                                                                                                                                                                                         740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001009; AAB89876.1; -. IIGR; AF1366; -.
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus.
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606 AAAEPHE 612
                                                                                         560 AADPHE 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAADPHE 7
                                1
                                   2 AADPHE
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                                                                                                                                                                                                                                                                      028905;
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                                                                                                                                                                                                                                            028905
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08PRL4
AC 08PRL
DT 01-0C
DT 01-0C
DT HYD-1-UC
CON XACEC
OS XACEC
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RESULT 9

028905

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=cv. Columbia;

Liu S., Chan A., Yu G., Lee J., Lenz C., Pham P., Sakano H.,

A Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,

Howng B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E.,

A Chao Q., Conn L., Conway A., Hannen N., Palm C., Shinn P.,

Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.;

Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AC00273; AAF78398.1;

InterPro; IPR03613; Znf_modRING.

REPRO; SWART; SM05504; Ubox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINEE FROM N.A.

MEDLINE=1608550; PubMed=11743193;

MODAGO D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

OKUTA V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kaymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley R., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.,

Whe genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cas Askenazi M., Halling C., Mullin L.,
Qurollo B., Goldman D., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
                                                                                                                                               TIN6.5.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryophyta; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sysermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ISS family transposase.
TNP OR ATU4436 OR AGR L 863GL.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group; Agrobacterium.
NCBL TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 AA; 35392 MW; CE53CFA27C77547D CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
TING.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AAADPH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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07 01-JU
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SEQUENCE FROM N.A.

SEQUENCE 23913 / NCPPB 528;

XA MEDINE-2202145; PubMed-12024217;

A da Silva A.C.R., Ferro J.A., Renach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Forto J.A., Refnach F.C., Camargo L.E.A.,

A da Silva A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Aves L.M.C., do Amaral A.M., Berrollini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cursino-Santos J.R., El-Dorry H.,

RA Formighieri E.F., Franco M.C., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Fubber A. A.

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RATSUYAMA A.M., Madeira A.M., Mayaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Fezza R.I.D.,

A Spinola L.A.F., Truiti M.A., Truiti D., Tsai S.M., White F.F.,

Sctubal J.C., Kitajima J.P.;

R Trindade dos Santos M., Truiti D., Tsai S.M., White F.F.,

Sctubal J.C., Kitajima J.P.;

R Trongarison of the genomes of two Xanthomonas pathogens with differing

Nature 417:459-468(2002).
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EMBL; AE012183; AAM40150.1; -.

GO; GO:0008276; F:DNA binding; IEA.

GO; GO:0008276; F:DNA binding; IEA.

GO; GO:0008276; F:Drotain methyltransferase activity; IEA.

GO; GO:0008776; F:S-adenosylmethionine-dependent methyltransfe. .; IEA.

GO; GO:0006479; F:S-adenosylmethionine-dependent methyltransfe. .; IEA.

GO; GO:0006479; F:S-adenosylmethylation; IEA.

InterPro; IPR004556; HemK.

InterPro; IPR005052; NG Mtase.

InterPro; IPR005052; NG Mtase.

InterPro; IPR0051; NG MTASE; 1.

Complete protecome.

SEQUENCE 283 AA; 30275 MW; ASF4E951E8E33479 CRC64;
                                                                                                                        Gaps
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Protoporphyvinogen oxidase.
HEMK OR XCC0835.
Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae; Xanthomonada.
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Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels
                                      86.8%; Score 33; DB 16; Length 238;
100.0%; Pred. No. 85;
.ive 0; Mismatches 0; Indels
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                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
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AC Q9LQ92;
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Length 308; 0; Indels

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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Fleischmann J., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Definition of the property of 
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"Whole genome comparison of Mycobacterium tuberculosis clinical and "Whole genome comparison of Mycobacterium tuberculosis clinical and Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL021287; CAA16117.1;
EMBL, AR007130; ARK47446.1;
PIR, C70859; C70859
A Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
A Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
T Agrobacterium tunnefaciens CS8 ",
B GMBL, AEG08932; AAL48230.1;
R EMBL, AEG08242; AAR48904.1;
R PIR; AH3101;
R PIR; B98185; B98185.
R InterPro; IPR00259; Transposase_11.
R Pfam; PF01609; Transposase_11, 1.
Complete proteome.
SEQUENCE 351 AA; 39162 MW; 8CS80BA75CBDF249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Glycosyl transferase).
RV3032 OR MTV012.47 OR MT3116.
Mycobacterium tuberculosia, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TAXID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.8%; Score 33; DB 16; Length 351;
85.7%; Pred. No. 1.3e+02;
tive 0; Mismatches 1; Indels
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Tuberculist; Rv3032; -.
GO; GO:0016/40; F:transferase activity; IBA.
GO; GO:0016/28; P:transferase IBA.
InterPro; IPR001296; Glyco_trans II.
Pfam; PF00534; Glycos_transferase; Complete proteome.
Hypochetical protein; Transferase; Complete proteome.
SEQUENCE 414 AA; 44805 MW; 64ADC7A4EA17A0DE CRC64;
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Best Local Similarity 85.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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20 053279
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Query Match 86.8%; Score 33; DB 16; Length 414; Best Local Similarity 85.7%; Pred. No. 1.5e+02; Matches 6; Conservative 0; Mismatches 1; Indels
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1 AAADPHE 7

66 AAQDPHE 72

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Search completed: April 19, 2004, 12:00:11 Job time : 4.70175 secs

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(without alignments)
480.375 Million cell updates/sec
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5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                   1586107 segs, 282547505 residues
                                                                                                                                                                   US-09-832-929-18_COPY_362_368
38
GenCore version
Copyright (c) 1993 - 2004
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqT1980s:\* geneseqT0900s:\* geneseqT2001s:\* geneseqT2001s:\* geneseqT2003as:\* geneseqT2003as:\* Geneseq 29Jan04:\* geneseqp2004s:\* Database

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abb56230 Vascular	Abb56225 Vascular		Aau15376 Schizophr	Aau33145 Novel hum	Aac02636 Human pol	Aay83948 Yeast cod	σ	3087	Aau33081 Novel hum	~	67	_	0	Aap90391 N-termina		Aar14179 Human ser	Nove	Aau32994 Novel hum	Aau29877 Novel hum	Abg72381 Mature hu	Aap93344 Sequence	3388	Aap91422 Human nor	Aarosale Human ser
SUMMARIES	ABB56230	ABB56225	AAU25032	AAU15376	AAU33145	AA002636	AAY83948	AAY83949	AAU33087	AAU33081	AAU33082	AAP90387	AAP90389	AAP90390	AAP90391	AAP90392	AAR14179	AAU33286	AAU32994	AAU29877	ABG72381	AAP93344	AAP90388	AAP91422	AAR05318
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Length	13	13	13	13	103	112	188	228	243	245	293	373	388	389	390	407	463	507	507	550	584	585	585	585	585
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Aar08457 Human ser	Aar26207 Human ser	Aar26362 Synthetic	Aar20029 Human ser	Aar80301 Human ser	Aao20111 HSA prote	Aaw59841 Mature pr	Aay84873 Amino aci	Aay83946 Yeast cod	Aam52567 Mature hu	Aae12417 Human alb	Aae12403 Human alb	Aae13129 Human alb	Aae13135 Human alb	Aae13311 Human alb	Aae13399 Human alb	Abb79006 Human mat	Aae08578 Human ser	Aau75220 Mature fo	Abj00986 B lymphoc	
AAR08457	AAR26207	AAR26362	AAR20029	AAR80301	AA020111	AAW59841	AAY84873	AAY83946	AAM52567	AAE12417	AAE12403	AAE13129	AAE13135	AAE13311	AAE13399	ABB79006	AAE08578	AAU75220	ABJ00986	
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26 3	7	8	6	0	-		m	4	35	36 3		38	39		-		2	4	r.	

## ALIGNMENTS

Vascular Dementia; VD; VD-associated protein isoform; VPI; screening; Vascular dementia-associated protein isoform (VPI) 430. diagnosis; prognosis; gene therapy ABB56230 standard; peptide; 13 AA. 15-MAR-2000; 2000GB-0006285. 24-NOV-2000; 2000GB-00028734. 28-NOV-2000; 2000US-00724391. 14-MAR-2001; 2001WO-GB001106. (first entry) WO200169261-A2. Homo sapiens. 20-SEP-2001. 15-FEB-2002 ABB56230; RESULT 1 ABBS6230 

(OXFO-) OXFORD GLYCOSCIENCES UK LTD. Rohlff C; Herath HMAC, Parekh RB, WPI; 2001-557937/62. Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.

Claim 6; Page 39; 151pp; English.

The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of erebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABBSS6195) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or

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severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                  Gaps
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                                                                                                                Query Match
100.0%; Score 38; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 7; Conservative 0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; prognosis; gene therapy
                                                                                                                                                                                                                                                                                                  ABB56225 standard; peptide; 13 AA.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-557937/62.
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Best Local Similarity
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                                                                                 Sequence 13 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebroopinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                            Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
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                                                                                  Schizophrenia-Associated Protein Isoform (SPI) peptide #261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 38; DB 4; Length 13; 100.0%; Pred. No. 0.57;
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                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD GLYCOSCIENCES UK LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 34; 148pp; English.
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AAU25032 standard; peptide; 13
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                                                                                                                                                                                                                                                                             2000GB-00004415.
2000US-00750395.
                                                                                                                                                                                                                                                                                                                                                   Herath HMAC, Parekh RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-570624/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 AA;
                                                                                                                                                                                         WO200162785-A2
                                                                                                                                                                                                                                                                             24-FEB-2000;
28-DEC-2000;
                                                                                                                                                             Homo sapiens
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                                                        18-DEC-2001
                                                                                                                                                                                                                     30-AUG-2001
                             AAU25032;
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Matches
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immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                        The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFB) and SCH Associated Protein Isoforms (SPB) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and monitoring SCH, cherapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH, and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFS, SPIS and related molecules (e.g. condary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifectations of antomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improve treatment of neuropsychiatric disorders. Aduls114-AUL15762 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                          Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
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    Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
neurological disorder; neuropathy.
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                                                                                                                                                                                                        (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #3636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU33145 standard; protein; 103 AA.
                                                                                                                                                                                                                                  Rohlff C;
                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 34; 160pp; English.
                                                                                                                                23-FEB-2001; 2001WO-GB000783.
                                                                                                                                                           24-FEB-2000; 2000GB-00004415.
28-DEC-2000; 2000US-00750395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                   Herath HMAC, Parekh RB,
                                                                                                                                                                                                                                                               WPI; 2001-502868/55.
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                                                                          WO200163293-A2
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                                                Homo sapiens
                                                                                                      30-AUG-2001
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated atth altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acides encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins to express them are also useful for producing the proteins. The proteins of an untitional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias. AAD29510-AAD33304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                            18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                        16-APR-2001; 2001WO-US008656.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAADPHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 103 AA;
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                                                                WO200179449-A2
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Homo sapiens.
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                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                                                               The invention relates to human polymucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerleotides and polymerleotides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiseis regulating activity, itssue growth factor activity, haematopoiseis regulating activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this parent did not form part directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant; human serum albumin; HSA; yeast codon bias; host cell; overlapping oligonucleotide; expression vector.
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                                                                                                                                                                                                          Claim 20; SEQ ID NO 16528; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 38; DB 4; Length 112; 100.0%; Pred. No. 5.9; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast codon-biased recombinant HSA protein fragment HSA-II.
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            26-FEB-2001; 2001WO-US004927
                                    28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                     Liu C, Drmanac RT;
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Best Local Similarity 100.
Matches 7; Conservative
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N-PSDB; AAA10093.
                                                                                                                             WPI; 2001-514838/56.
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                                                                          (HYSE-) HYSEQ INC
                                                                                                                                            N-PSDB; AAI82567
                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 112 AA;
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                                                                                                  Tang YT,
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                                                                                                  The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonuclecide fragments that were extended. This sequence represents the sequence of the HSA fragment HSA-II encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression the process for producing human serum albumin in the yeast host cells especially in secretory mode
Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast codon-biased recombinant HSA protein fragment HSA-III.
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                                                                 Example 1; Fig 5; 44pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                Sequence 188 AA;
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7; Conservative
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  Matches
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AAU33081
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AAU39510-AAU393304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
vector, yeast host cells carrying the recombinant expression vector and the process for producing human serum albumin in the yeast host cell, especially in secretory mode
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                       Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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0
                                                                       100.0%; Score 38; DB 3; Length 228; 100.0%; Pred. No. 13;
                                                                                                0; Indels
                                                                                             Mismatches
                                                                                                                                                                                                       AAU33087 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                 Novel human secreted protein #3578.
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                         (first entry)
                                                                                              Conservative
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                                                                                                                                             AAADPHE 11
                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                       1 AAADPHE
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                                                Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                                                              WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                  RESULT 9
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DB 4; Length 243;

100.0%; Score 38; DB 100.0%; Pred. No. 14;

Query Match Best Local Similarity

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used a survitional supplements. They may be used to increase stem cell proliferation; to requiate haematopoiesis; and in bone, cartiage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimulation; as anti-inflammatory agents; and in treatment of leukaemias. Secreted proteins of the invention
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                                                                                                                                                                                                                                 AAU33081 standard, protein, 245 AA.
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26-JAN-2001; 2001US-00770160.
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Best Local Similarity 100.
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                                                            64 AAADPHE 70
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1 AAADPHE 7
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N-terminal portion of human serum albumin. Used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
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Pred. No. 21;
                                                             Human serum albumin polypeptide; plasma expanders.
                     N-terminal of human serum albumin polypeptide.
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Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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25-MAR-2003
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stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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                                                                                                                                                          Novel human secreted protein #3573.
                       AAU33082 standard; protein; 293 AA
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26-JAN-2001; 2001US-00770160.
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N-terminal portion of human serum albumin. Used to make new N-terminal fragments which are used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                              New N-terminal fragments of human serum albumin - esp. useful as blood
                                                                                                                N-terminal portion of human serum albumin; plasma expanders.
AAP90391 standard; protein; 390 AA.
                                                                                                                                                                                                                                                            (DELZ ) DELTA BIOTECHNOLOGY LTD.
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                                                                                           N-terminal human serum albumin.
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                                                                                                                                          Homo sapiens; (Human)
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                                                                                                                                                                                                                                                                                                                                               plasma expanders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal portion of human serum albumin. Used to make plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field.)
                                              N-terminal fragment of human serum albumin used as plasma expander, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New N-terminal fragments of human serum albumin - esp. useful as blood
plasma expanders.
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                                                                                                                                                                                                                                                                                                                                                                                  N-terminal portion of human serum albumin; plasma expanders.
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                                                                                                                             Match 100.0%; Score 38; DB 1; Length 388; Local Similarity 100.0%; Pred. No. 22; local Similarity 0, Mismatches 0; Indels
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                                                                                                                                                                                                                                                                AAP90390 standard; protein; 389 AA.
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                                                                                                                                                                                                                                                                                                                                                            N-terminal human serum albumin.
                          Claim 2; Page 9; 20pp; English.
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Best Local Similarity lov...
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens; (Human)
                                                                                                                                                                                                     362 AAADPHE 368
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                                                                                                                                                                              1 AAADPHE 7
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   plasma expanders.
                                                                                                          Sequence 388 AA;
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01-NOV-1989
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Best Local S:
Matches 7
                                                                                   field)
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Senior PJ;

Geisow MJ,

87GB-00025529. 88EP-00310000.

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Query Match
100.0%; Score 38; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels
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Gaps

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362 AAADPHE 368

RESULT 15 AAP90391

1 AAADPHE 7

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Soto, Ana M. TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
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; Patent No. US2002012080A1
; GENERAL INFORMATION:
APPLICANT: Sonnenschein, Carlos
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAADPHE
1 AAADPHE
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Sequence 2, Appli
Sequence 445, App
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                                                                                                                                                                                     April 19, 2004, 12:00:25 ; Search time 2.94737 Seconds (without alignments) 654.724 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/PCT_RM_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/PCT_RM_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/PCT_RM_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_DSP:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB_DSP:*
| cgn2_6/ptodata/2/pubcomBSP:*
| cgn2_6/pto
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-984-010-26
US-09-883-117-18
US-09-833-117-18
US-09-833-118-18
US-09-833-118-18
US-09-833-118-18
US-09-833-118-18
US-10-424-999-11
US-10-425-000-31
US-10-425-000-31
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US-09-929-552-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1124875 segs, 275673149 residues
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                                                                                                                                                                                                                                                                                   US-09-832-929-18_COPY_362_368
38
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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Sequence 26.1, Application US/09791378
Sequence 26.1, Application US/09791378
Fatent No. US20020142303A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: SCHIZOPHRENIA
FILIE REPRENCE: 9195-661-999
CURRENT APPLICATION NUMBER: US/09/791,378
CURRENT FILING DATE: 2001-02-23
PRIOR PAPPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SEQ ID NOS: 677
SEQ ID NO 261
LENGTH: 13
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Sequence 2, Appli
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Sequence 37, Appli
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Sequence 2, Appli
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Sequence 15, Appli
Sequence 17, Appli
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels
US-10-319-263-1
US-10-319-263-2
US-10-319-263-2
US-10-414-469-1
US-10-413-831-1
US-10-413-831-1
US-10-413-832-1
US-10-413-832-1
US-10-414-386-1
US-10-414-386-1
US-10-414-386-1
US-10-33-675A-11
US-10-33-675A-11
US-09-984-010-7
US-09-984-010-7
US-09-984-010-7
US-09-984-010-7
US-10-153-064-7
US-10-153-684-7
US-10-153-684-7
US-10-153-684-7
US-10-153-684-7
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US.10-237-667-2
US.10-237-866-2
US.10-237-871-2
US.10-237-871-2
US.10-433-108-13
US.10-433-108-14
US.10-433-108-15
US.10-433-108-15
US.10-433-108-15
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RESULT 4
10S-0944-010-26
1 Sequence 26, Application US/09984010
1 Publication No. US20030104578A1
2 GENERAL INFORMATION:
2 APPLICANT: Ballance, David James
1 TILE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
2 TITLE OF INVENTION: AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER,
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: DATE: Peterlin FC-DOS/MS-DOS
SOFTWARE: Peterlin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR APPLICATION DATA:
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100.0%; Score 38; DB 10;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-833-041-18

US-09-833-041-18

Sequence 18, Application US/09833041

PUBLICATION NO. US20030125247A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Reseltine, William A.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REPERENCE: PF545

CURRENT APPLICATION NUMBER: US/09/833,041

CURRENT PILING DATE: 2001-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMERR: US 09/091,873
FILING DATE: 25-40N-1998
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 19-DEC-1996
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERSTICS:
LENGTH: 585 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: linear
WOLECTLE TYPE: protein
HYPOTHETICAL: NO
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     362 AAADPHE 368
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| Sequence 445, Application US/09932613
| Publication No. US2003009156SA1
| Publication No. US2003009156SA1
| APPLICANT: Human Genome Sciences, Inc.
| APPLICANT: Beltzer, James P. APPLICANT: Pleming, Tony J. APPLICANT: Rosen, Craig A. ITLE REPERENCE: DAY-025.1 US PLICANT: ROSen, Craig A. ITLE REPERENCE: DAY-025.1 US CURRENT ALPLICATION NUMBER: US/09/932,613
| CURRENT FILING DATE: 2001-08-17
| NUMBER OF SEQ ID NGS: 458
| SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: FREADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/929,552

FILING DATE: 14-Aug-2001

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/769,746

FILING DATE: 19-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G

REGIETRATION NUMBER: 32,837

REPERRATION NUMBER: 32,837

REPERRATION NUMBER: 32,837

REPERRATION NUMBER: 32,837

REPERRATION NUMBER: 32,838

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH : 585 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 38; DB 9; Length 585; Best Local Similarity 100.0%; Pred. No. 49; Matches 7; Conservative 0; Mismatches 0; Indels
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-929-552-2
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; ORGANISM: HomoSapiens
US-09-932-613-445
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US-09-932-613-445
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LENGTH: 585
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                          Indels
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VESOLI 9.

Sequence 18, Application US/09833118

Sequence 18, Application US/09833118

Publication No. US20030219875A1

GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Heseltine, William A.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF5-4
CURRENT PLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/26,931
PRIOR PRILING DATE: 2000-12-21
PRIOR PRILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-14-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PALENTING DATE: 2000-14-25
NUMBER OF SEQ ID NOS: 35
LENGTH: 595
                                                                                                                                                                                                                                                                                                                 APPLICANT: Ballance, David J.
APPLICANT: Ballance, Darrell
APPLICANT: Sleep, Darrell
APPLICANT: Sadeghi, Homa
APPLICANT: Funcer, Christopher P.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF542
CURRENT FILING DATE: 2001-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 585
  Pred. No. 49;
; Mismatches
                                                                                                                                                                                                  RESULT 8
US-09-832-501-18
; Sequence 18, Application US/09832501
; Bellication No. US20030199043A1
; GENERAL INFORMATION:
Best Local Similarity 100.0%; P. Matches 7; Conservative 0;
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo Sapiens
US-09-832-501-18
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Sequence 445, Application US/09932322
Sequence 445, Application VG20030194743A1
GENERAL INFORMATION:
APPLICANT: DATA COUR.
APPLICANT: Fleming, Tony U.
APPLICANT: Fleming, Tony U.
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REPERENCE Dyx-01B.1 PCT; DYX-01B.1 US
CURRENT APLICATION NUMBER: US/09/932,322
CURRENT APLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 445
LENGTH: 585
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                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels
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US-09-833-117-18
Sequence 18, Application US/09833117
Publication No. US20030171267A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Prior, Christopher P.
APPLICANT: Prior, Christopher P.
APPLICANT: TILTER, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF543
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE PRICED NOS: 36
SEGID NO 18
LENGTH: 585
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Best Local Similarity 100.
Matches 7; Conservative
             ; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-833-041-18
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Sequence 31. Application US/10425000
| Sequence 31. Application WS/10425000
| Publication No. US2004062777A1
| GENERAL INFORMATION:
| APPLICANT: Cameron, Mark
| APPLICANT: Blanche, Francie
| TITLE OF INVENTION: Anglogenesis
| FILE REPRENCE: STOT1027-B
| CURRENT FILING DATE: 2003-04-29
| PRIOR FILING DATE: 2003-09-04
| NUMBER OF SEQ ID NOS: 105
| SOFTWARE: Patentin version 3.2
| LENGTH: 585
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Publication No. US20020142814A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Human derived fusion protein US-10-425-000-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-10-433-108-34
Sequence 34, Application US/10433108
Publication No. US20040053370A1
GENERAL INPORMATION:
APPLICANT: Bil Lilly and Company
TITLE OF INVENTION: GLP-1 FUSION PROTEINS
FILE REFERENCE: X-13991
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: US/10/433,108
CURRENT FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
LENGTH: 585
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Pred. No.
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-10-433-108-34
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105-10-424-999-11

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100.0%; Score 38; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                    RESULT 10
US-09-833-245-18
US-09-833-245-18
Sequence 18, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILLE OF INVENTION: Albumin Fusion Proteins
FILE REPRENCE: PF546FER:
CURRENT FRIENCATION NUMBER: 06/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR PRILING DATE: 2000-04-12
PRIOR PRILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTIN NUMBER: 66/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTIN VOY: 2.1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo Sapiens
US-09-833-245-18
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   1 AAADPHE 7
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Search completed: April 19, 2004, 12:54:59 Job time : 2.94737 secs

362 AAADPHE 368

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April 19, 2004, 11:37:09; Search time 3.47368 Seconds (without alignments) 817.479 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                   US-09-832-929-18_COPY_280_288
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O86yq0 homo sapien	O7ysq3 felis silve	O7wgw3 bordetella	Q7wly5 bordetella	Q8c7c7 mus musculu	Q95vb7 schistosoma	Q8c7h3 mus musculu	Q94c01 hordeum vul	Q81fb3 arabidopsis	Q7uq53 rhodopirell	Q8kla6 rhizobium e	Q97f20 clostridium	Q8i621 plasmodium	O9pmw9 campylobact	001495 caenorhabdi	Q40001 hordeum vul
SUMMARIES	ID	Q86YG0	Q7YSG3	Q7WQW3	Q7W1Y5	080707	Q95VB7	Q8C7H3	Q94C01	QBLFB3	Q70Q53	Q8KLA6	Q97F20	Q81621	Q9PMW9	001495	Q40001
	DB	4	φ	16	16	11	ın	11	10	10	16	N	16	ហ	16	Ŋ	10
	% Query Match Length DB	417	584	245	245	576	809	608	1381	191	480	123	156	226	301	1265	1380
	% Query Match	100.0	83.0	78.7	78.7	78.7	78.7	78.7	78.7	76.6	76.6	74.5	74.5	74.5	74.5	74.5	74.5
	Score	47	39	37	37	37	37	37	37	36	36	35	35	35	35	35	35
	Result No.	П	7	m	4	เบ	ω	7	60	ማ	10	11	12	13	14	15	16

Q8mpv7 caenorhabdi Q8mpv6 caenorhabdi Q84bi8 streptococc Q81sb7 bacillus an	o wolinella homo sapie homo sapie	4 C H M	QYZTCZ Brachydanio Q9D985 saccharomyc Q9Urel saccharomyc Q9D986 saccharomyc Q9J288 saccharomyc Q8J288 saccharomyc Q7YSp6 caenorhabdi	Q9rlbB ruminococcu Q9xwf9 caenorhabdi Q8xqm0 salmonella Q96kg5 rhizobium 1 Q9h855 homo sapien Q7vK53 helicobacte Q8xly6 clostridium
Q8MPV7 Q8MPV6 Q84BI8 6 Q81SB7	0000	1 Q9CQQ4 1 Q9DAD7 068651 6 Q87Y51 0 Q94YY3	000000	Q9KLB8 Q9KWF9 Q9KWF9 6 Q9EQM0 6 Q9BES5 6 Q7VK53
2227	14444	44444	758660 748660 748660 748660 748660	<b>44444</b>
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	. 4 4 4 4 4 4 1 4 4 4 4 4 4	~~~~~~~ ********	* * * * * * * * * " ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	~~~~~~ ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
11 118 120 120	2 2 2 2 2 2 2 4 2 5 4 5 5 6 4 5 6 4 5 6 6 6 6 6 6 6 6 6 6	22 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	N m 4 m m m m m	w 4 4 4 4 4 4 0 0 4 61 61 61 61

## ALIGNMENTS

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Gaps
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 47; DB 4; Length 417; 100.0%; Pred. No. 0.5; or Mismatches 0; Indels
                                                                                                                                                                                                                        A Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BCO41789; AA441789.1; --
R GO; GC:0005615; C:extracellular space; IEA.
GO; GC:0005386; F:extrace acclivity; IEA.
R GO; GC:0006810; P:transport; IEA.
R InterPro; IPR000264; Serum_albumin.
R FRINTS; PR00612; SERUMALBUMIN.
R PRDOM; PD002486; Serum_albumin; 1.
R SMART; SM00103; ALBUMIN; 2.
R PROSITE; PS002012; ALBUMIN; 2.
R PROSITE; PS002012; ALBUMIN; 2.
                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                              417 AA.
                              PRT;
                                                                                                      Similar to alpha-fetoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                            PRELIMINARY;
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                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Liver;
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                            Q86YG0
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Matches
RESULT 1
              086YG0
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RESULT 2

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110 EVPLLERSH 118
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=RB50 / ATCC BAA-588;

MEDIINE=25873954, PubMed=12910271;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Goble A., Hamiln N., Hauser H., Holroyd S., Jagels K.,

Retwell T., Goble A., Hamiln N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Sanders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

Comparative analysis of the genome sequences of Bordetella pertussis,

Thordetella parapertussis, and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                       Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                              TISSUE-Liver;
Reininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P.,
Rumpold H., Valenta R., Spitzauer S.,
Rumpold H., Valenta R., Spitzauer S.,
"Bacherichia coli expression and purification of recombinant calbumin. Tage recognition, induction of basophil activation and lymphoproliferative responses in atopic patients.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ487677; CAD32275.1; -.
NON TER 1
SEQUENCE 584 AA, 65908 MW; BS1002F12902C9CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.7%; Score 37; DB 16; Length 245; 77.8%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                    83.0%; Score 39; DB 6; Length 584; 87.5%; Pred. No. 28; ive 1; Mismatches 0; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                               Created)
Last sequence update)
Last annotation update)
                     584 AA
                   PRT;
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EMBL; BX640437; CAE30710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylase family protein.
                                             01-0CT_2003 (TrEMBLrel, 25, 01-0CT-2003 (TrEMBLrel, 25, 01-0CT-2003 (TrEMBLrel, 25, Albumin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                  PRELIMINARY;
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Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KPLLEKSH 9
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE 245 AA
                                                                                                                                                                    NCBI_TaxID=9685;
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Q7WQW3
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SEQUENCE FROM N.A.

STAIN=12822 / ATCC BAA-587;

STAIN=12822 / ATCC BAA-587;

RA TAIN=12822 / ATCC BAA-587;

RA FARIN=12822 / FubMed=12910271;

PATKIN-1282 / Bobainia M., Preston A., Murphy L.D., Thomson N.,

RA Harris D.E., Holden M. TG., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A chtman M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Ouail M.A.,

A chtman M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

Relianing M., Connoin A., Davis P., Doggett J.,

Relianing M., Crohlin A., O'Neil S., Ormond D., Price C.,

Rabbinowitsofh E., Rutter S., Sanders M., Squares B., Seeger K.,

Rabbinowitsofh E., Rutter S., Sanders B., Seeger K.,

Rabbinowitsofh E., Whitchead S., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome sequences of Bordetella pertussis,

Rodetella parapertusis and Bordetella bronchiseptica.";

Rabbin B., Skid A., Sanders R., Sanders R.,

Rabbin B., Skid A., Skelton J., Squares R.,

Romplete proteome.

SW Complete proteome.

SW Complete Proteome.
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STRAIN-CS 7BL/6J; TISSUE=Thymus;
STRAIN-CS 7BL/6J; TISSUE=Thymus;
MEDLINS-22334683; PubMed=12466851;
The FAMTOM CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
AA1874518 of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
NATURE 420:563-573 (2002).
MGD; MGI:87991; Albi.
GQ; GO:0005615; C:extracellular space; IEA.
GQ; GO:0005386; F:carrier activity; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.
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                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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     PRT;
                                                                                                                                                                                                                                                 Phosphorylase family protein.
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                                                                                                                                                                                                                                                                                                                                                Bordetella parapertussis.
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nes 7; Conservative
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PRELIMINARY;
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1; Indels

1, Mismatches

Conservative

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SEQUENCE FROM N.A.
STRAIN=cv. Svaloef's Bonus;
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QBLFB3;
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Q94C01;
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Q94C01
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2 SEQUENCE FROM N.A.
3 SEQUENCE FROM N.A.
4 Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
5 Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
6 Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
7 "Albumin precursor homolog is a novel T helper cell immunogenic component in murine infection with Schistosoma mansoni.";
8 The Media (SEP-2001) to the EMBL/GenBank/DDBJ databases.
8 EMBL; AF418550; AAL08579.1;
8 EMBL; AF418550; AAL08579.1;
8 CG) GO:0005615; C:extracellular space; IEA.
8 CG) GO:0005810; P:transport, IEA.
8 CG) GO:0005810; P:transport, IEA.
8 CG) GO:0005810; P:transport, John I.
8 FRINTS; PRO0273; transport, Drot; 3.
8 FRINTS; PRO0802; SERUMALBUMIN; 1.
8 PRINTS; PRO0129; ALBUMIN; 3.
8 PROSTIE; SO00212; ALBUMIN; 3.
8 SEQUENCE 608 AA; 68225 MW; ESEABB20BEIC66E54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                       Score 37; DB 11; Length 576;
Pred. No. 68;
3; Mismatches 0; Indels
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                                                                                                                                                                                                            NON TER 1 1
SEQUENCE 576 AA; 65002 MW; F85733E99AE37F04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC_2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Albumin.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608 AA
GO, GO.0006810; P.transport; IEA.
InterPro: IPR002024; Serum albumin.
Péan, PR00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
PRDOM: PROCA346; Serum albumin; 1.
SYMRT; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Albumin 1.
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Best Local Similarity 66...
Best Local Similarity 66...
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Best Local Similarity 66.7
Matches 6; Conservative
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272 DKPLLKKAH 280
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SEQUENCE FROM N.A.
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095V87
AC 095V87
AC 095V87
DT 01-DD
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38 KPLLKRSH 45
            Hypothetical protein.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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MEDLINE=22735913; PubMed=12835416;
MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                  SEQUENCE FROM N.A. Has a sequence of trouchan M., Alexandrov Faldmann K.A., Flavell R.B., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.6%; Score 36; DB 16; Length 480; 87.5%; Pred. No. 91; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.6%; Score 36; DB 10; Length 191; 77.8%; Pred. No. 37; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Peldmann K.;
Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY084948; AAM61509.1;
Hypothetical protein.
SEQUENCE 191 AA; 21908 MW; F7434F97C7520294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL. BX294144 CAD74852.1;
Hypothetical protein; Complete proteome.
SEQUENCE 480 Aa; 53002 MW; 82B07EA8798FB7A2 CRC64;
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Best Local Similarity 77.00.,
And 77 Conservative
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                                                                                                                                                                                                                                                                   annotation.";
Genome Biol. 0:0-0(2002)
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01-OCT-2003 (
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01-OCT-2002
01-JUN-2003
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Q8KLA6
ID Q8KLA
AC Q8KLA
DT 01-OC
DT 01-OC
DT 01-OC
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27UQ53
AC 07UQ53
DT 01-0C
DT 01-0C
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SEQUENCE FROM N.A.
STRAIN=ATCC 814 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=1466286;
MOEDLING=21359325; PubMed=1466286;
MOEDLING J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Tatuscov R.L., Sabathe F., Duccette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium [Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL, AE007790, AAK80877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CRN42;
MEDLINE=974921; PubMed=9274036;
MEDLINE=9749219; Dustos P., Girard L., Rodriguez O.,
Cevallos M.A., Davila G.;
"Sequence, Localization and characteristics of the replicator region
of the symbiotic plasmid of Rhizoblum etli.";
Microbiology 143:2825-2831(1997).
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                                                                                                                                                                                                                                                                           MEDLINES-91199195; PubMed=2013564; Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.; Structural complexity of the symbiotic plasmid of Rhizobium leguminosarum bv. phaseoli."; J. Bacteriol. 173:2411-2419(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CF742;
Quintero V., Cevallos M.A., Davila G.;
Quintero V., Cevallos M.A., Davila G.;
Quintero V., Cevallos M.A., Davila G.;
As lite-specific recombinates and RecA are required to exert
incompatibility towards the symbiotic plasmid of Rhizobium etli.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U80928; AAM54641.1; -.
GO; GO:0046821; C:extrachronsomal DNA; IEA.
Hypothetical protein; Plasmid.
SEQUENCE 123 AA; 13938 MW; 7349C06DC4D4766A CRC64;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Rhizobium etli.
Plasmid symbiotic plasmid p42d.
Plasmid symbiotic plasmid p42d.
Raceria, Proteobacteria, Alphaproteobacteria, Rhizobium.
Rhizobiaceae, Khizobium/Agrobacterium group, Rhizobium.
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Pred. No. 38;
2; Mismatches 0; Indels
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GO; GO:0008080; F:N-acetyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
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01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
predicted acetyltransferase.
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Best Local Similarity 75.0°
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STRAINSTOCT 1168;

XX MEDLINE=2015.9912; FubMed=10688204;

XB MEDLINE=2015. FubMed=10688204;

XA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

A Jagels K., Xarlyshev A.V., Moule S., Pallen M.J., Penn C.M.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitchead S., Barrell B.G.;

The genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences.";

Nature 403:665-668(2000).

REMBL; AL13078; CAB73757.1; -.

REMSL; AL13078; CAB73757.1; -.

RHYDOTHERICAL protein; Complete proteome.

SQUENCE 301 AA; 35002 MW; 3A14BB93BA6F61D9 CRC64;
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0000524; F:ATP binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006106; F:nucleotide binding; IEA.
InterPro; IPR0013593; AAA ATPaee.
InterPro; IPR00140; ABC TM transpt.
InterPro; IPR00140; ABC TM transpt.
Pfam; PF00066; ABC TEAN; 2.
ProDom; PD000606; ABC Lransporter.
ProDom; PD000006; ABC Lransporter; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%; Score 35; DB 16; Length 301; 87.5%; Pred. No. 91; ive 0; Mismatches 1; Indels
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
EMBL; U97407; AAB52482.2;
-PIR; D87789; D87789.
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STRAIN=Bristol N2;
Langston Y., Rohlfing T.;
"The sequence of C. elegans cosmid C34G6.";
submitted (AFR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O01495;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1265 AA.
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MEDLINE=99069613; PubMed=9851916;
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
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7; Conserve
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Best Local S
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Matches
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X MEDLINE=22255705; PubMed=1236864;

X MEDLINE=22255705; PubMed=1236864;

X Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W.,

XA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

X Gardner M.J., Ratherford K.E., Salzberg S.L., Craig A., Kyes S.,

X Sisen J.A., Rutherford X., Salzberg S.L., Nather M.W., Vaidya A.B.,

RA Chan M.-S., Nene V., Shallom S.J., Haft D., Mather M.W., Vaidya A.B.,

RA Artin D.M.A., Farilamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

RA Mcradden G.I., Cummings L.M., Subramanian G.M., Mungall C.,

RA Fraser C.M., Barrell B.;

R Fraser C.M., Barrell B.;

R France J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

R France G. C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

R France G. C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

R France H.J. Appl4844; AAN36113.1;

DR GO; GO:0006457; P:protein folding; IBA.

DR GO; GO:0006457; P:protein folding; IBA.
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Batteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Campylobacteraceae; Campylobacter.
VCBI_TaxID=197;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                  74.5%; Score 35; DB 16; Length 156; 66.7%; Pred. No. 48; arive 1; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.5%; Score 35; DB 5; Length 226; 100.0%; Pred. No. 68; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISWRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 226 AA; 26429 MW; 9A1E790BB457E181 CRC64;
InterPro; IPR000182; GCNSacetyl_trans.
Pfam; PR00833; Acetyl_transf; 1.
Transferase; Complete proteome.
SEQUENCE 156 AA; 17998 MW; ADF750D0FCS953E8 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Cj1330.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             226 AA.
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0816215

01-MAR-2003 (TrEWBLrel. 23, Cz

01-MAR-2003 (TrEMBLrel. 23, Le

01-JUN-2003 (TrEMBLrel. 24, Le

Cyclophilin, putative.
                                                                                                             Local Similarity 100.
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                                                                                                                                                                                                                                                                                                           137 EKPLIETDH 145
                                                                                                                                                                                                                                                1 EKPLLEKSH 9
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OQPNWA
DID QQPNWA
AC QQPNWA
DDT 01-0C
DT 01-0C
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RESULT 13
C081621
LD C081622
AC C081622
DT O1-MP

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74.5%; Score 35; DB 5; Length 1265;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
SWART; SM00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PSS0833; ABC_TRANSPORTER_2; 2.
HYDOCHHELICAI protein; ATP-binding; Transport.
SEQUENCE 1265 AA; 140465 MW; 4948EP5G5A402757 CRC64;
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13 KPLLKRSH 20
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Search completed: April 19, 2004, 12:00:09 Job time : 5.47368 secs

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Best Local Similarity 85.7
Matches 6; Conservative
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SEQUENCE FROM N.A.
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Best Local S
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QBSXM8
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Q8NST2
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MEDLINE=22709107; PubWed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. US.A. 100:7877-7882 (2003).
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SEQUENCE FROM N.A.
STRAINS-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; Pubmed=11572948;
OMUTA S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Genome sequence of an industrial microorganism Streptomyces
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
probable succinyl-CoA synthetase (Beta chain) SUCC (SCS-beta)
SUCC OR MB0976.
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Bacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.6%; Score 29; DB 16; Length 387;
85.7%; Pred. No. 3.98+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                        Score 29; DB 16; Length 315;
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40897 MW; DC055A7CD5E987CC CRC64;
                InterPro; IPR006140; 2-Hacid_DH_C.
Pfam; PP00389; 2-Hacid_DH; 1.
Pfam; PP02826; 2-Hacid_DH_C; 1.
Plasmid; Hypochatical profein; Complete proteome.
SEQUENCE 315 AA; 34163 MW; A335784D7608BE26 CRC64;
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            IPR006140; 2-Hacid_DH_C.
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                                                                                                                                                                                                 90.6%;
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387 AA; 40897
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Best Local Similarity 85...
6; Conservative
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                                                                                                                                                                                                                                                            6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                31 EAADKAA 37
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                      1 QAADKAA 7
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SEQUENCE
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082PD6
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DT 01-JU
DT 0
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207102
AC 07102
DT 01-0C
DT 0
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP005275, BAB9778.1; Hypothetical protein; Complete proteome.
SEQUENCE 503 AA; 52191 MW; 7C257A5457A515C1 CRC64;
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                                                                                              STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=222608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                             "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531 (2003).

EMBL, AP00505; BACG8697.1; -

Hypothetical protein; Complete proteome.

SEQUENCE 466 AA; 48152 MW; 436EEEFSAC2E3FD2 CRC64;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.6%; Score 29; DB 16; Length 503;
85.7%; Pred. No. 5.2e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 85.7%; Pred. No. 4.88+02; 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Cg10885.
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Last annotation update)
metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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01-UTN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
LD23509p (CG12141-PA).
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Q7YSG3
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Q7YSG3
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REDINDE-20196006; Pubbded-10731132;
RAdams M.D. Celniker S.E., 16 P.W., Hoskins R.A., Galle R.F.,
RA Amantides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfelifer B.D.,
RADII J.F., Agbayani A., An H.J., Andrews-Fannkoch C.R., Balbor B.D.,
RADII J.F., Bencs P.V., Bernam B.P., Bandari D., Belabarkov S.,
Radeson K.Y. Bencs P.V., Bernam B.P., Bandari D., Botharkov S.,
Radeson K.J., Bencs P.V., Bernam B.P., Brottler P.,
Borkova D., Bocchen M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Bocchen M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Bocchen M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Bocchen M.S., Buller H., Cadieu E., Center A., Chandra I.,
RADESON K., Doup L.E., Downes M., Dugan-Rocha S., Punkov S.,
RADESON K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferrac C., Ferrac
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Celliker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.
Brans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.
A Banzon J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A.,
A Pacleb J., Paragas V., Park S., Patel S., Péciffer B.,
A Pacleb J., Paragas V., Svirskas R., Tector C., Tyler D.,
A stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Milliams S.M., Zaveri J.S., Smith H.O., Venez J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy O.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
STRAIN=Berkeley;
Laplacon M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
                                                                                                                                Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
Reininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P.,
Rumpold H., Valenta R., Spitzauer S.;
Rumpold H., Valenta R., Spitzauer S.;
Escherichia coli expression and purification of recombinant cat
albumin: IgE recognition, induction of basophil activation and
lymphoproliferative responses in atopic patients:";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ487677; CAD32275.1;
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Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         90.6%; Score 29; DB 6; Length 584;
85.7%; Pred. No. 6.1e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 5; Length 574; Pred. No. 5.9e+02;
                                                                                                                  Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PSSGB62; AA TRNA_LICASE II; 1.
SEQUENCE 574 AA; 64661 MW; 861DAEA9C53E0DBE CRC64;
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Last annotation update)
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01-00T-2003 (TrEMBLrel. 25,
01-00T-2003 (TrEMBLrel. 25,
Albumin (Fragment).
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Matches 6; Conserva
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                                                                                                     SEQUENCE FROM
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170 EAADKAA 176

Search completed: April 19, 2004, 12:00:05 Job time : 4.70175 secs

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April 19, 2004, 11:24:29; Search time 4.11727 Seconds (without alignments) 480.375 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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11. geneseqp1980s:*
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43. geneseqp2000s:*
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67. geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription		משוושוו	71 Human	875	00	0022	3947 Yeast	9874 Novel	7051	4				æ	88	83	ø	78	4 Novel	Aau29942 Novel hum	2995 Novel	87 Nov	87 N-t	œ	90 N-t	Aap90391 N-termina
SUMMARIES	ID		AACOULUS		AAU29875	AA017048	ABU10022	AAY83947	AAU29874	AA017051	AA016984	ABU10025	AA016985	AA016986	AA016987	AA016988	AA016989	ABU10026	AAR14178	AAU32564	AAU29942	AAU32995	AAU33287	AAP90387	AAP90389	39	33
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AAU29876 AAR14179 AAR14179 ADD32019 ADD32019 ADP2901381 AAR90388 AAR90388 AAR90318 AAR26362 AAR80301 AAC20111 AAC3011 AAC3011	ALIGNMENT	116 AA.			14000.	feration tem cell omodulat rthritis				27.	26. 09.		RT;		polypeptide, inflammat:	139900 +	The invention relates to human polymucleo the encoded proteins (AAO00010-AAO13910) cytokine, cell proliferation or cell diff production of other cytokines in other ce polymucleotides and polymeptides are usef peptide therapy. The polymeptides have va cell strowth factor activity, activity, tissue growth factor activity, activity, tissue growth factor activity, activity, tissue growth factor activity, activity, in activity and may be useful treatment of cancer, leukaemia, nervous s
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0.000000000000000000000000000000000000		1 38 4000108	AA000108;	6-NOV-20	Human pol	Human; cy vaccine; tissue gr nervous s	Homo sapie	WO20016483	07-SEP-200	26-FEB-20	28-FEB-20 18-MAY-20	(HYSE-)	Tang YT,	WPI; 2001 N-PSDB; A	Isolated and treat	Claim 20;	The inver the encode cytokine, productic polynucle peptide e.g. sten activity, activity, treatment
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OAADKAA

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Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 206; 765pp; English
                                                                                                     AAU29875 standard; protein; 192 AA
                                                                                                                                                                                             Novel human secreted protein #366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US008656.
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26-JAN-2001; 2001US-00770160
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                           17 QAADKAA 23
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                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                  AAU29875;
                                                                        RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to grothshine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoldesis regulating activity, issue growth factor activity, immunomodulatory activity and activity, issue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                     Query Match
100.0%; Score 32; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            AAO02571 standard; protein; 143 AA.
                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 16463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT;
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18-MAY-2000; 2000US-00577409.
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                                                               Sequence 116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins or useful in genetic vaccination, testing and therapy, and can be used as unitional supplements. They may be used to increase stem cell proliferation, to requiate haematopoissis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stillulation, as anti-inflammatory agents; and in treatment of leukaemias. AM129510-AAU33304 represent the amino acid sequences of novel human
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Best Local Similarity luv...
7; Conservative
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170 QAADKAA 176
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                                                                                                                   US2002193332-A1.
                                                           serum albumin
                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual existence from or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthitis, asthma, sepsis, cirthosis, dermatitis, psorlaais, contact hypersenstivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, luque, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                  Alpha-MSH; inflammation, autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive, antiinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antiasthmatic; antibacterial; dermatological; antidiabetic; ophthalmological; meuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 195; 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                        albumin (1-195) SEQ ID NO: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU10022 standard; protein; 195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human serum albumin residues 1-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 46; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                              2000US-0218381P.
2000US-0226382P.
2000US-0238380P.
2000US-0258764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aziz N,
                                                                                                                                                                                                                                                                                                                    16-JUL-2001; 2001WO-US022263.
                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0298317P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                             (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hedley ML, Urban R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 QAADKAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-195801/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QAADKAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYCO-) ZYCOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 195 AA;
                                                                                                                                                                                                                                                      WO200206316-A2
                                                                                                                                                                                                                                                                                                                                                              18-AUG-2000;
06-OCT-2000;
29-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001;
                                                                                                                                                                                                                            Homo sapiens
                                             29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                 .4-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2003
                                                                           Human serum
                                                                                                                                                                                                                                                                                      24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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                AAO17048;
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The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having a bander disorder, and administering; (a) an isolated nucleic acid (NI) comprising an un-methylated CpG sequence to the mammal; (b) an isolated nucleic acid (NI) comprising sequence encoding alpha-MSH to the mammal; (c) a peptide that binds to a melanocortin receptor to the mammal; (n) an encoding alpha-MSH to the mammal; (n) a peptide that binds to a melanocortin receptor to the mammal; (n) control is useful for modulating immune response in a mammal having an amelioration of cone or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (NI) results in a modulation of the cystitis (where administration of (NI) results in a modulation of the improved immune response from Th2 response to a Th1 response). The method is also immune response from Inflammation which is associated with symptoms that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of the bladder liming This is the amino acid sequence of human serum albumin residues 1-195 that can be used in the creation of melanocyte cumulating hormone (alpha-MSH) concertances resulting in secretion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating immune responses in a mammal with a bladder disorder e.g.
bladder cancer, by administering nucleic acids comprising un-methylated
CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
Bladder disorder; cytostatic; antiinflammatory; immune response; un-metylated CpG sequence; alpha-MSH; melanocortin receptor; bladder chancer; tumour; interstitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast codon-biased recombinant HSA protein fragment HSA-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion protein when expressed in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY83947 standard; protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 9; 17pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2001; 2001US-0268175P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2002; 2002US-00074956.
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Best Local Similarity 100.
Matches 7; Conservative
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Li S,

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimulation, as anti-inflammatory agents; and in treatment of leukaemias. AMU29910-AAU33304 represent the amino acid sequences of novel human
                                                                                                                        Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-mSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; antiathmatic; antibacterial; dermatological; antipsoriatic; antidiabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 32; DB 4; Length 214; 100.0%; Pred. No. 43; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human albumin-thrombin-alpha-MSH SEQ ID NO: 82.
                                                                                                                                                                                            Claim 20; Page 205; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO17051 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-2000; 2000US-0218381P.
18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-0238380P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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                                          Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2002 (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 QAADKAA 201
                                                                                  WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
(HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QAADKAA
                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200206316-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2002
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                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as there synthetic fragments (AAA10092-A10094) joined by recombinant DNA oligonucleoide fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping the sequence of the HSA fragment HSA-I encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression the process for producing human serum albumin in the yeast host cell, especially in secretory mode
                                                                                                                                                                                                                                                                                                                                                                                                                                           Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 32; DB 3; Length 204; 100.0%; Pred. No. 41; o; Indels ive 0; Mismatches 0; Indels
overlapping oligonucleotide; expression vector.
                                                                                                                                                                                                                                                                                      (HAIJ-) HAIJI BIOENGINEERING CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU29874 standard; protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3; 44pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                 98CN-00102506.
                                                                                                                                                                                                                                           98CN-00102506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 QAADKAA 183
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-351198/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAADKAA 7
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA10092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179449-A2.
                                            Homo sapiens.
                                                                                                                                                                                                 17-JUN-1998;
                                                                                                                                                                                                                                           17-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                Lu D;
                                                                                                          CN1239103-A,
                                                                                                                                                  22-DEC-1999.
                                                               Synthetic.
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Gaps

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Length 241;

5, DB 49;

Score 32; Pred. No.

100.0%;

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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (NSH) concaramer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, astima, sepsis, cirrhosis, dermattis, psoriasis, concact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveltis and coeliac disease. The present sequence is a protein described in the exemplification of the
                         Example 2; Page 4-5; 89pp; English.
                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
or autoimmune disorders.
                                                                                                                                                                                                             Sequence 241 AA;
                                                                                                                                                                                     nvention
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                                                                                                                                                   The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatory arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a peptide described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
                                                                    Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antibosis; antidabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                                                                                          DB 5; Length 236; 48;
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               Etemad-Moghadam B,
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-MSH construct protein fragment SEQ ID NO: 59.
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 32; DE 100.0%; Pred. No. 48; ive 0; Mismatches
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               Chen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO16984 standard; protein; 241 AA
                                                                                                                           Example 2; Page 48; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-2000, 2000US-0218381P.
18-AUG-2000; 2000US-0226382P.
06-OCT-2000, 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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               Aziz N,
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                               or autoimmune disorders.
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             Hedley ML, Urban R,
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                                                                                                                                                                                                                                                                                                                Sequence 236 AA;
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bladder disorder; cytostatic; antiinflammatory; immune response; un-methylated CpG sequence; alpha-MSH; melanocortin receptor; bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human;
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0; Indels
Mismatches
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bladder disorder, where administration of (NI) results in an amelioration of one or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where or conducting immune response in a mammal having interstitial or for modulating immune response in a mammal having interstitial or systitis (where administration of (NI) results in a modulation of the immune response to a ThI response). The method is also useful for modulating immune response in a mammal having bladder disorder that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of the bladder lining. This is the amino acid sequence of a human serum melanocyte stimulating hormone (alpha-MSH) concatamer useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences useful for treating an individual suffering from, or at risk of, a disorder of the immune system
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100.0%; Pred. No.
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06-OCT-2000; 2000US-0238380P.
29-DEC-2000; 2000US-0258764P.
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Best Local Similarity 100...
7; Conservative
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                                                                                                                                                                                                                                                              Sequence 241 AA;
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e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
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Pred. No. 49;
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18-AUG-2000, 2000US-0226382P.
06-OCT-2000, 2000US-0238380P.
29-DEC-2000; 2000US-025864F.
14-JUN-2001, 2001US-0298317P.
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Best Local Similarity 100.
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                                                                                                                        Sequence 242 AA;
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AAO16986
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Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antiasthmatic; antiacthritic; dispersive; obthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.

Alpha-MSH construct protein fragment SEQ ID NO: 73.

(first entry)

29-MAY-2002

AA016988;

AAO16988 standard; protein; 245 AA

194 QAADKAA 200

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AA016988
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                                         100.0%; Score 32; DB 5; Length 244; 100.0%; Pred. No. 49;
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                                                                                      0; Indels
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                                                                                      0; Mismatches
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06-0CT-2000; 2000US-028890P.
29-DEC-2000; 2000US-0258764P.
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7; Conservative
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Sequence 244 AA;
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AA016987
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2000US-0226382P. 2000US-0238380P. 2000US-0258764P.

18-AUG-2000; 06-OCT-2000; 29-DEC-2000;

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14-JUN-2001; 2001US-0298317P

(ZYCO-) ZYCOS INC.

16-JUL-2001; 2001WO-US022263.

WO200206316-A2.

24-JAN-2002

Unidentified.

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Chen H, Etemad-Moghadam B,
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100.0%; Pred. No. 49;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 5; 89pp; English.
        Aziz N,
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The Conservative of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or autoimmune disorders.
Hedley ML; Urban R,
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                                                                                                                                                                 WPI; 2002-195801/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention
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AAO16989
ID AAO16
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5; Length 245;

Query Match 100.0%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 49; Matches 7; Conservative 0; Mismatches

1 QAADKAA 7

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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                                                                     Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory; antiheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidiabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yin P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen H, Etemad-Moghadam B,
                                                                        Alpha-MSH construct protein fragment SEQ ID NO: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 5; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aziz N,
                                                                                                                                                                                                                                                                                                                                                                              14-JUL-2000, 2000US-0218381P.
18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
                                                                                                                                                                                                                                                                                                                                               16-JUL-2001; 2001WO-US022263
                                              29~MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hedley ML, Urban R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-195801/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 268 AA;
                                                                                                                                                                                                                                                                               WO200206316-A2
                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                 24-JAN-2002.
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               AA016989;
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Score 32; DB 5; Length 268;
Pred. No. 54;
Mismatches 0; Indels
 Query Match 100.0%; St
Best Local Similarity 100.0%; P:
Matches 7; Conservative 0;
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1 QAADKAA 7

194 QAADKAA 200

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Search completed: April 19, 2004, 11:51:18 Job time : 5.11727 secs

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1 QAADKAA 7
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Sequence 24, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 445, Appl
Sequence 18, Appl
Sequence 11, Appl
                                                                                                   April 19, 2004, 12:00:25; Search time 2.94737 Seconds (without alignments) 654.724 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications_AA:*

1: /cgn2_6/prodata/2/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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13 US-10-074-956-24

13 US-10-074-956-27

13 US-10-074-956-28

9 US-09-929-552-2

10 US-09-932-613-445

10 US-09-932-613-445

10 US-09-833-041-18

10 US-09-833-117-18

10 US-09-833-118-18

11 US-09-833-118-18
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                                                                                                                                                                                                                                                                                              1124875 seqs, 275673149 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                  US-09-832-929-18_COPY_170_176
32
1 QAADKAA 7
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                              score:
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Perfect
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## ALIGNMENTS

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TRESULT 3

TRESULT 3
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Gaps

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Sequence 445, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
TITLE OF INVERTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON FILE REFERENCE: Dyx-025.1 PCT; DXX-025.1 US
                                                                                                                                                                                                                              Sequence 2, Application US/09929552
Patent No. US20020123080A1
GENERAL INPORMATION:
APPLICANT: Sonnenschein, Carlos
TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF SEQUENCE: 2
CORRESPONDENCE ADDRESS:
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 32; DB 9; Length 585;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: Patentin Nelease #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/929,552
FILING DATE: 14-Aug-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/769,746
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: CATATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMOUNICATION INFORMATION:
TELEFATION INFORMATION:
TELEFATION (1415) 705-8410
TELEFAX: (415) 397-8338
                        Indels
                        ö
100.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Illuar

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-929-552-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 585 amino acids
TYPE: amino acid
    Best Local Similarity 100.
Matches 7; Conservative
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US-10-074-956-28

Sequence 28, Application US/10074956

Sequence 28, Application US/10074956

SEQUENCE 28, Application US/10074956

PULL APPLICANT: Hedley, Mary Lynne

TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS

TILE REFERENCE: 08191-022001

CURRENT FILING DATE: 2002-06-10

PRIOR PILICATION NUMBER: 60/268,175

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 268
                                                                                                                                                                                                                                                                                                                                      DB 13; Length 195; 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/10074956
Publication No US20020193332A1
GENERAL INFORMATION:
APPLICANT: Hediev, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFREENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
PRIOR APPLICATION NUMBER: 06/268,175
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 241
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
  TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS FILE REFERENCE: 0819-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR PEPLICATION NUMBER: 60/268,175
NUMBER OF SEQ ID NOS: 29
SEQ ID NOS: 29
SEG ID NO 24
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 32;
100.0%; Pred. No.
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-10-074-956-28
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                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-074-956-24
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US-10-074-956-27
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170 QAADKAA 176
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US-09-833-117-18
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09984010
Publication No. US20030104578A1
GENERAL INFORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION:
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: INPORT LIFE: FLOPEY LIFE
COMPUTER: BY PC Compatible
CORRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-UNH 1998
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 19-DEC-1996
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: protein
HYPOTHETICAL: NO
ANTIL SENSE: NO
ANTIL SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-984-010-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 32; DB 10; Length 585; 100.0%; Pred. No. 82;
                                                                                                                                                                                                      100.0%; Score 32; DB 10; Length 585; 100.0%; Pred. No. 82; cive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 445
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                        TYPE: PRT ORGANISM: HomoSapiens
                                                                                                                                                                                                                                                                                                                            170 QAADKAA 176
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                                                                                                                                                                 US-09-932-613-445
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US-09-984-010-26
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RESULT 8 US-05-833-041-18 Sequence 18, Application US/09833041 ; Publication No. US20030125247A1

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| Western inventor | Western inv
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US-10-42-999-11

1 Sequence 11, Application US/10424999

1 Sequence 11, Application US/10424999

2 Sequence 11, Application No. US20040052810A1

3 GENERAL INFORMATION:

4 APPLICANT: Cameron, Beatrice

5 APPLICANT: Blanche, Francis

7 TITE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for TITE OF INVENTION: Using Them to Inhibit Angiogenesis

7 TITE OF INVENTION: USING Them to Inhibit Angiogenesis

7 TITE OF INVENTION: USING Them to Inhibit Angiogenesis

7 TITE OF INVENTION: USING Them to Inhibit Angiogenesis

8 FILE REFERENCE: 2002-04-04

9 PRIOR APPLICATION NUMBER: 10/233,675

9 PRIOR FILING DATE: 2002-09-04

9 NUMBER OF SEQ ID NOS: 70

9 SOFTWARE: Patentin Version 3.2

9 SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels C
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Sequence 18, Application US/09833245
Sequence 18, Application US/09833245
Publication NO. 220040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FITLE REPERENCE: PF546FCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
RIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN VOS: 2267
SOFTWARE: PATENTIN VOS: 2267
SOFTWARE: PATENTIN VOS: 2267
TYPE: PRT
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 585
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-833-245-18
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GORGANISM: Homo Sapiens
US-09-833-118-18
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  APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Eleming, Tony J.
APPLICANT: Ladder, Robert
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: Dyx-018.1 PCT; DYX-018.1 US
CURRENT PAPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
ENGTHA: 585
LENGTH: 585
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Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels (
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Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roseltine, William A.
TILE OF INVENTION: Albumin Fusion Proteins
TILE REFERENCE: PF544
CURRENT FILING DATE: 2001-04-12
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NESOLI II.

NESOLI II.

Sequence 18, Application US/09832501

Sequence 18, Application US/09832501

SUBJICATION OF US20030199043A1

SPELICANT: Ballance, David J.

APPLICANT: Sleep, Darrell

APPLICANT: Turner, Andrew J.

APPLICANT: Brieg, Darrell

APPLICANT: Brieg, Darrell

APPLICANT: Prior, Christopher P.

TITLE OF INVEXTION: Albumin Fusion Proteins

FILE REFERENCE: PF542

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/229,358

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/256,931

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
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US-09-832-501-18
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; ORGANISM: HomoSapiens
US-09-932-322-445
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RESULT 15

US-10-425-000-31

US-10-425-000-31

SEQUENCE 31, Application US/10425000

Publication No. US20040052777A1

GENERAL INFORMATION:
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Anglogenesis
FILE REFRENCE: ST0102-B

PRIOR REPLICATION NUMBER: US/10/425,000

CURRENT FILING DATE: 2003-04-29

PRIOR PILING DATE: 2003-09-04

NUMBER OF SEQ ID NOS: 105

SSCPIND NO 31

LENGTH: 585
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                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Human derived fusion protein US-10-425-000-31
                                                        FEATURE:

OTHER INFORMATION: Fusion protein human abrogen US-10-424-999-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                    TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 585
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Search completed: April 19, 2004, 12:54:58 Job time : 2.94737 secs

170 QAADKAA 176

1 QAADKAA 7

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LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
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CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
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                                                                                                          April 19, 2004, 11:40:29 ; Search time 2.14589 Seconds (without alignments) 336.813 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
Sequence
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Sequence 5
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Sequence 3
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2: /cdT2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgD2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgD2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgD2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgD2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-702-572-2
US-08-8970-64-5
US-08-8970-64-5
US-08-8970-64-2
US-08-8970-64-2
US-09-976-594-977
US-09-984-186-2
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US-09-984-186-2
US-10-153-064-133
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                       US-09-832-929-18_COPY_76_89
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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127, App
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125, App
123, App
92, App
101, App
2, Appli
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16, Appl
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US-10-153-064-127
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US-10-153-064-125
US-10-153-064-125
US-10-153-064-121
US-10-153-064-101
US-08-256-938-2
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US-08-448-196A-4
US-08-448-196A-4
US-08-448-196A-4
US-08-448-196A-4
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US-08-448-196A-4
US-08-448-196A-4
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## ALIGNMENTS

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COMPUTER: USA

ZIP: USA
ZIP: USA
ZIP: USA
ZIP: USA
ZIP: USA
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUCHENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE: US 07/847975
FILING DATE: OS-MAR-1992
RAICH APPLICATION NUMBER: US 07/847975
FILING DATE: 29-AR-1992
PRICK APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 29-AR-1999
PRICK APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 29-AR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SWOPE: PS-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SWOPE: PRICK HAIN
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 24864
REFERENCE/DOCKET NUMBER: 24804
Sequence 14, Application US/08153799;
Sequence 11 No St6883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
ITLE OF INVENTION: POLYpeptides
NUMBER OF SEQUENCES: 23
CORRESSORBESSER: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 219484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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14

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CARTER, DANIEL C

APPLICANT: CARTER, DANIEL C

APPLICANT: RUKER, FLORIAN

APPLICANT: RUKER, FLORIAN

TITLE OF INVENTION: CXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT

TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

FILE REFERENCE: 08/984,176

CURRENT APPLICATION NUMBER: US/08/984,176

CURRENT FILING DATE: 1997-12-03

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

SEQ ID NO 1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5965366

GENERAL INFORMATION:

APPLICANT: Rerry-Williams, Sean M
APPLICANT: Gilbert, Sarah C
TITLE OF INVENTION: Yeast Strains and Modified Albumins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Centeen L.L.C.
STREET: 1020 First Avenue
CITY: King of First Avenue
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFRATING SYSTEM: MS-DGS
SOFTWARE: MICROSOft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,572
FILING DATE: 11-MOV-1996
CLASSIFICATION NUMBER: GB 9404270.2
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wasani Biswas
REFERENCE/DOCKET NUMBER: CE0114 US
TELECOMMUTATION INFORMATION:
TELEPAX: 610/878/4221
INFORMATION POR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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100.0%; Pred. No. 5.4e-05;
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Patent No. 5965386
                                                                                                                                       US-08-984-176-1; Sequence 1, Application US/08984176; Patent No. 5948609
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                                             76 rvarireryceman 89
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Best Local Similarity 100.
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-08-984-176-1
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TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NARA
STREET: MARSHALL SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
COUNTRY: USA
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Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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100.0%; Score 70; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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HSA(1-n)"
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGRNT INFORMATION:
NAME: BROAD UR., FOBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEFAX: 205-544-0258
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                 /note= "Amino acid sequence of
natural HSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 35812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08448196A; Patent No. 5780594; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Innear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTL-SENSE: NO
FRAGMENT TYPE: N-terminal
MOLECULE 111...

HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Home sapiens
FEATURE:
NAME/KEY: Region
JOCATION: 369..419
OTHER INFORMATION: HSA(
FEATURE:
NAME/KEY: Region
LOCATION: 1.585
OTHER INFORMATION: HSA(
JOCATION: 1.585
OTHER INFORMATION: na
US-08-153-799-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TVATLRETYGEMAD 14
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Length 585;

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; Sequence 3, Application US/08222619
; Patent No. 565235
; GENERAL INFORMATION:
APPLICANT: Lyons, David
APPLICANT: Lyons, David
APPLICANT: Warfel, Mark
APPLICANT: Warfel, Samuel
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 70; DB 1; Length 609; 100.0%; Pred. No. 5.7e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PALENTIN VERSION 3:1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sreekrishna, Kotikanyadan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08433037; Patent No. 5707828; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TVATLRETYGEMAD 14
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Best Local Similarity 100.
Matches 14; Conservative
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MOLECULE TYPE: protein
US-08-222-619-3
                                                                                                                                                                    ; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-064-5
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US-08-433-037-4
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US-08-769-746.

Sequence 2, Application US/08769746

Patent No. 6274305

GENERAL INFORMATION:

APPLICANT: Sonnenschein, Carlos

APPLICANT: Soncenschein, Carlos

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPE CAlifornia

COUNTRY: United States of America

ZIP: 94104

COMPUTER: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: DATE: PACCHOSY MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/769,746

FILING DATE: 19-DEC-1996

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: CARTOIL, Peter G.

REFERENCE/DOCKET NUMBER: 32,837

REFERENCE/DOCKET NUMBER: 32,837

REFERENCE/DOCKET NUMBER: 32,837

TELEPHONE: (41s) 705-8410

TELEPHONE: (41s) 705-8410

TELEPHONE: GHARACTERISTICS:

LENGTH SES amino acids

TYPER: Amino acids

TYPER: Amino acids
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                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-153-064-5
US-10-153-064-5
Sequence 5, Application US/10153064
Patent No. 665485
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 585 amino acids
amino acid
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          SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-572-2
                                                                                                                                                                                                                                                                                                                  76 TVATLRETYGEMAD 89
                                                                                                                                                                                                                                                                                 1 TVATLRETYGEMAD 14
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hes 14; Conservative
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MOLECULE TYPE: protein

US-08-769-746-2
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US-08-769-746-2
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RESULT 11
US-09-976-594-977
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100.0%; Score 70; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 70; DB 1; Length 609; Best Local Similarity 100.0%; Pred. No. 5.7e-05; Matches 14; Conservative 0; Mismatches 0; Indels
APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Thill, Gregory P.
APPLICANT: TSCHOOP, Users F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: T1530-0299

COMPUTER: F10ppy disk

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APPLICANT: Philip Lake
FILE REFERENCE: 600-7244(CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SSENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-897-956A-2

Sequence 2, Application US/08897956A

Patent No. 6423512

; GENERAL INFORMATION:
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CRGANISM: Homo Sapiens
US-08-897-956A-2
                                                                                                                                                                                                                                                                                                                                                                  STREET: 400 cur
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Garde...
STATE: New York
COUNTRY: U.S.A.
71P: 11530-0299
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Sequence 977, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Burness, Michael
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOGTWARE: PERL PROGRAM
SEQ ID NO 977
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 70; DB 4; Length 609; Best Local Similarity 100.0%; Pred. No. 5.7e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 609;
                                                                                                                                                               Sequence 7, Application US/10153064

Sequence 7, Application US/10153064

GENERAL INFORMATION

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT APPLICATION NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SEQ ID NO 7

LENGTH: 609
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OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 70; DB 4; I 100.0%; Pred. No. 5.7e-05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application PC/TUS9504075; GENERAL INFORMATION:
APPLICANT: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 rvariksrydsmap 113
                                      100 TVATLRETYGEMAD 113
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1 TVATLRETYGEMAD 14
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Best Local Similarity 100.0
....has 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo Sapiens
US-10-153-064-7
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TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                            Score 70; DB 2; I
Pred. No. 5.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION NUMBER: US/09/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/797,689
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: B 92/01064
APPLICATION NUMBER: P 92/01064
APPLICATION NUMBER: P 92/01064
APPLICATION NUMBER: P 92/01085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REPRENCE/COCKT NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEPHONE: (610) 454-3839
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                        P-38,619
3R: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (610) 454-383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09984186 Patent No. 6686179 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
                                                                                                                                                                                                         TOPOLOGY: 11mer-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-797-689-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
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US-09-984-186-2
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Detent No. 5876-99

Patent No. 5876-99

Patent No. 5876-99

GENERAL INPORMATION:

APPLICANT: Fleer, Reinhard

APPLICANT: Fleer, Alain

APPLICANT: Fleer, Alain

APPLICANT: Guitton, Jan-Dominique

APPLICANT: Jung, Gerard

APPLICANT: Jung, Gerard

APPLICANT: Jung, Gerard

APPLICANT: Work Parine

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 30

TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 30

CITY: Collegevile

STREET: 500 Arcola Road, 3C43

CITY: Collegevile

STREET: SOO Arcola Road, 3C43

CONTAY: USA

ZIP: 1942-6

STREET: PAPPLICATION DATA:

MEDIUM TYPE: Ploppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOOTMARE: Wad 5.1 (Patentin)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-UUL-1994

FILING DATE: 28-UUL-1994

FILING DATE: 31-AN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 70; DB 5; Length 609; 100.0%; Pred. No. 5.7e-05; tive 0; Mismatches 0; Indels
        Afamin: A Human Serum Albumin-Like
                                                                               100 TVATLRETYGEMAD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TVATLRETYGEMAD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
    TITLE OF INVENTION: Pr.
TITLE OF INVENTION: Pr.
NUMBER OF SEQUENCES: 3.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-04075-3
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100.0%; Score 70; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-153-064-133
Sequence 133, Application US/10153064
Patent No. 6663485
GENERAL INFORMATION:
APPLICANT: Bell at 1.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT PILING DATE: 2002-05-24
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
LENGTH: 651
SEQUENCE CHARACTERISTICS:

LENGTH: 610 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 19, 2004, 12:05:19 Job time : 2.14589 secs
                                                                                                                                                                                                                                                            100 TVATLRETYGEMAD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TVATLRETYGEMAD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT

) ORGANISM: Homo sapiens

US-10-153-064-133
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April 19, 2004, 11:37:59 ; Search time 1.09695 Seconds (without alignments) 789.208 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                           Run on:
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US-09-832-929-18\_COPY\_92\_100 47 1 AKQEPERNE 9 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	serum albumin prec		lbumin	-01	serum albumin - mo	serum albumin prec							6.2		ı	component of type	πſ	nuclear autoantige	thif protein - Esc	thiamin biosynthes	thiamin biosynthes	hypothetical prote	ABC transporter BH	probable sigma-70	hypothetical prote	H	74K albumin precur	C (im	hypothetical 84K p
SUMMARIES	ID	A47391	ABRTS	ABHUS	JC5838	A05139	ABBOS	ABSHS	ABHOS	ABPGS	857632	S59517	ABCHS	G96787	A60272	BOAG58	AF3249	A43800	A48819	C65206	C91243	A86091	H84607	H84108	G83477	B82965		ABXL72	AC3220	JQ1383
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	Score	47	47	47	47	43	43	43	43											33				33	33	33	33	33	33	33
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906 1364 106	204 2014 2014 2014	486 559 721	1032	1172 1291 3051
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## ALIGNMENTS

RESULT 1

	serum albumin precursor - rhesus macaque Cispecies: Macaca mulatta (rhesus macaque)
	n n n
- ,	Riwatkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.
-	A, Title: CDNA and protein sequence of polymorphic macaque albumins that differ in bilin
	A;Reference number: A47391; MUID:93211971; PMID:8460152 A:Contents: B/B homozyqote
	A,Accession: A47391
	Astatus preliminary AsMolecule tyre: mRNA; protein
	A.Residues: 1-600 (MAI)
	A.Note: sequence extracted from NCBI Dackbone (NCBIN:128280, NCBIP:128281)
	Cysuperiaminty: estum albumin estum albumin repeat inmology F:21-194/Domain: serum albumin repeat homology <8Al>
	F/213-386/Domain: serum albumin repeat homology <sa2></sa2>
	F/405-584/Domain: Berum albumin repear nomology ksAs>
_	100.0%;
	Best Local Similarity 100.0%; Pred. No. 0.26; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-	Cy 1 AKQEPERNE 9
	D5 108 AKQEPERNE 116
	RESULT 2 ABRTS
	serum albumin precursor - rat
	N.Atternate names: preprogrammn C.Species: Rattus norvedicus (Norvey rat)
	C,Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 22-Jun-1999
	C.ACCESSION: ASSOLV; ASZZII; ASISTO, ASTSTO, GEOCO, ISTOLI, ACSZSS R.Sargent, T.D.; Yang, M.; Bonner, J.
	Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981 A:Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
	A; Accession: A93872
	A. Nesidues: 1-608 <5AR>
	A;Cross-references: GB:V01222; GB:J00698; NID:g55627; FIDN:CAA24532.1; FID:g55628 R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
	J. Biol. Chem. 252, 6846-6855, 1977
	A) ILLIE: Kal IIVel pleaforming Compiler and Compiler of Compiler
-	A;NOTe: cleavages cutting process macutarios

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A,Molecule type: mRNA
A,Residues: 1-419, KV,421-609 <LAW>
A,Residues: 1-419, KV,421-609 <LAW>
A,Residues: 1-419, KV,421-609 <LAW>
A,Crosal-creferences: EMBL:V00495, GB:U00132; GB:L00133; NID:g28591; PIDN:CRAZ: R,Dagaccyk, A.; Law, S.W.; Dennison, O.E.
B,Dugaccyk, A.; Law, S.W.; Dennison, O.E.
A,FUCI. Acid. Sci. US.A. 79, 71-75, 1982
A,FILL: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.
A,Reference number: A9936; MUID:82105994; PMID:6275391
A,Rocession: A93936
A,Molecule type: mRNA
A,Residues: 1-120, G',122-609 <CDG>A,MOLECULE type: mRNA
A,Rocession: A,Wollecule type: MRNA
A,Residues: Lamanabe, K.; Sakai, M.; Tamaoki, T.
J. Biol. Chem.261, 3244-3251, 1986
A,FILL: The human albumin gene. Characterization of the 5' and 3' flanking regions and A,Rocession: 139427
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./Residues: 25-117, EQ',120-154,'Q',156-193,'E',195-387,'H',389-390,'Y',392-393,'A',395
./Residues: 25-117, EQ', Tripier, D.
./Roetu U.; Spiteller.'G', Tripier, D.
hustus Liebigs Ann. Chem. 9, 881-884, 1988
./Title: Isolation and structure elucidation of middle-molecular weight peptides from u.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserveferences: GB:M13075; NID:g178330; PIDN:AAAS1688.1; PID:g553173
; Matkins, S.; Madison, J.; Galliano, M.; Minchiotti, b.; Putnam, F.W.
roc. Natl. Acad. Sci. U.S.A. 91, 2275-2279; 1994
; Title: A nucleoride insertion and frameshift cause analbuminemia in an Italian family; Reference number: IS9286; MUID:94181575; PMID:8134387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4) Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 282-290, KSRFDLQ' <WAT>
A; Notices references: GB: S69192; NID: 9546032; PIDN: AAB30282.1; PID: 9546033
A; Note: this frame-bhift variant, designated albumin Roma, leads to analbuminemia
A; Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putnam, A; Trile: Genetic variants of human serum albumin Italy: point mutants and a carboxyl
A; Reserved enumber: IS9313; MUID: 94294404; PMID: 8022807
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A; Residues: 1-120, 'G', 122-455 < MEN>
A; Residues: 1-120, 'G', 122-455 < MEN>
A; Residues: 1-120, 'G', 122-455 < MEN 
Bioderwood, B.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J. 308, 321-325, 1995
A; Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kex
A; Accession: S55314
A; Accession: S55314
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Arch. Biochem. Biophys. 305, 595-599, 1993
A.Title: Mass spectrometric identification of modifications to human serum albumin trea
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.Molecule type: DNA
.Molecule type: DNA
.Molecule type: DNA
.Creaidues: 589-590 'ALPERVKNLLLQVKLP' «MAD>
.Creaidues: 589-590 'ALPERVKNLLLQVKLP' «MAD>
.Cross-references: GB:S70799; NID:G547231; PIDN:AAB31177.1; PID:G547232
.Cross-references: GB:S70799; NID:G547231; PIDN:AAB31177.1; PID:G547232
.Cross-references: GB:S70799; NID:G547231; PIDN:AAB31177.1; PID:G547232
.Cross-references: GB:S70799; NID:G547231; PIDN:AB31177.1; PID:G547232
.Cross-references: GB:S70799; NIS:AB31177.1; PID:G547232
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AyResidues: 19-27 aLED->

AyResidues: 19-27 aLED->

AyResidues: 19-37 algorithms and 18-137, 1975

PEBS Lett. 58, 134-137, 1975

Tyttle: Complete amino acid sequence of human serum albumin.

AyReference number: A91420; MUID:76187907; PMID:1225573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 806422
A; Note: this paper is in German, with an English abstract
A; Accession: 806422
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Accession: G01747
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A;Residues: 25-48 <ROE>
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A. M. Cession. A9221

A. M. Cession. A9221

A. M. Cession. A9221

A. R. Lesanza. S. Tisenza. T.

T. Biochem. 33. 15-48, 19-29

A. Tille: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage A. Accession. A91346

A. M. Colochem. A A. 
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Serum albumin precursor [validated] - human

Serum albumin precursor [validated] - human

Nalternate names preproalbumin

Nicontains: kinetensin

C;Species: Homo sapiens (man)

C;Species: 29-031-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000

C;Accession: A93743; A33936; T39427; I59286; I59313; G01747; S55314; A91420; S06422; S36

R;Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seebun

Nucleic Acids Res. 9, 6103-6114, 1981

Nucleic Acids Res. 9, 6103-6114, 1981

A;Title: The sequence of human serum albumin cDNA and its expression in Escherichia coli

A;Reference number: A93743; WUID:82081882; PMID:6171778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 100.
Matches 9; Conservative
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A,Title: Lysine residue 240 of human serum albumin is involved in high-affinity binding A, Reference number: A00299; MUID.78186630; PMID.656055
A; Contents: annotation; bilirubin-binding site
In Albumin: Structure, Blosynthesis, Function, Peters, J., and Sjoholm, I., eds., 11-20
A,Tothens: annotation; binding sites
A,Tothens: annotation; binding sites
A,Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein gene: A,Reference number: A0028; MUID.83279982; PMID:6192711
A,Ritle: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein gene: A,Reference number: A0028; MUID.83279982; PMID:6192711
A,Reference number: A0028; MUID.8279082; PMID:6192711
A,Contents: annotation; gene position
A,Title: Lysine residue 199 of human serum albumin is modified by acetylsalicyclic acid A,Title: Lysine residue 199 of human serum albumin is modified by acetylsalicyclic acid A,Contents: annotation
A,Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:118990; OMIM:103600
A;Map position: 4g11-4g13
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyrido:
E;1-18/Domain: signal sequence #status predicted <SIG>
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F;413-592/Domedin: serum albumin repeat homology <SA3>
F;413-592/Domedin: serum albumin repeat homology <SA3>
F;413-592/Domedin: serum albumin repeat homology <SA3>
F;713-592/Domeding site: copper (His) #status experimental (Jy 24-270, 269-277, 289-303, 302-313, 340-385, 384-393, 78-214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ťЪ
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Cipacies: Mariones unguiculatus (Mongolian jird)
Cipaces 105-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
Cipacesion: JC5838 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
Riyoshida, K.; Setc-Ohshima, A.; Sinohara, H.
DNA Res 4, 351-354, 1997
A.Title: Sequencing of CDNA encoding serum albumin and its extrahepatic synthesis in A.Title: Sequencing of CDNA encoding serum albumin and its extrahepatic synthesis in A.Faccession: JC5838
A.Faccession: JC5838
A.Molecule type: mRNA
A.Residues: 1-609 «YOS»
A.Cross-references: DDBJ:AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278
A.Experimental source: liver
C.Superfamily: serum albumin; serum albumin repeat homology
F;222-395/Domain: serum albumin repeat homology «SA2»
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F;25-609/Product: serum albumin #status experimental <MPT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;166-174/Product: kinetensin #status experimental <KIP>
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Best Local Similarity
Matches 9; Conserv
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A.Molecule type: prot
A; Reference number: 836882; MUID: 93384321; PMID: 8373198
A; Molecule type: procein
A; Molecule type: procein
A; Molecule type: procein
A; Residues: 45-7;111-160;311-337;469-490;570-581 cFIN>
B; Kauler, E.; Spiteller, G.
Biol. Chem. Hoppe-Sepier 322, 489-855, 1991
A; Reference number: Slass Sepier 322, 489-855, 1991
A; Reference number: Slass Sepier 322, 489-855, 1991
A; Reference number: Slass Sepier 322, 489-855, 1991
A; Residues: 25-4;334-337;431-447 cKAU>
A; Roceine type: protein
A; Residues: 25-4;334-337;431-447 cKAU>
A; Roceine type: protein
A; Residues: 25-4;334-337;431-447 cKAU>
A; Roceine type: protein
A; Residues: 516-513,345-337;431-447 cKAU>
A; Nolecule type: protein
A; Reference number: A45800; MUID: 89341406; PMID: 2474609
A; Reference number: A45800; MUID: 89341406; PMID: 2474609
A; Reference number: A45800
A; Reference number: A63039; MUID: 893-988, 1986
A; Reference number: A0339; MUID: 863-988, 1986
A; Reference number: A0339; MUID: 863-988, 1986
A; Reference number: A0339; MUID: 8642180; PMID: 308352
A; Residues: 166-173, L. ANOA;
A; Residues: 166-173, L. ANOA;
B; Realidues: 166-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <GAL1>
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A,Residues: 76-111 <GAL1>
A,Accession: B38255
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A, Modecule type: protein
A, Residues: 529-536;569-572 < WER>
A, Residues: 529-536;569-572 < WER>
A, Residues: 529-536;569-572 < WER>
C, Superfamily: serum albumin; serum albumin repeat homology
C, Superfamily: serum albumin; copper binding; duplication; plasma
C, Keywords: carrier propedide #status experimental < SIG>
F;19-24/Domain: sproperide #status experimental < PRO>
F;29-201/Domain: serum albumin repeat homology < SA1>
F;29-201/Domain: serum albumin repeat homology < SA2>
F;20-393/Domain: serum albumin repeat homology < SA3>
F;210-393/Domain: serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: S10780
A, Residues: 25-41, H', 43-57,59-64 <STR>
A, Residues: 25-41, H', 44-57,59-64 <STR>
A, Residues: 25-41, H', 44-57,59-64 <STR>
A, Residues: 25-41, H', 44-57,59-64 <STR>
J. Immunol. 143, 1680-1684, 1989
A, Title: Structures of histamine-releasing peptides formed by the action of acid protean A, Rolecule type: protein
A, Accession: 045800
A, Rolecule type: protein
A, Residues: 163-172 <CAR>
R, Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5568-5973, 1987
A, Active some number: A26693; MUD:87194805; PMID:2437111
A, Reference number: A26693; MUD:87194805; PMID:2437111
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;Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,')
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Contents: annotation; disulfide bonds
Merlen, R.C.; Offord, R.E.; Rose, K.
Jochem, J. 302, 907-911, 1994
Pritle: Preparation and characterization of novel substrates of insulin proteinase (EC)
                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: procein
A;Reaidues: 25-41 <H81>
R;Strawich, E.; Glimcher, M.J.
Bur. J. Blochem. 191, 47-56, 1990
A;Title: Tooth, 'enamelins' identified mainly as serum proteins. Major 'enamelin' is alb'
A;Reference number: S10780; MUID:90336641; PMID:2379503
          A;Molecule type: protein
A;Residues: 1.32 kMG>
R;Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A;Title: Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing
A;Reference number: A60808; MUID:88267456; PMID:3389500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: protein ,Residues: 165-172,'L' <CA2> ,Residues: 165-172,'L' <CA2> ,Residues: 161-172,'L' <CA2> ,Residues: 161, BT-869, 1980 ,100chem. J. 191, BT-869, 1980 ,100chem. J. 191, BT-869, 1980 ,1980 ,1981 ,Title: Sequence of residues 400-403 of bovine serum albumin. ,Reference number: A90309; MUID:82023364; PMID:7283978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....: structure of bovine serum albumin.
Reference number: A91458
Accession: "Affice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein;
Residues: 402-433 <REE>;Brown, J.R.
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Residues: 190-195 <BR2>
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tle: Structure of bor
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Molecule type: pro
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serum albumin precursor [validated] - bovine
NyAlternate names: 67K protein; preproalbumin
C;Species: Bos primigenius taurus (catte)
C;Date: 24-Apr.1984 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C;Accession: A38885; A36401; A91258: B60808; S10780; D45800; A26693; A90309; A91458; A94
R;HGlowachuk, E.W.; Stoltenborg, J.K.; Reed, R.G.; Peters Jr., T.
submitted to the EMBL Data Library, August 1991
A;Description: Bovine serum albumin: cDNA sequence and expression.
A;Accession: A38885
A;Molecule type: mRNA
A;Resernce number: A38885
A;Molecule type: mRNA
A;Resernces: EMBL: M3215
B;Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.
Biochem Biophys. Res Commun. 173, 639-646, 1990
A;Title: Rapid confirmation and revision of the primary structure of bovine serum albumin A;Reference number: A36401; MUID:91083649; PMID:2260975
A;Accession: A36401
A;Molecule type: protein
A;Residues: 25-41, H', 43-189, E', 191-213, T', 215-323, 'D', 325-393, TS', 396-607 AHR>
Eur. U Blochem. 99, 477-485; 1979
A;Title: Blosynthesis of bovine plasma proteins in a cell-free system.
A;Reference number: A91258; MUID:80024278; PMID:488109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: About - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Accession: A05139; HesGas Musculus (house mouse)
C.Accession: A05139; HesGas Musculus (house mouse)
R.Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
Mol. Biol. Evol. 2, 347-358; 1985
A.Accession: A05139
A.Molecule rype: mRNA
A.Reference number: A93055; MUID:88216123; PMID:2452956
A.Accession: A05139
A.Molecule rype: mRNA
A.Residues: 1-418 «MIN>
A.Residues: 1-418 «MIN>
A.Residues: 1-418 «MIN>
A.Reference number: H8638; MUID:9026960; PMID:1971802
A.Accession: H8638; MUID:9026960; PMID:1971802
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0
100.0%; Score 47; DB 2; Length 609; 100.0%; Pred. No. 0.27; ive 0; Mismatches 0; Indels
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Pred. No. 1.2;
0; Mismatches 0; Indels
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100.0%; Pre/
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                                                                                                           Conservative
                                                                                                                                                                                                                                                                                              117 AKOEPERNE 125
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Best Local Similarity
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                                                        Best Local Similarity
Matches 9; Conserv
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A.Note: albumin and other serum proteins are also found in bone
C,Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
C,Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
C,Comment: Serum albumin; serum albumin repeat homonesy promote their transfer across the membra
C,Superfamily: serum albumin; serum albumin repeat homology
C,Keywords: carrier protein; duplication; metal binding; plasma
F,11-6/Domain: signal sequence (fragment) #status predicted <NGS-
F,27-Domain: propeptide #status predicted <NAT-
F,27-199/Domain: serum albumin repeat homology <SA2-
F,218-31/Domain: serum albumin repeat homology <SA2-
F,410-589/Domain: serum albumin repeat homology <SA3-
F,410-589/Domain: serum albumin repeat homology <SA3-
F,410-113,112-123,145-190,189-198,221-267,266-274,286-310,299-310,337-382,381-390,
F,261/Binding site: bilirubin (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,Cross-references: EMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
;Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
Bone Miner. Res. 4, 235-241, 1989
. Form Miner. Res. 4, 235-241, 1989
.;Title: Serum albumin and its acid hydrolysis peptides dominate preparations of minera ,Reference number: A61006; MUID:89269769; PMID:2728927
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A,Residues: 1-608 cHI2>
A,Cross-references: EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g886485
A;Experimental source: liver
C;Comment: This protein is the major protein component in plasma. It functions as a mul-
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CiSpecies: Felis silvestris catus (domestic cat)
CiDate: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
CiAccession: UG4660, S57632
R;Hilger, C.; Grigioni, F.; Hentges, F.
Gene 169, 295-296, 1996
A;Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A;Reference number: JC4660; MJID:96194824; PMID:8647469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serum albumin precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Dace: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S01382; A61006
R;Weinstock, J; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Ritle: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:3174440
A;Reference number: S01382; MUID:89016582; PMID:3174440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 23-51,'X',53-54;'XXXGY',146,'E',148,'E',150-151,'XVN',155 <LIM>
A;Experimental source: dental enamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                    91.5%; Score 43; DB 1; Length 607; 100.0%; Pred. No. 1.6; tive 0; Mismatches 0; Indels
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Pred. No. 6.2;
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F,263/Binding site: bilirubin (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                             Query Match 91.5
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                     117 KOEPERNE 124
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C;Species: Equue caballus (domestic horse)
C;Date: 31929
C;Date: 31939
C;Date: 31903
C;Date: 319053
C;Date: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: S06936
A, Folecule type: mRNA
A, Residues: 1-607 - 6BRO-
A, Cross-references: EMBL:X17055, NID:g1386; PIDN:CAA34903.1; PID:g1387
A, Ross-references: EMBL:X17055, NID:g1386; PIDN:CAA34903.1; PID:g1387
C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membra C; Superfamily: serum albumin; serum albumin; metal binding; plasma
C; Leywords: carrier protein; duplication; metal binding; plasma
C; Leywords: carrier protein; duplication; metal binding; plasma
C; L-18/Domain: signal sequence #status predicted <ROO-
F; 22-4/Domain: serum albumin #status predicted <AMN-
F; 22-201/Domain: serum albumin repeat homology <AA3-
F; 220-393/Domain: serum albumin repeat homology <AA3-
F; 220-393/Domain: serum albumin repeat homology <AA3-
F; 27/Binding site: copper (His) #status predicted
F; 263/Binding site: bilirubin (Lys) #status predicted
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S06936
R;Brown, W.M.; Daiegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10455, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MJID:90098888; PMID:2602160
                                                                                                                                            Gaps
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                                                   DB 1; Length 607;
1.6;
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Pred. No. 1.6;
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                                                                                                                                            0; Indels
                            91.5%; Scor.
100.0%; Pred. No. 100.0%;
'... 0; Mismatches
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91.5%; Score 43; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 8; Conservative 0; Mismatches
                                                                                                                                            Conservative
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                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977

A;Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.
A;Reference number: Al3451; MUID:78019943; PMID:911327
A;Accession: Al3451
A;Accession: Ala551
A;Accession: Ala57
A;Accession: Ala551
A;Accession: Ala57
A;Accession: Ala57
A;Accession: Ala56
A;Accession: Ala57
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();Species: Arabidopsis thaliana (mouse-ear cress)
();Date: 02-Mar-2001
();Accession: G96787
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Ajmolecule Type: DNA
Ajsesidues: 1-884 <STO>
Ajcoss-references: GB:AE005173; NID:g8778819; PIDN:AAF26771.2; GSPDB:GN00141
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Pred. No. 89;
0; Mismatches 1; Indels
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Pred. No. 61;
2; Mismatches 1; Indels
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R;Gilbert, J.V.; Plaut, A.G.; Wright, A.
Infect. Immun. 59, 7-17, 1991
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
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A60272
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1999
C;Accession: S1571; A05078; A1341
R;Cassady, A.I.; Salklid, C.K.; Baverstock, P.; Wallace, J.C.
submitted to the EMBL Data Library, July 1991
A;Reference number: S1571
A;Molecule type: mRNA
A;Residues: 1-615 < CAS>
A;Cross-references: EMBL:X60688; NID:g63747; PIDN:CAA43098.1; PID:g63748
A;Residues: 1-615 < CAS>
A;Cross-references: EMBL:X60688; NID:g63747; PIDN:CAA43098.1; PID:g63748
B;Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
J. Biol. Chem. 258, 4556-4564; 1983
A;Title: The S' noncoding and flanking regions of the avian very low density apolipoprot A;Recession: A05078; MUID:83161037; PMID:618737
A;Accession: A05078
A;Molecule type: DNA
A;Residues: 1-28 < AAC>
A;Cross-references: GB:V00381; NID:g63038; PIDN:CAA23680.1; PID:g63039
R;Rosen, A.M.; Geller, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sebels Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C;Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C;Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-2000
C;Accession: S59517
R;Wang, X: Havsteen, B.; Hansen, H.
Biol. Chem. Hoppe-Seyler 376, 545-55, 1995
Biol. Chem. Hoppe-Seyler 376, 545-55, 1995
A;Title: Svidence of the coevolution of a snake toxin and its endogenous antitoxin. Clorr
A;Reference number: S59517; MUID:96145734; PMID:8561913
A;Note: the source is designated as Naja naja kaouthia, but referred to as Chinese cobra
A;Accession: S59517
A;Status: preliminary; nucleic acid sequence not shown
A;Accession: S59517
A;Status: preliminary; nucleic acid sequence not shown
A;Accession: S59517
A;Status: preliminary; nucleic acid sequence homology
C;Csuperiamily: serum albumin serum albumin repeat homology cs12
F;17-614/Product: serum albumin repeat homology cs22
F;225-398/Domain: serum albumin repeat homology cs23>
F;217-6596/Domain: serum albumin repeat homology cs32>
F;217-6596/Domain: serum albumin repeat homology cs32>
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83.0%; Score 39; DB 2; Length 608;
Best Local Similarity 87.5%; Pred. No. 9.9;
Matches 7; Conservative 1; Mismatches 0; Indels
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                                                       ein has 35 conserved cysteine residues.
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: liver; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-24/Domain: propeptide #status predicted <RRP>F;25-608/Product: serum albumin #status predicted <MAT>F;29-202/Domain: serum albumin repeat homology <SA1>F;221-394/Domain: serum albumin repeat homology <SA2>F;413-592/Domain: serum albumin repeat homology <SA3>
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74.5%; Score 35; DB
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches
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RESULT 15
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virB10 procein - Agrobacterium tumefaciens plasmid priC58
C;Species: Agrobacterium tumefaciens
C;Accession: S12360, 511835; S10525
R;Shirsau, K.; Morel, P.; Kado, C.I.
Mol. Microbiol. 4, 1153-1163, 1990
A;Fitle: Characterization of the virB operon of an Agrobacterium tumefaciens Ti plasmid:
A;Reference number: S12341; MUID:91041724; PMID:223352
A;Accession: S12350
A;Molecular type: DMA
A;Residues: 1-377 cSHI
A;Residues: 1-377 cSHI
A;Accession: S11835
A;Accessi
A; Title: Analysis of the immunoglobulin A protease gene of Streptococcus sanguis.

A; Reference number: A60272; MUID: 91100011; PMID: 1987065

A; Accession: A60272

A; Status: not compared with conceptual translation

A; Status: not compared with conceptual translation

A; Residues: 1-1668 cGIL>
C; Comment: This protein is shown from the start of translation of this gene as determine the start codon is shown in entry B60272.
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A,Start codon: GTG
C,Superfamily: Streptococcus sanguis IgA-specific metalloendopeptidase
C,Keywords: hydrolase; metalloproteinase; tandem repeat; zinc
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72.3%; Score 34; DB 1; Length 377;
Best Local Similarity 66.7%; Pred. No. 57;
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C,Superfamily: tumor-inducing plasmid pTiC58 virB10 protein
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TISSUE=Plasma;
MEDLINE=87194805; PubMed=2437111;
Carraway R.E., Mitra S.P., Cochrane D.E.;
"Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(8).";
J. Biol. Chem. 262:5968-5973(1987);
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608 AA;
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P02770; P11382;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-38, AND PROCESSING.
MEDIATE=7724657; PubMed=883447;
Strauss A.W., Bennett C.D., Donohue A.W., Rodkey J.A., Alberts A.W.;
"Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece, Analysis of the direct translation product of albumin messenger RNA.";
J. Biol. Chem. 252:6846-6855(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isenura S., Ikenaka T.,
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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SEQUENCE FROM N.A.
MEDLINE-81223722; PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
Sargent T.D., Yang M., Bonner J.;
"Nucleotide sequence of cloned rat serum albumin messenger RNA.";
Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
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MEDLINE=78109429; PubMed=564345;
Isemura S., Ikenaka T.;
'Amino acid sequences of fragments I and bromide cleavage of rat serum albumin."
J. Biochem. 83:35-48(1978).
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100.0%;
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[5]
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WEDLINE-79001617; PubMed=80265;

A POYAGI Y., IKenaka T., IChida F.;

A AOYAGI Y., IKenaka T., IChida F.;

A AOYAGI Y., IKenaka Dility of human alpha-fetoprotein.";

Cancer Res. 38:483-486(1978).

Cancer Res. 38:483-483-486(1978).

Cancer Res. 38:483-486(1978).

Cancer Res. 48:483-486(1978)
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NEUROTENSIN-RELATED PEPTIDE.
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FISSP; PO2768; LBTB.
InterPro; IRR00264; Serum albumin.
Pfam; PF00273; transport prot; 3...
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Esrum albumin; 1...
SMART; SM00103; ALBUMIN; 3...
PROSITE; PS00212; ALBUMIN; 3...
Metal-binding; Lipid-binding; Repeat; Signal; Copper. SIGNAL
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5BB497A282411AB7 CRC64;
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ALBUMIN 3.
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larity 100.0%;
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Best Local Similarity
9, Conserve
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SECUENCE FROM N.A.
MEDLIFES 64595112; PubMed=3009475;
MINGhetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,
Beattie W.G., Dugaiczyk A.;
"Molecular structure of the human albumin gene is revealed by
nuclectide sequence within q11-22 of chromosome 4.";
J. Biol. Chem. 261:6747-6757(1986).
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TISSUB=Liver, and Skeletal muscle;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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ZHANG C. YU Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,

Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;

Functional prediction of the coding sequences of 121 new genes
deduced by analysis of CDNA clones from human fetal liver.";
submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANT LYS-420.
MEDLINE=82081882; PubMed=6171778;
MEDLINE=82081882; PubMed=6171778;
Majarian T., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;
"The sequence of human serum albumin cDNA and its expression in E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT GLY-121.
MEDILINE-82105994; PubMed=6275391;
Dugaiczyk A., Law S.W., Dennison O.E.;
Nucleotide sequence and the encoded amino acids of human serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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"The cDNA sequences of human serum albumin.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          ALBU HUMAN STANDARD; PRT; 609 AA.
P02768; 095574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0; 21-UTL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Serum albumin precursor.
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Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Gord, Schmutz, Schmutz, J., Myers R.M., C., Grimwood J., Schmutz J., Myers R.M., Schein J.S., Schmutz, Procenation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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MEDLINE=86140099; PubMed=2419329;
Urano Y., Watenabe K., Sakai M., Tamaoki T.;
Urano Y., Watenabe K., Sakai M., Tamaoki T.;
The human albumin gene. Characterization of the 5' and 3' flanking regions and the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
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PUBDLINE=25203287; PubMed=7895732;

Corbett J.M., Wheeler C.H., Baker C.S., Yaccub M.H., Dunn M.J.;

"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobsen C.; "Lysher residue 240 of human serum albumin is involved in high-affinity binding of bilirubin."; Biochem. J. 171:453-459(1978).
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MEDLINE-88068523; PubMed-3479777;
Takshashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lysine residue 199 of human serum albumin is modified by
                                                                                                                                                                                                                             SEQUENCE OF 25-609.
MEDLINE=76187907; PubMed=1225573;
Meloun B., Moravek L., Kostka V.;
"Complete amino acid sequence of human serum albumin.";
FEBS Lett. 58:134-137(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Menaya J., Parrilla R., Ayuso M.S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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Brennan S.O., Herbert P.;
"Albunin Canterbury (313 Lys--Asn). A point Biochim. Biophys. Acta 912:191-197(1987).
                                                                                                                                                                                                                                                                                                                                                       Brown J.R., Shockley P., Behrens P.Q., (In) Bing D.H. (eds.);
The chemistry and physiology of the hum
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MEDLINE-78186630; PubMed=656055;
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SEQUENCE FROM N.A.

STATNISMES IDR, TISSUE-Liver;

STATNISMES IDR, TISSUE-Liver;

MEDLINE-98116663; PubMed=9455485;

MEDLINE-98116663; PubMed=9455485;

A. Yoshida K., Seto-Ohshima A., Sinohara H.;

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin, the main protein of plasma, has a good

"In DNA Res. 4:351-354(1997)

"In PUNCTION: Serum albumin, the main protein of plasma, has a good

"In FUNCTION: Serum albumin, the main function is the regulation of the colloidal osmotic pressure of blood.

"Issues SPECIFICITY: Plasma.

"Issues SPECIFICITY: Blasma.

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                                                                                                                                                             Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                           Serum albumin precursor.
                                                                                                                                                                                                                                                            NCBI_TaxID=10047;
              ALBU MERUN
035090;
              Two alloalbumins with identical electrophoretic mobility are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=11316157; Pubmed=1859851;
Peach R.J. Brennan S.O.;
"Structural characterization of a glycoprotein variant of human serum albumin: albumin Casebrook (494 App--Aen).";
Biochim. Biophys. Acta 1097:49-54 (1991).
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MEDLINE=92052189; PubMed=1946412;
Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsuda Y.-I., Amaki I., Putnam F.W.;
"Genetic variants of serum albumin in Americans and Japanese.";
Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
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Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
"Albumin Redhill (-1 Arg, 320 Ala -- Thr): a glycoprotein variant of
human serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91062352; PubMed=2247440;
Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.
Watkins S., Putnam F.W.;
"Mutations in genetic variants of human serum albumin found in
                                                                                                                                                                                                                                                            VARIANTS MANAUS; OSAKA, NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
MEDLINE-90115905; PubMed-2404284; Arai K., Madison J., Shimuzu A., Putnam F.W.; "Point substitutions in albumin genetic variants from Asia."; Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92190239; PubMed=1347703;
Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.;
                                                                                                     MEDLINE-89345611; HIR-1; HIR-2 AND TOCHIGI.
MEDLINE-89345611; PubMed=2762316;
Aral K., Medison U., Huss K., Ishioka N., Satoh C., Fujita M., Neel J.V., Sakurabayashi I., Putnam F.W.;
Point substitutions in Japanese alloalbumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
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100.0%; Score 47; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
                                         Amerindian and Japanese populations.";
Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                              3; Repeat; Signal; Copper. BY SIMILARITY. BY SIMILARITY. SERUM ALBUMIN, ALBUMIN 1.
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PIR; UC5838; UC5838.
HSSP; P02768; 1E7B.
Interpro; IPR00264; Serum albumin.
Péam; PR00273; Iransport prot; SRINTS; PR00802; SERUMALBUMIN.
ProDom; P0002486; Serum albumin; 1.
SWART; SW00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
MOCALL-binding; Lipid, binding; Repeat;
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EMBL; M73993; AAA51411.1; -. EMBL; X58989; CAA41735.1; -. EMBL; Y17769; CAA76847.1; -.
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MEDLINE=80024278; PubMed=488109;
MCGillivzay R.T.A., Chung D.W., Davie E.W.;
"Blosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin.";
Eur. J. Biochem. 98:477-485(1979).
                            Gaps
                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                IISSUE-Liver;
Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
Submitted (JUL-1998) to the EMBL/GenBank/DDEJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=77134075; PubMed=843354;
Patterson J.E., Geller D.M.;
"Bovine microsomal albumin: amino terminal sequence of bovine proalbumin.";
proalbumin.";
[10]
                                                                                                                                                                                                                                            Holowachuk E.W., Stoltenborg J.K., Reed R.G., Peters T. Jr., Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
        100.0%; Score 47; DB 1; Length 609; 100.0%; Pred. No. 0.17; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=82023364; PubMed=7283978;
Reed R.G., Putnam F.M., Peters T. Jr.;
"Sequence of residues 400-403 of bovine serum albumin.";
Biochem. J. 191:867-868(1990).
                                                                                                                                                                                                                                                                                                                                                                             Wu H.T., Huang M.C.;
"The complete cDNA sequence of bovine serum albumin.";
submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  IISSUE=Liver;
Barry T., Power S., Gannon F.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214.
                                                                                                                    P02769; 002787;
21-UUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 31, Last sequence update)
Serum albumin precursor (Allergen Bos d 6).
                                                                                                             607 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown J.R.;
Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT THR-214.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT THR-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of bovine serum albumin."; Fed. Proc. 34:591-591(1975).
                 Similarity 100.
9; Conservative
                                                                                                             STANDARD;
                                                              117 AKQEPERNE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 190-195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 19-28.
                                             1 AKQEPERNE
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  NCBI_TaxID=9913;
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      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fed. Proc. 33:1389-1389(1974).

-I-PUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-I-SUBCELLULAR LOCATION: Secreted.

-I-SINIERREN: Causes an allergic reaction in human.

-I-SIMILARITY: Belongs to the ALB/APP/VDB family.
SEQUENCE, AND REVISIONS TO 118-119 AND 180.
MEDLINE=91083649; PubMed=2260975;
Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
"Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";
Biochem. Biophys. Res. Commun. 173:639-646(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                   isolating proteins
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PRINTS; FR00802; SERUMALBUMIN.
Prodom; PD002486; Serum albumin; 1.
SMART; SW00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
                                                                                                                                                                                                                                                                 SEQUENCE OF 25-41.

BIGLINE-82567456; PubMed=3389500;
Hsich J.C., Lin F.P., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating is for N-terminal microsequencing.";
Anal. Biochem. 170:1-8(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of serum albumin: disulfide bridges.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF542068; AAN17824.1; -.
HSSP; P02768; 1E7B.
InterPro; IPR000264; Serum_albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vilbois F.;
Submitted (AUG-1998) to Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                               117 KOEPERNE 124
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581
607 AA;
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Best Local Similarity
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PROPEP
CHAIN
DOMAIN
DOMAIN
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                                             DOMAIN
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CISSUE-Liver,

MEDLINE-93345495; PubMed-8344282;

MEDLINE-93345495; PubMed-8344282;

A MILLINE-93345495; PubMed-8344282;

A D.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

A D.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

A D.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

A D.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

B D.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

C I- Tabochem. 215:205-212 (1993).

C I- SUBCELLULAR LOCATION: Secreted.

C I- SUBCELLULAR LOCATION: Secreted.

C I- TISSUE SPECIFFCITY: Plasma.

C I- ALLERGEN: Causes an allergic reaction in human. Binds IgE.

C I- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstandnumber the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              ô
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                    Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR00002; SERUMALBUMIN.
PRODOM; PR001346; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
SIGNAL
                                                                                                                                                        Score 43; DB 1; Length 607;
Pred. No. 0.97;
                                                                                                                                                                              0; Indels
                                                      A -> T.

C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

N -> D (IN REF. 6).

ST -> TS (IN REF. 6).

K -> R (IN REF. 6).
                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Equ c 3).
                                                                                                                                                                 100.0%; Pred. ...
                                                                                                                                    69293 MW;
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PIR; S34053; ABHOS.
                                                                                                                                                         91.5%;
                                                                                                                                                                    Local Similarity 100.
nes 8; Conservative
                                                                                                                                                                                                                                                                                 STANDARD;
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302
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607 AA;
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ALBU_HORSE
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Mammalia, Metazoa, Ctertiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
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BY SIMILARITY.
SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
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01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Kawawa T., Hara A., Shibata K., Komo H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D07724; Q61802;
101-APR-1988 (Rel. 07, Created)
115-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Serum albumin precursor.
ALB OR ALB1 OR ALB-1.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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TISSUB-Liver;
van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
R HASP; 806936; ABSHS.
R HASP; POTOR8; 1E7B.
R InterPro; 1ER000264; Serum_albumin.
R Pfam; PF00273; transport_pro; 3.
DR PRINTS; PR00802; SERUMIABUMIN.
DR SWART; SM00103; ALBUMIN; 3.
DR SWART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
TW Metal-binding; Lipid-binding; Repeat; Signal; Copper.

24 BY SIMILARITY.
THUS.
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Pred. No. 0.97;
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COPPER (BY SIMILARITY).
BY SIMILARITY.
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100.0%; Pred. No. ...
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607 AA;
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ALBU_MOUSE
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A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Zeeberg B., Brain G.M., Hong L.,

B Altschul S.F., Zeeberg B., Brain G.M., Hong L.,

A Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Roka S.S., Loquellano N.A., Peters G.J., Malek J.A., Glubs R.A.,

B Dosak S.A., McEwan P.J., McKernan K.J., M., Glubs R.A.,

B Norley W., McIny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Ratherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Generation and initial analysis of more than 15,000 full-length

R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbech C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., "Punctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88216123; PubMed=2452956;
Minghetti P.P., Law S.W., Dugaiczyk A.;
"The rate of molecular evolution of alpha-fetoprotein approaches that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=9026966; PubMed=1971802; Boccaccio C., Deschatrette J., Meunier-Rotival M.; Boccaccio C., Deschatrette J., Meunier-Rotival M.; Empty and occupied insertion site of the truncated LINE-1 repeat located in the mouse serum albumin-encoding gene."; Gene 88:181-186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of pseudogenes.";
Mol. Biol. Evol. 2:347-358(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 477-551 FROM N.A. STRAIN=BALB/c;
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STRAIN=FVB/N; TISSUE=Liver;
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     ALLINEABULINE # SOUGESTOR TO THE WEBDAMEN BY THE WEBDAMEN G.S., Weinstock J.;
Baldwin G.S., Weinstock J.;
"Nucleic Acids Reserved of Porcine liver albumin.";
"Nucleic Acids Res. 16:3045-9045 (1988).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- SINCELIVITAE NOCATION: Serveted.
-!- SUBCELIVITAE LOCATION: Serveted.
-!- TISSUE SPECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X12422; CAA30970.1; -.
EMBL; M36787; AAA30988.1; -.
PIR; S01382; ABPS.
HSSP; P02768; LBTH.
InterPro; IPR000264; Serum albumin.
Pfam; PP00273; transport.prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum albumin; 1.
SMART; F000121; ALBUMIN; 3.
PROSITE; P900121; ALBUMIN; 3.
PROSITE; P900121; ALBUMIN; 3.
PROSITE; P900121; ALBUMIN; 3.
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Best Local Similarity 87.5
Matches 7; Conservative
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ALBU_CANFA
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                                           EMEL; AJ011413; CAA006617.1; --
REMEL; AX010025; BAB26650.1; --
REMEL; X13060; CAA31458.1; --
REMEL; ROST68; PAD13; ALPUMIN.
REFEAR; PROC0273; transport prot; 3.
REMORT; SNO0103; ALBUMIN; 3.
RECSITE; PSO0212; ALBUMIN; 3.
RECSITE; PSO0212; ALBUMIN; 3.
RECSITE; PSO0212; Lipid-binding; Repeat; Signal; Copper.
RECPAIN 25 608 SERUM ALBUMIN.
RECPAIN 25 608 ALBUMIN; 3.
RECPAIN 212 397 ALBUMIN; 3.
RETAL 77 86 88 ALBUMIN; 3.
RETAL 77 86 88 ALBUMIN; 3.
RETAL 77 86 89 ALBUMIN; 3.
RETAL 77 86 80 ALBUMIN; 3.
RETAL 
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-> D (IN REF. 6).
-> I (IN REF. 6).
292F7C7EED3A61B4 CRC64;
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Best Local Similarity
8; Conserv?
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41
608 AA;
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SEQUENCE FROM N.A.
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87.5%; Pred. No. 3.7;
iive 1; Mismatches 0; Indels
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BY SIMILARITY.
SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 1.
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ALBUMIN 3.
COPPER (BY SIMILARITY).
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TISSUE-Salivary gland;

MEDLINE-SALO1492; PubMed=7512102;

MEDLINE-SALO1492; PubMed=7512102;

Mehl S., Echeric C., Scherr W.R., Pandjaitan B., Valent P.,

A Mehl S., Echer C., Scheiner O., Kraft D., Rumpold H.;

T Molecular characterization of dog albumin as a cross-reactive

T allergen.";

T allergen.";

T allergen.";

T allergen.";

T bunding capacity for water. (a(2+). Na(+), K(+), fatty acids, or memoric pressure of blood.

C c fe the colloidal cemoric pressure of blood.

C c fe the colloidal cemoric pressure of blood.

C c fe the colloidal semoric pressure of blood.

C c i- SumcELLUTAR LOCATION: Secreted.

C i- ALERGEN: Causes an allergic reaction in human.

C i- ALERGEN: Causes an allergic reaction in human.

C i- SIMILARITY: Belongs to the ALE/ARPYOB family.

C i- SIMILARITY: Contains 3 albumin domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-48.
MEDLINE=75011422; PubMed=4414013;
Dixon J.W., Sarkar B.;
"Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-24) of dog serum albumin.";
J. Biol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn M.J., Corbett J.M., Wheeler C.H., "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE20148667; PubMed=10669948;
MEDLINE20148667; PubMed=10669948;
Pandjaican B., Swoboda I., Brandejsky-Pichler F., Rumpold H.,
Valenta R., Spitzauer S.;
"Escherichia coli expression and purification of recombinant dog albumin, a cross-reactive animal allergen.";
J. Allergy Clin. Immunol. 105:279-285(2000).
                                                                                                                                                                                                                                                        Hilger C.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
P49822; O77705; Q9TSZ4;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Can f 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSC-2DPAGE; P49822; DOG.
InterPro; IPR00264; Serum albumin.
Pfam; PF00273; transport_prot; 3.
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EMBL; Y17737; CAA76841.1; -.
EMBL; S72946; AAB30434.1; -.
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Beagle; TISSUE=Liver;
                                                                                                                    Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ALBUMIN 1.
ALBUMIN 2.
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ALBUMIN 3.
COPPER (BY SIMILARITY).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                        Metal-binding; Lipid-binding; Repeat; Signal, Copper; Allergen. SIGNAL 18 PROPEP 29 4 SERUM ALBUMIN. CHAIN 212 205 ALBUMIN 1. DOMAIN 212 377 ALBUMIN 3. DOMAIN 404 595 ALBUMIN 3.
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01-FEB-1996 (Rel. 31, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Fel d 2).
              ProDom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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PRINTS; PR00802; SERUMALBUMIN
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87.5%;
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Best Local Similarity 87.50.
Matches 7; Conservative
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448
474
608 AA;
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P49064;
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ALBU_FELCA
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Sheffield W.P., Syed S., Schuyler P.D., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, blilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SINSELLULAR LOCATION: Secreted.
-!- SINSUB SPECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anon-37Gs protein (Fragment).
CG10561 OR ANON-37GS OR CS.
Drosophila simulans (Fruit fly).
                                                                                                                                                                                                                                                                                                                                        EMBL, U18144, AAB58347 1; -.
HSSP, P02768; 1E7B.
InterPro.; IRRO00264, Serum albumin.
Pfan, PF00273; transport prot; 3.
PRINTS, PR00802; SERUMALBUMIN.
ProDom; P0002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; SIGNAL.
1 18 BY SIMILARITY.
PR00BP 19 24 BY SIMILARITY.
CHAIN 25 608 SERUM ALBUMIN.
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ALBUMIN 2.
ALBUMIN 2.
COPPER.
BY SIMILARITY.
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1; Mismatches
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                                                                                                                                                                                                   R EMBL; X84842; CAA59279.1; -.

R PIRI; VC4660; S5758.1

R HSSP; PO2768; LB7B.

R Fam; PF00273; transport Drot; 3.

R PRINTS; PR00802; SERUMALEUMIN.

R PRINTS; PR00802; SERUMALEUMIN.

R PRAFT; SM00103; ALBUMIN; 3.

MCALL'binding; Lipid-binding; Repeat; Signal; Copper; Allergen.

R PROSITE; PS00212; ALBUMIN; 3.

MCALL'binding; Lipid-binding; Repeat; Signal; Copper; Allergen.

T SIGNAL

R SERUMALIARITY.

T CHAIN 25 608 SERUMALONIN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Best Local Similarity 87.5%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07E629CACSF60ESF CRC64;
         -!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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ALBUMIN 2.
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BY SIMILARITY.
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SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Liver;
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582
608 AA;
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ID ALBU RABIT
AC P49065;
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Biochem. Biophys. Res. Commun. 78:1060-1066(1977).

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                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF091327; AAG67579.1; -. FlyBase; Fgg002565; Dain\CG10561.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR000205; NAD BS.
Pfam; PF01593; Amino oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83161037; PubMed=6187737; Hache R.J. Lau P.C.K., Deeley R.G.; Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.; "The 5' noncoding and flaming regions of the avian very low density apolipoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                              SEQUAND.
SEQUENCE.
SEQUENCE.
STRAIN=St. Lucia;
MEDLINE=99280256; PubMed=10231575;
MEDLINE=99280256; PubMed=10231575;
Tatarenkov A., Saez A.G., Ayala F.J.;
"A compact gene cluster in Drosophila: the unrelated Cs gene is compressed between duplicated and and Ddc.";
Gene 231:111-120(1999)
-!- FUNCTION: Has a nonvital function (By similarity).
-!- FUNCTION: Has a nonvital function (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 19-30.
MEDLINE=78019943; PubMed=911327;
Rosen A.M., Geller D.M.;
"Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.";
Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NCV-1990 (Rel. 16, Created)
1-ACG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Alpha-livetin) (Allergen Gal d 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.5%; Score 35; DB 1; Length 501; 75.0%; Pred. No. 28; Cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Liver;
Cassady A.I., Salklld C.K., Baverstock P., Wallace J.C.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 501 AA; 56018 MW; 1F140F1E45FC1249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 615 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te protein genes.";
Biol. Chem. 258:4556-4564(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                        SEQUENCE FROM N.A.
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                                                        NCBI_TaxID=7240;
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A Quirce S., Marano, F., Umplerrez A., de las Heras M.,
A Ternandez-Caldas E., Sastre J.;
A Fernandez-Caldas E., Sastre J.;
Thicken serum albumin (Gal d 5*) is a partially heat-labile inhalant
and food allergen implicated in the birdegg syndrome.";
Allergy Sci754-762(2001).

1. FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2*), Na(*), K(*), fatty acids,
binding capacity for water, Ca(2*), Na(*), K(*), fatty acids,
controlled to smootic pressure of blood.

2. SUBCELLULAR LOCATION: Secreted.
C. SUBCELLULAR LOCATION: Secreted.
C. SUBCELLULAR LOCATION: Secreted.
C. MERGEN: Causes an allergic reaction in human. Binds 1gE.
Partially heat-labile allergen that may cause both respiratory and food-allergy symptoms in patients with the bird-egg syndrome.
C. SIMILARITY: Belongs to the ALB/ARPP/VDB family.
C. SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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F -> M (IN REF. 3).
E5924BBCAEC066C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IRR00264; Serum albumin.
Pfam; PR00273; transport prot; 3.
PRINTS; PR006040; SERUM-EDMIN.
PRODOM; PR002486; SERUM-EDMIN.
SMART; SW00103; ALBUMIN; 3.
PROSITE; PS00211; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
SIGNAL.
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ALBUMIN 1.
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COPPER (BY SIMILARITY).
BY SIMILARITY.
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                                                                 ALLERGENIC PROPERTIES.
MEDLINE=21381307; Pubmed=11488569;
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615 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibiai: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
NCBI_TAXID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Wolff C.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in a nucleolar function (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
-!- SIMILARITY: Belongs to the SURF6 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.3%; Score 34; DB 1; Length 341; Best Local Similarity 77.8%; Pred. No. 30; Matches 7; Conservative 0; Mismatches 2; Indels
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InterPro, IPR007019; SURF6.
Pfam, PF04935; SURF6, 1.
Nuclear protein.
SEQUENCE 341 Aa, 39901 MW, 280A066920D653A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Surfeit locus protein 6 homolog.
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1 AKOEPERNE 9
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SUR6 XENLA
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Search completed: April 19, 2004, 11:52:49 Job time : 1.65651 secs

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033764 streptococc 033765 streptococc 033765 streptococc 033762 streptococc 033762 streptococc 03762 streptococc 039893 mus musculu 099ke9 mus musculu 099ke9 mus musculu 099ke4 homo sapien 05499 mus musculu 099cs homo sapien 05400 streptochia 09bu3 beudomonas 09bub4 pseudomonas 09bub4 pseudomonas 09bub4 pseudomonas 09bub4 pseudomonas 025777 plasmodium 08us6 agrobacteri
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCR-2003 (TrEMBLrel. 25, Last annotation update)
Similar to serum albumin precursor.
Similar to serum albumin precursor.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUB-Liver;
Straubberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035969; AAH35969.1; -..
GO, GO.0005615; C:extracellular space; IEA.
GO; GO:0005816; P:carrier activity; IEA.
InterPro; TRR00264; Serum albumin.
Pfam; PF00273; transport, prot; 2.
PRINTS; PR00802; SERUMALBUMIN.
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PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 396 AA; 45159 MW; 756519C096463A9B CRC64;
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00996KB
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          AKOEPERNE 124
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Best Local Similarity
Best Local 91 Conserva
             NCBI_TaxID=9606;
             116
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Q8CG74
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Q8c7c7 mus musculu
Q8c7c3 mus musculu
Q7v8g3 felis silve
Q8mrz4 drosophila
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Albumin precursor homolog is a novel T helper cell immunogenic egg

T "Albumin precursor homolog is a novel T helper cell immunogenic egg

T component in murine infection with Schistosoma mansoni.";

RECO. SECURINE (SEP-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, AF418850; AAL08579.1;

RO; GO:0005185; P:carriac-lular space; IEA.

GO; GO:0005185; P:carriac activity; IEA.

RO; GO:000510; P:transport, IEA.

RO; GO:0005410; P:transport, IEA.

REMINTS; PRO00204; SERUMALBUMIN.

PRODOM: PRO0213; ALBUMIN; 1.

REMINTS; ROWO1013; ALBUMIN; 1.

SMART; ROWO1012; ALBUMIN; 2.

SEQUENCE GOS AA; GS225 MW; ESEABBZBEICG6E54 CRC64;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTUN-2003 (TrEMBLrel. 24, Last annotation update)
Albumin.
Schistosoma mansoni (Blood fluke).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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nes 8; Conservative
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SEQUENCE FROM N.A.

STRAIN=CSTSHI663; TRISSUB=Thymus;

RAIN=CSTSHI663; PubMed=12466851;

The FANYOM Consortium,

The FANYOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of the Malysis of the mouse transcriptome based on functional annotation of the Malysis of the mouse transcriptome based on functional annotation of the Malysis of the mouse transcriptome based on functional annotation of the Malysis of the mouse transcriptome based on functional annotation of the Malysis of the mouse transcriptome based on functional annotation of the Malysis of the mouse transcriptome, is malbumin.

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RICHARD: PRO0802; SERUMALBUMIN.

PRINTS; PRO0802; SERUMALBUMIN.

PRINTS; SMARR; SMO0103; ALBUMIN; 3.

PROSSITE; PSO0212; ALBUMIN; 3.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NOSI_TaxID=10090;
                                                                                                                                                                                      Albumin (Fragment).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mammalia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SvevTACfBr;
A van Reeth T., Dreze P.L., Gabant P., Szpirer J.;
STRAIN=129/SvevTACfBr;
Van Reeth T., Dreze P.L., Gabant P., Szpirer J.;
Usubmitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ277794 CACCA9103.1;
R GO; GO:0005615; C:extracellular space, IEA.
R GO; GO:000586; F:carrier activity; IEA.
R GO: GO:0006810; P:transport; IEA.
R InterPro; IPRO00264; Serum albumin.
R Pfam; PF00273; transport Drot; 1.
R PRINTS; PR0080273; LSBUNALBUMIN.
SMRAT; SM0103; ALBUMIN, 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin 1 (Fragment).
                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Best Local Similarity 100.
Matches 8; Conservative

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Q8C7C7 Q8C7C7;

RESULT 3 Q8C7C7

Query Match Best Local Similarity

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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dreenek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Xronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P., Rumpold H., Valenta R., Spitzauer S.; ification of recombinant ca "Escherichia coli expression and purification of recombinant albumin: IgE recognition, induction of basophil activation and lymphoproliferative responses in atopic patients."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ489677; CAD32275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophila, Drosophila.
                                                                                                                                                                                                                                            91.5%; Score 43; DB 11; Length 608;
llarity 100.0%; Pred. No. 4.2;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.0%; Score 39; DB 6; Length 584;
87.5%; Pred. No. 25;
ive 1; Mismatches 0; Indels
InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_broi; 3.
PRINTS; PR00822; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
SEQUENCE 608 AA; 68722 MW; 292F600EED3A61B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 AA; 65908 MW; B51002F12902C9CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7XSG3
Q7XSG3
Q7XSG3
01-OCT-2003 (TERMELrel. 25, Cx
01-OCT-2003 (TERMELrel. 25, La
01-OCT-2003 (TERMELrel. 25, La
Albumin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.55,
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 KKEPERNE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                     117 KOEPERNE 124
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conservat
                                                                                                                                                                                                                                                                                                                                                                         2 KOEPERNE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KOEPERNE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBMRZ4;
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Q8MRZ4
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Q778G3

1D Q778G3

AC Q778G4

Q778G4

DD 01-00

DD 01-00
      SOR BRANCES
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PERSONT 8

REBUIL 8

GRINGO PRELIMINARY, PRT; 203 AA.

ADD GRINGO PRELIMINARY, PRT; 203 AA.

RESPONDED TO GRINGHELED 32, Leaf sequence update)

DT 01-WAR-2003 (TERMELTED 32, Leaf sequence update)

DT 01-WAR-2003 (TERMELTED 32, Leaf sequence update)

DT 01-WAR-2003 (TERMELTED 32, Leaf sequence update)

DE GO31174-N.

GO31174-N.

GO31174-N.

GO31177-N.

RESPONDED FROW N.A.

RESPONDED FROM N.A.

RESPONDED FROW N.A.

RESPONDED FROW N.A.

RESPONDED FROM N.A.

RESPONDED FROW N.A.

RESPONDED FROM N.A.

RESPONDED FR
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Gaps

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5; Length 115; 0; Indels

Query Match 76.6%; Score 36; DB Best Local Similarity 75.0%; Pred. No. 19; Matches 6; Conservative 2; Mismatches

2 KQEPERNE 9

Celniker S.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AT119187; AAMS1047.1; -. Flybase; FEBN062887; BCDNA:SD11171. SEQUENCE 115 AA; 13534 MW; F680D64C7C967AEC CRC64;

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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeron K.Y., Busam D.A., Carlen A., Champe M. Davenort L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hoostin D., Howland T.U., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Parts S., Pteiffer B., Scheeler F., A. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Fmilh H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D.,
Tupy J.L., Berman C., Berman B., Carlson J.W., Celniker S.E.,
Tupy J.L., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Mnitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003736; AAN13887.1; -.
Flybase EMBL/GROS1174; CG31174.
SEQUENCE Z03 AA; 23859 MW; 3C3E8F93F3434B33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase;
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Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.W., Cawley S., Darlike C., Davenport L.B., Davies P.,

RA Chebrry J.W., Cawley S., Darlike C., Davenport L.B., I. Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Fosler C., Gabrielian A.E., Garraz C., Ferriera S., Fleischmann M.,

RA Glock A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Werl M.-H., Ibegwam C.,

RA Lanko P., Lei Y. Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y. Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y. Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y. Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y. Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y. Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y., Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y., Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y., Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lanko P., Lei Y., Levylsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.,

RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacle J. M.,

RA Reinert K., Remington K., Saunders R.D., Puri V., Rang A.H., Wang X.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M., Walssenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zao Q., Zheng L.,

RA Sheng X.H., Myers E.W., Rubin G.M., Vang S., Zho X., Zhu X., Zho X., Zho

0; Gaps 5; Length 203; 0; Indels Ouery Match
76.6%; Score 36; DB
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches

34 KREPERNO 41 2 KOEPERNE 9 ò g

PRELIMINARY; RESULT 9
(2917X6
(2017X6
(2017X7
(2017X6
(2017X7
(2017

PRT; 439 AA

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;

Bphydroidea, Drosophilidae, Drosophila. 01-WAR-2001 (TrEMBLrel. 16, Created) 01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) EG:39E1.1 protein (L04222'p).

SEQUENCE FROM N.A.

STAIN=Berkeley;

MEDLINE=2019606; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adamsatidee P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

ô Gaps ö 5; Length 439; 0; Indels Score 36; DB 5; Pred. No. 74; 2; Mismatches 76.6%; Local Similarity 75.0 les 6; Conservative Query Match Best Local S Matches 6 

SEQUENCE FROM N.A.

408 EQOPERNE 415 σ 2 KOEPERNE 임 ò

O46078, Q9WS/01 046078, Q9WS/01 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-2003 (TrEMBLrel. 06, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) EG:39E1.1 protein. EG:39E1.1 OR CG11596. Drosophila melanogaster (Fruit fly). Drosophila melanogaster (Fruit fly). BUMARYOCA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopteray; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. PRT; 456 AA PRELIMINARY; RESULT 10
0046078
1D 04607
AC 04607
DT 01-JU
DT

STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N. SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).

425 EQOPERNE 432

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RESULT 11 Q7WSR5

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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA April J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Easledin D.,

Ra Besson K.Y., Bengan B.P. Bhandari D., Bolshakov S.,

Burker S.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center R., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Bratis N.L., Harvey S., Danner R.A., Hourd J., Hermandez J.R., Houck J.,

RA Hartis N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hermandez J.R., Houck J.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., ij J., Isang Y., Lin X.,

Anteta B., Mollosh T.C., McLeod M.P., Morbherson D.,

RA Mount S.M., Now M., Winghy B., Murphy B., Murshy D.M., Nelson R.A.,

Raleson D.R., Nelson K.A., Wanskern D.R., Pacieb J.M.,

Raleson D.R., Nelson K.A., Sandson M., Stupeki M.P.,

Raleson D.R., Nelson K.A., Stangeon M., Stupeki M.P.,

Spirekas R., Tector C., Thurner R., Venter E., Wang X.,

Mullams S.M., Woodaget T., Wolley K.C., Wu D., Yang S.,

RA Spier E., Spaadling A.C., Stapleton M., Stupeki M.P.,

Sylrekas R., Tector C., Thurner R., Venter E., Wang X.,

Mullams S.M., Woodaget T., Wolley K.C., Wu D., Yang S.,

RA Sheng X.H., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Sheng X.H., Zhong F.N., Rubing G.M., Zhao Q., Zheng S.,

Ralence Z87:2185-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAINSON N.A.
STRAINSONE FROM N.A.
STRAINSONE FROM N.A.
STRAINSONE FROM N.A.
STRAINSONE S. V. Gallaure V. Mottier S., Gallbert F., Borkova D., Minana B., Ratatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schottler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schafer U., Jackhe H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Momillan P.J., Salles C., Tait E.A., Valenti P., Saunder R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Shoit,

is EMBL; AE003422; AAF45697.1; -.

R EMBL; AE003422; AAA15698.1; -.

R EMBL; AE003191; CAAA15684.1; -.

DR FlyBase; FBgn0023522; EG:39E1.1.

KW Alternative splicing; Hypothetical protein.

Missing (in isoform Short).

Frida-VSP 050174.

/Frida-VSP 050174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "From sequence to chromosome: the tip of the X chromosome of melanogaster."; Science 287:220-2222(2000).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.6%; Score 36; DB 5; Length 456; Best Local Similarity 75.0%; Pred. No. 77; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=046078-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glover D.M.;
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A SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB=Olfactory brain;

X MEDLINE-2534683; PubMed=12466851;

RA The FANTOM Consortium,

BENEL; AK032238; BAC27775.1; -.

DR MED; AG1:1920950; 2410051C13Rik.

DR MED; METIT 1920950; 2410051C13Rik.

DR Ffam; PF00571; CBS; 4.

DR SMART; SM00116; CBS; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Parschat K., Hauer B., Kappl R., Kraft R., Huettermann J., Fetzner S., "Gene Cluster of Arthrobacter ilicis R.61a Involved in the Degradation of Quinaldine to Anthranilate. Characterization and Functional Expression of the Quinaldine 4-oxidase qoxLMS Genes."; J. Biol. Chem. 278:27483-27494 (2003).

Biol. Chem. 278:27483-27494 (2003).

Monooxygenase, Transmembran.

SEQUENCE 414 AA; 45307 MW; 00BD746F673C0486 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NOBI_TaxID=10090;
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0
                                                                                                                                                                                  Arthrobacter ilicis.
Bacteria, Actinobacteridae, Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=43665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.5%; Score 35; DB 11; Length 443; 87.5%; Pred. No. 1.2e+02; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.5%; Score 35; DB 2; Length 414; 66.7%; Pred. No. 1.1e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLINE, 2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 24, Last annotation update) Similar to AMP activated protein kinase gamma 1. 2410051C13RIK.
                          OTWSES;
01-OCT-2003 (TEBMBLrel. 25, Created)
01-OCT-2003 (TEBMBLrel. 25, Last sequence update)
01-OCT-2003 (TEBMBLrel. 25, Last annotation update)
Putative transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 AA.
414 AA
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PRT;
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STRAIN-Rue61a;
MEDLINE-22753791; PubMed=12730200;
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Best Local Similarity 87.5
Best Local 7; Conservative
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Best Local Similarity 66...
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PRELIMINARY;
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   Q7WSR5
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Length 614;

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Query Match 74.5%; Score 35; DB 13; Length 61
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
Pfam, PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 2.
PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 614 AA; 69798 MW; 3DB2D3CC4BDBCBFD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
241051C13RIK.
Buks musculus (Musse).
Bukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Muschleriares (NCBI_TaxID=10090;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shao J., Shen H., Havsteen B.;
"Purification, characterization and binding interactions of the Chinese-cobra (Naja arra) serum antitoxic protein CSAP.";
Biochem. J. 293:559-566(1993).
BMBL, X78589; CAA55333.1;
GO; GO:0005618; Caxtracellular space; IEA.
GO; GO:0005618; Caxtracellular space; IEA.
GO; GO:0005610; P:transport; IEA.
InterPro; IPR000264; Serum_albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC015283, AAH15283.1;
InterPro, MSI:1290550; 2410051C13Rik.
InterPro, IPR000644; CBS_domain.
Ffam, PP00571; CBS; 4.
SMART; SM00116; CBS; 4.
Hypothetical protein.
SEQUENCE 566 AA; 62997 MW; 754DE4D696102C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         091134;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Cobra serum albumin.
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Best Local Similarity 87.5
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NCBI_TaxID=35670;
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A Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
A Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
A Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
A Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
A Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
A Theologis A., Ecker J.;
A Theologis A., Ecker J.;
B. Embl., AC007366; AAPZ6771.2;
B. Embl., AC07366; AAPZ6771.2;
REBL., AC07366; AAPZ6771.2;
REBL., PROS535; VP835.
R. PIR, G96787; G96787.
R. PIR, G96787; G96787.
R. PIR, G96787; G96787.
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
euroaids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                     01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
174012-9.
Arabidopais thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                         PRT;
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119 AKADPDRNE 127
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Query Match 74.5%; Score 35; DB 10; Length 884; Best Local Similarity 87.5%; Pred. No. 2.4e+02; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps

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Search completed: April 19, 2004, 12:00:03 Job time : 5.47368 secs

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Post-processing: Minimum Match	Minimum Match 0%	RE	RESULT 1					
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AAP90389 AAP90390 AAP90391 AAP90391 AAP90398 ABG72381 AAP90384 AAP91422 AAR965318 AAR26362 AAR26364	ALIGNMENTS	116 AA.		1 #71.	herapy; nut aematopoies stimulation				. 9					range of human therapy.	English.	to the poor to the poor predis or predis or predis or septide. It is septide. It is septimentally to poly the poly for poly for poly for partion, te They may
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0 C G G G E E E E E E E E E E E E E E E E	RESULT 1	e; e;	8			DS Homo	-	55- 58-	16	18	PA (HYSE	PI Tang	OR WPI	PT Nucl	PS Claim	CC Phy CC Phy CC CC Mich CC CC Phy CC Phy CC CC CC CC Phy CC CC CC CC Phy CC CC CC CC Phy CC CC CC CC CC Phy CC CC CC CC CC CC CC CC CC Phy CC CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying a pents (agonists and antagonists) that bind to them. Cells oxpressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukeemias. AAU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                             ö
proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU20510-AAU33104 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                               0; Gaps
                                                                                                    100.0%; Score 47; DB 4; Length 116; 100.0%; Pred. No. 0.49;
                                                                                                                             0; Indels
                                                                                                                             Mismatches
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                                                                                                                                                                                                                                          AAU29574 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #65.
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26-JAN-2001; 2001US-00770160.
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                                                                                        Query Match
Best Local Similarity 100.
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                                                                             Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                  AAU29574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; mmunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                 Gaps
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Score 47; DB 4; Length 116;
Pred. No. 0.49;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                   AAO12088 standard; protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 25980.
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   Query Match
Best Local Similarity 100.0%; P:
Matches 9; Conservative 0;
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                        AA012088;
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Matches
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Human, vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

16-APR-2001; 2001WO-US008656.

WO200179449-A2. Homo sapiens.

25-OCT-2001.

18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160.

HYSE-) HYSEQ INC

Drmanac RT;

Liu C,

Tang YT,

WPI; 2001-611725/70.

Novel human secreted protein #3564.

(first entry)

18-DEC-2001

AAU33073;

AAU33073 standard; protein; 156 AA

RESULT 5 4AU33073

111 AKQEPERNE 119

1 AKOEPERNE 9

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27352 encode the human ORFX in the specification). ABN15762 to ABN27352 encode the human ORFX proteins given in ABP60010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated with an ORFX-associated with ORFX-associated with ORFX-associated disorder. ORFX polymucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, circhosis of liver, contains, benign tumours, keloid, degenerative disorders, haemorinage, osteoarthritis, neurodegenerative disorders, circhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, infectious cortange in the contains and partial or an infectious disorders, disorders, infectious cortange disease, autoimmune disorders send and disorders, infectious disease, autoimmune inflammatory eye disease. ORFX proteins are also arthitis, autoimmune inflammatory eye disease. ORFX proteins are also disease and autoimmune inflammatory eye disease. ORFX proteins are also consein for treating burns, indications, ulcers, for treating observation and treatment of lung or liver fibrosis, bone degenerative diseases, autoinfliens rissues and conditions resulting from part of the printed specification, but was obtained in electronic former directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                               Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 10118; 1037pp; English.
                                                                                                                                                          Human ORFX protein sequence SEQ ID NO:10118.
                         ABP05068 standard; protein; 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                         myasthenia gravis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2001.
                                                                   ABP05068;
ABP05068
ID ABP0
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapentic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the runciel cacids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or atimulation; as anti-inflammatory agents; and in treatment of leukaemias. AMU29510-AAMU3304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU33271 standard; protein; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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Matches 9; Conserv
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ID AAU
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0; Indels

100.0%; Score 47; DB 5; Length 143; 100.0%; Pred. No. 0.61;

Mismatches

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Conservative

Query Match Best Local Similarity Matches 9; Conserv

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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted proteins of the invention
                                                                                                                                        18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                16-APR-2001; 2001WO-US008656.
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9, Conserve
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                                                                WO200179449-A2.
                                          Homo sapiens.
                                                                                         25-OCT-2001.
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                                                                                                                                                                                                     Tang YT,
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     The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins of as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoisals, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                      Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune stimulation, anti-inflammatory, leukaemia.
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                                                                  Novel human secreted protein #3762.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 751; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted protein #366.
                                                                                                                                                                                                                    16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                           18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                        Tang YT, Liu C, Drmanac RT;
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Best Local Similarity 100.0
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                                                                                                                                            Homo sapiens.
                                         18-DEC-2001
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                  AAU33271;
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AAU29875
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to each state also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to requiate hemanatopiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. Adults of the present the amino acid sequences of novel human
Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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(HEDL/) HEDLEY M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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                                                                                                                                                                                               Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                        Yin P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bladder disorder; cytostatic; antiinflammatory; immune response; un-methylated (pG sequence; alpha-MSH; melanocortin receptor; bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human;
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 47; DB 5; Length 195; 100.0%; Pred. No. 0.82; ive 0; Mismatches 0; Indels
                                                                                                                                                        Etemad-Moghadam B,
                                                                                                                                                         Chen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU10022 standard; protein; 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human serum albumin residues 1-195.
                                                                                                                                                                                                                                        Example 2; Page 46; 89pp; English.
                                                                                                                                                         Aziz N,
                                                                     14-JUL-2000; 2000US-0218381P.
18-MG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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                                                   2001WO-US022263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2003 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKQEPERNE 100
                                                                                                                                                         Hedley ML, Urban R,
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                                                                                                                                                                          WPI; 2002-195801/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKQEPERNE
                                                                                                                                     (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 195 AA;
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             WO200206316-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serum albumin
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                                                   16-JUL-2001;
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                                 24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                          nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU10022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
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The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having comparising identifying a mammal that has or is at risk for having comprising an un-methylated CDG sequence to the mammal, (NI) an isolated nucleic acid (NI) comprising sequence to the mammal, the mammal; or nucleic acid (NI) comprising sequence encoding alpha-MSH to the mammal. The cor or (c) a peptide that binds to a melanocortin receptor to the mammal. The method is useful for modulating immune response in a mammal having a complating immune response. Preferably, the method is useful cof one or more symptoms of the disorder. Preferably, the method is useful cor for modulating immune response in a mammal having bladder cancer (where daministration of (NI) results in a modulation of the cystitis (where administration of (NI) results in a modulation of the cystitis (where administration of (NI) results in a modulation of the immune response in a mammal having bladder disorder concerning immune response in a mammal having bladder disorder that is characterised by inflammation which is associated with superconforming the bladder lining in the craption of the integrity of the bladder lining in the craption of melanocyte calbumin residues 1-195 that can be used in the creation of melanocyte cor fusion protein when expressed in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                    Modulating immune responses in a mammal with a bladder disorder e.g. bladder cancer, by administering nucleic acids comprising un-methylated CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to the mammal.
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Pred. No. 0.82;
; Mismatches 0; Indels
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Best Local Similarity
9; Conserv?
                                                                                                                            WPI; 2003-447327/42.
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                                                                Hedley ML;
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LTD.

BIOENGINEERING CO

98CN-00102506

2; Page 48; 89pp; English.

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The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A.10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonucleotide fragments that were extended. This sequence represents the sequence of the HSA fragment HSA-I encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression the process for producing human serum albumin in the yeast host cell, especially in secretory mode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
                                                             Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-MSH; inflammation, autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antispsoriatic; antianthalmological; neuroprotective; ophthalmological; dermatological; antiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 47; DB 3; Length 204; 100.0%; Pred. No. 0.86;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA017051 standard; protein; 236 AA.
                                                                                                                  Example 1; Fig 3; 44pp; Chinese.
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18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-195801/25.
                WPI; 2000-351198/31
N-PSDB; AAA10092.
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                                                                                                                                                                                                                                                                                                                                                          Sequence 204 AA;
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autoimmune disorders

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                                     The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concataent. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatory arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a peptide described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-MSH, inflammation, autoimmune disease, gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive, antiinflammatory, antirheumatic; antiarthritic; antiathathritic; antidatetic; antibacterial; dermatological; antibsoriatic; antidabetic, ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                 5; Length 236;
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO16984 standard; protein; 241 AA.
                                                                                                                                                                                                                                                            Similarity 100.0%;
9; Conservative 0;
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18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-0238380P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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                                                                                                                                                                                                                                                                                                                                                                      116 AKQEPERNE 124
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                                                                                                                                                                                                                                                                                                                                      1 AKOEPERNE
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                   Sequence 236 AA;
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                                                                                                                                                                                                    invention
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Matches
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The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having a badder disorder. And administering: (a) an isolated nucleic acid (NI) comprising an un-methylated CpG sequence to the mammal; (b) an isolated nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal; or (c) a peptide that binds to a melanocortin receptor to the mammal. The method is useful for modulating immune response in a mammal having a bladder disorder, where administration of (NI) results in an amelioration of one or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (NI) results in a decrease in tumour size or activity), or for modulating immune response in a mammal having interstitial cystitis (where administration of (NI) results in a modulation of the immune response from Th2 response to a Th1 response). The method is also useful for modulating immune response in a mammal having bladder disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating immune responses in a mammal with a bladder disorder e.g. bladder cancer, by administering nucleic acids comprising un-methylated CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to the mammal.
e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uvoitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bladder disorder, cytostatic, antiinflammatory, immune response, un-methylated CpG sequence; alpha-MSH; melanocortin receptor; bladder cancer; tumour; interestitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human; serum albumin; fusion protein; H9.
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                     Query Match
100.0%; Score 47; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-MSH/Serum albumin fusion protein H9.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABU10025 standard; protein; 241 AA.
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                                                                                                                                                                                                                                                                                                       116 AKQEPERNE 124
                                                                                                                                                                                                                                                                        1 AKQEPERNE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HEDL/) HEDLEY M L.
                                                                                                                                                Sequence 241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU10025;
                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of the bladder lining. This is the amino acid sequence of a human serum melanocyte stimulating hormone (alpha-MSH) concatamer useful in the trearment of bladder disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis asthma; cirrhosis; dermatitis; psociasis; inflammatory bowel disease; immunosuppressive; antinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antiasthmatic; antibacterial; dermatological; antiasthmatic; antiathritic; disease; obthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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100.0%; Pred. No. 1;
iive 0; Mismatches 0; Indel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA016985 standard; protein; 242 AA
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18-MG-2000; 2000US-0226382P.
06-OCT-2000, 2000US-0238380P.
29-DEC-2000; 2000US-0259831PP.
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Best Local Similarity 100...
9, Conservative
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AA016985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                  Gaps
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100.0%; Score 47; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels
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Length 242;
                                  0; Indels
                                                                                                                                                                                                                                                                                                            Alpha-MSH construct protein fragment SEQ ID NO: 71.
Query Match
100.0%; Score 47; DB 5;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0
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                                                                                                                                                                                                 AA016986 standard; protein; 244 AA.
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18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-0238380P.
29-DEC-2000; 2000US-025854P.
14-JUN-2001; 2001US-0298317P.
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                                                                                                      116 AKOEPERNE 124
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                                                                       1 AKOEPERNE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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                                                                                                                                                                                                                                      AA016986;
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AAO16986
ID AAO16
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Search completed: April 19, 2004, 11:51:17 Job time : 5.29363 secs 116 AKQEPERNE 124 a

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Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 11, Appli Sequence 24, Appli Sequence 26, Appli Sequence 27, Appli Sequence 2, Appli

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 9; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-110-074-956-24

| Sequence 24, Application US/10074956
| Sequence 24, Application US/10074956
| Publication No. US2002019332A1
| GENERAL INFORMATION:
| APPLICANT: Hedley, Mary Lynne
| TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
| FILE REFERENCE: 08191-022001
| CURRENT APPLICATION NUMBER: US/10/074,956
| CURRENT APPLICATION NUMBER: 2002-06-10
| PRIOR PILING DATE: 2001-02-12
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: FESTSEQ for Windows Version 4.0
| SEQ ID NO 24
| LENGTH: 195
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-10-074-956-24
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US-10-074-956-27
US-10-074-956-27
Sequence 27, Application US/10074956
Fublication No. US20020193332A1
GENERAL INFORMATION:
APPLICANT: Hedley, MATY Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
ALIGNMENTS
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                                                                                April 19, 2004, 12:00:25 ; Search time 3.78847 Seconds (without alignments) 654.724 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_BMP_PUB_PEP:*
3: \cgn2_6/ptodata/2/pubpaa/BCT_BMP_PUB_PEP:*
4: \cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP:*
5: \cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP:*
6: \cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP:*
7: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP:*
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12: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: \cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: \cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP:*
17: \cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP:*
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-074-956-27

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3 US-09-932-522-8

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Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAM, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
STREET: 1300 I Street, NW
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Publication No. US20030104578A1
GENERAL INFORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beltzer, James P.
APPLICANT: Beltzer, James P.
APPLICANT: Beltzer, James P.
APPLICANT: Potter D.
APPLICANT: Potter D.
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON FILE REFERENCE: Dyx-025.1 US
CURRENT PEPLICANT: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: 2001-08-17
LENGTH: 585
LENGTH: 585
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/769,746
FILING DATE: 19-DEC-196
ATTORNEY/AGENT INFORMATION:
NAME: CARTOLL, Peter G.
REGISTRATION NUMBER: 32,837
REFRENCE/DOCKET NUMBER: MBRI-02584
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 47; DB 100.0%; Pred. No. 2.7 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-09-932-613-445
Sequence 445, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 585 amino acids
TYPE: amino acid
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Best Local Similarity 100.0%;

Matches 9; Conservative 0
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Best Local Similarity 100.
Matches 9; Conservative
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CRGANISM: HomoSapiens
US-09-932-613-445
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                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 241;
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US-10-074-956-28
US-10-074-956-28
US-10-074-956-28
Sequence 28, Application US/10074956
Publication No. US2002019332A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REPREMENCE: 08121-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR APPLICATION NUMBER: 60/268,175
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
IENGTH: 268
IENGTH: 268
TYPE: PRI
CORGANISM: Home sapiens
US-10-074-956-28
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/929,552
FILING DATE: 14-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                               PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 27
LENGTH: 241
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
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Patent No. US20020123080Al
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-10-074-956-27
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US-09-929-552-2
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Sequence 18, Application US/09833117
Publication No. US20030171267A1
GENERAL INFORMATION:
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STATE: DC
COUNTRY: USA

COUNTRY: USA

ED: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,010
FILING DATE: 12.MAY-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 25-UN-1998
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 12-DEC-1996
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: Anno acids
TYPE
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09833041

Sequence 18, Application US/09833041

Sublication No. US20030125247A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Heseltine, William A.

TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF545

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/229,358

PRIOR APPLICATION NUMBER: 60/226,931

PRIOR APPLICATION NUMBER: 60/199,384

PRIOR PILING DATE: 2000-04-12

PRIOR PILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 18
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ORGANISM: Homo Sapiens
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US-09-833-117-18
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KEQUENCE 445, Application US/09932322

FUBLICANT US2030194743A1

FUBLICANT: Dyax Corp.

APPLICANT: Dyax Corp.

APPLICANT: Petter, M. Daniel

APPLICANT: Potter, M. Daniel

APPLICANT: Potter, M. Daniel

APPLICANT: Potter, M. Daniel

APPLICANT: Potter, M. Daniel

APPLICANT: Ladner, Robert Charles

FILE REFERENCE: Dyx-018.1 PCT; DXx-018.1 US

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: PatentIn version 3.1

SEQ ID NO 445

LENGTH: 585

LENGTH: 585

TYPE: RT

CRANIES PRT

CRANIESM: HomoSapiens

US-09-932-322-445
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels
JOHERAL INFORMATION:
JAPPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Thoma
APPLICANT: Sadeghi, Homa
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF54
CURRENT APPLICATION NUMBER: US/09/833,117
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: S85
TYPE: PRT
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Sequence 18, Application US/09832501
Publication No. US20030199043A1
GENERAL INFORMATION:
APPLICANT: Ballance, David J.
APPLICANT: Sleep, Darrell
APPLICANT: Turner, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AKOEPERNE 100
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Sequence 11, Application US/10424999

Sequence 11, Application US/10424999

Publication NO. 10220040052810A1

GENERAL INFORMATION:
APPLICANT: Generon, Beatrice
APPLICANT: Generon, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Using Them to Inhabit Anglogenesis
TITLE OF INVENTION: Using Them to Inhabit Anglogenesis
FILE REFERENCE: STO1027-A

CURRENT APPLICATION NUMBER: US/10/424,999

CURRENT PILING DATE: 2003-04-29

PRIOR PILING DATE: 2003-09-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE PATENTIN VERSION 3.2

SEQ ID NO 11

LENGTH: 585
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Publication No. US20040052777A1
GENERAL INFORMATION:
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Mark
APPLICANT: Mark
APPLICANT: Mark
APPLICANT: Mandiogenesis
TITLE OF INVENTION: Anglogenesis
FILE REFERENCE: ST01027-B
CURRENT APPLICATION NUMBER: US/10/425,000
CURRENT FILING DATE: 2003-04-29
FRIOR APPLICATION NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 11; Length 585; 100.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. 2.7;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Fusion protein human abrogen US-10-424-999-11
       PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR PELING DATE: 2000-12-21
PRIOR PELING DATE: 2000-12-21
PRIOR PELING DATE: 2000-12-31
PRIOR PELING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 18
LENGTH: 585
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo Sapiens
US-09-833-245-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 10; Length 585; Pred. No. 2.7; Mismatches 0; Indels (
APPLICANT: Sadeghi, Homa
APPLICANT: Prior, Christopher P.
ITLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PF$42
CURRENT APPLICATION NUMBER: US/09/832,501
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 18
LENGTH: 585
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WESULI 11

SEQUENCE 18, Application US/09833118

SEQUENCE 18, Application US/09833118

PUBLICANT NORMATION:
APPLICANT Haseline, William A.
TITLE OF INVENTION: Abbumin Fusion Proteins
FILE REFRENCE: PF544

CURRENT PAPLICATION NUMBER: US/09/833,118

CURRENT PILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/229,358

PRIOR APPLICATION NUMBER: 60/226,931

PRIOR APPLICATION NUMBER: 60/256,931

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PARCH PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 35

LENGTH: 585
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100.0%; Score 47; DB
Best Local Similarity 100.0%; Pred. No. 2.7
Matches 9; Conservative 0; Mismatches
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Publication No. US20040010134A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPRENCE: PP546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 AKOEPERNE 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo Sapiens
US-09-833-118-18
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKOEPERNE 9
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US-09-833-245-18
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Length 585; Indels

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                                                                                                                                                                            Query Match 100.0%; Score 47; DB 12; Length 585; Best Local Similarity 100.0%; Pred. No. 2.7; Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
US-10-425-000-31
                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-433-108-34
Sequence 34, Application US/10433108
Sequence 34, Application US/10433108
Sequence 34, Application US/10433108
SUBJECT OF UNIVERSETION:
TITLE OF INVENTION: GLD-1 FUSION PROTEINS
TILE REFERENCE: X-13991
CURRENT FILING DATE: 2003-65-29
PRIOR PILING DATE: 2003-65-29
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 19, 2004, 12:54:58 Job time : 3.78947 secs
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 585
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CRGANISM: Homo sapiens
US-10-433-108-34
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Sequence Sequence Sequence

equence 1238, Appl lequence 1238, A sequence 102, Appl Sequence 98, Appl Sequence 104, Appl Sequence 129, Appl Sequence 129, Appl Sequence 125, Appl Sequence 123, Appl Sequence 101, Appl Sequence 2, Appl

Run on:

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PROTEIN FRAGMENTS
BINDING REGIONS OF SERUM ALBUMIN OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTED TO SATISTICS OF STATE OF STATE
                              US-10-153-064-90
US-10-153-064-93
US-10-153-064-93
US-10-153-064-95
US-10-153-064-95
US-10-153-064-95
US-10-153-064-127
US-10-153-064-127
US-10-153-064-127
US-10-153-064-123
US-10-153-064-123
US-10-153-064-123
US-10-153-064-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 1, Application US/08448196A |
| Patent No. 5780594 |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: BIOLOGICALLY ACTIVE PRO TITLE OF INVENTION: CONTAINING SPECIFIC BIN TITLE OF INVENTION: RELATED PROTEINS |
| NUMBER OF SEQUENCES: 9 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: NASA |
| STREET: MARCHALL SPACE FLIGHT CENTER |
| STATE: ALABANA |
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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1 HGDLLE
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                                                                                                                            April 19, 2004, 11:40:29; Search time 0.919668 Seconds (without alignments) 336.813 Million cell updates/sec
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Sequence 2, App
Sequence 2, App
Sequence 133, A
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Sequence 3, Ar
Sequence 1, Ar
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Sequence 1
Sequence 4
Sequence 5
Sequence 6
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Sequence 2
Sequence 5
Sequence 3
Sequence 4
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Sequence
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Sequence
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1. /cgn2 = /ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2 = /ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2 = /ptodata/2/iaa/6A_COMB.pep:*

3. /cgn2 = /ptodata/2/iaa/6A_COMB.pep:*

5. /cgn2 = /ptodata/2/iaa/PCTUS_COMB.pep:*

6. /cgn2 = /ptodata/2/iaa/PCTUS_COMB.pep:*

6. /cgn2 = /ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                           389414 segs, 51625971 residues
                                                                                                                                                                                            US-09-832-929-18_COPY_247_252
33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                 Sequence:
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Result

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Gaps

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DANIEL C.
BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
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Sequence 1, 473050

RENERL INFORMATION:
APPLICANT: Strand, Frederick T
TITLE OF INVENTION: Denatured Bovine Serum Albumin Milk
TITLE OF INVENTION: Denatured Bovine Serum Albumin Milk
TITLE OF INVENTION: Products and Method Therefor
NUMBER OF SEQUENCE: 1
CORRESPONDENCE HODRESS:
ADDRESSE: Frederick T. Strand
STREET: Phoenix
STREET: Phoenix
STREET: Anizona
COUNTRY: USA
ZIP: Phoenix
STREET: BAPAGE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb storage
COMPUTER: USA
SOFTWARE: WordPerfect 5.1
COMPUTER: WordPerfect 5.1
COMPUTER: WORDPER: US/08/134,638
FILING DATE: US/12/93
CLASSIFICATION NUMBER: US/08/134,638
FILING DATE: US/12/93
FILING DATE: US/12/94
F
                                                                                                                                                              Query Match
100.0%; Score 33; DB 4; Length 547;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels
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100.0%; Score 33; DB 1; Length 582;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels
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Patent No. 5780594
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: BIOLOGICALLY
TITLE OF INVENTION: CONTAINING SP
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27640
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STRANDEDNESS: single
TOPOLOGY: linear
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Patent No. 6551795
GENERAL INFORMATION:
PAPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 33; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BIENKOWSKI, MICHAEL J.
TITLE OP INVENTION: NOVEL KIDNEY ATP-DEPENDENT POTASSIUM
TITLE OP INVENTION: GRANNELS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPDY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT PEDLICATION DATA:
REPLICATION NUMBER: US/08/709,923
FILING DATE:
CLASSIFICATION NUMBER: US/08/709,923
FILING DATE:
CLASSIFICATION NUMBER: 6001.N CP
REGISTRATION NUMBER: 6001.N CP
TELEPHONE: 616-833-7914
TELEPHONE: 616-833-7914
TELEPHONE: 380 antho acids
SEQUENCE CHARACTERISTICS:
LENGTH: 380 antho acid
STRANDEDNESS: SINGle
TYPE: antho acid
STRANDEDNESS: SINGle
TOPOLOGY: linear
MOLECULE TYPE: POTCHIN
ANTI-STREET NO
                                                                                                                                                                            Sequence 3, Application US/08709923 Patent No. 5831055
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US-09-252-991A-27640
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Sequence 6, Application US/08448196A
Patent No. 5780594
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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ZIP: 35812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: MS/NES-28402-2
REFERENCY FOOCHER IN PSOF AT TELECOMMUNICATION INFORMATION:
TELEBROME: 205-544-0028
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TELEBRAX: 583 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                    XX/MFS-28402-2
                                                                                REFERENCE/DOCKET NUMBER: XX/X
TELECOMUNICATION INFORMATION:
TELEFAX: 205-544-0021
TELEFAX: 205-544-0021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-448-196A-5
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-08-448-196A-6
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Best Local Similarity 100.
Matches 6; Conservative
                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 HGDLLE 251
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US-08-448-196A-5

Sequence 5, Application US/08448196A

Patent No. 578059

TOTAL OF INVENTION:
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS

TITLE OF INVENTION: RELATED PROTEINS

TORRESPONDENCES: 9

CORRESPONDENCES: 19

CORRESPONDENCES: 19

STREET: MARSHALL SPACE FLIGHT CENTER

CITY: HUNTSVILLE
STRATE: ALABAMA

COUNTY: HUNTSVILLE
STATE: ALABAMA

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: DEN PC Compatible

OPERATING SYSTEM: DC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/448,196A

FILING DATE: 23-MAY-1995

CLASSIFICATION: S3-MAY-1995

CLASSIFICATION: ROBERT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 33; DB 1; Length 583; 100.0%; Pred. No. 50; tive 0; Mismatches 0; Indels
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NASA
STREET: MASAASILE SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
COUNTRY: USA
ZIP: 35812
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: 205-544-0221
TELEPHON: 205-544-0228
INFORMATION FOR EQUID NO: 4:
TELEPHONE TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE:
CARACTERICAL: NO
ANTI-SENSE:
CARACTERICALINAL
FRAGMENT TYPE: N-terminal
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Matches 6; Conservative
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18,757

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Sequence 3, Application US/08448196A

Patent No. 5780594

GENERAL INFORMATION:
APPLICANT: CRAFER, DANIEL C.
TITLE OF INVENTION: ELOLOGICALLY ACTIVE PROTEIN FRAGMENTS
TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NASA
STREET: MARSHALL SPACE FLIGHT CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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JOCATION: 369.419
COCHER INPORMATION: HSA(1-n)"
FEATURE:
NAMEAKEY: Region
JOCATION: 1.585
OTHER INPORMATION: MOLE= "Alternative C-termini of FEATURE:
FEATURE:
OTHER: NEORWATION: Mole= "Amino acid sequence of OTHER: INPORMATION: natural HSA"
US-08-153-799-14
     ZIP: 079/4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/153,799
FLING DATE: OF-MAR-1992
PILING DATE: OF-MAR-1992
PRICH APPLICATION NUMBER: US 07/847975
PRICH APPLICATION NUMBER: US 07/775952
PRICH APPLICATION NUMBER: PCT/GB90/00650
PRICH APPLICATION NUMBER: US 07/775952
PRICH APPLICATION NUMBER: US 07/775992
PRICH APPLICATION NUMBER: US 06/90997
PRICH APPLICATION NUMBER: US 06/
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100.0%; Score 33; DB 1;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 6; Conservative 0; Mismatches 0
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US-08-448-196A-3
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                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08448196A
| GENERAL INFORMATION:
| TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRACHENTS
| TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR SEQUENCES: 9
| CORRESPONDENCE ADDRESS: 9
| CORRESPONDENCE ADDRESS: 9
| CORPUTER INVENTION: FRACE FLIGHT CENTER OF SERUM ALBUMIN OR STREET: MAKSHALL SPACE FLIGHT CENTER OF SERVING SYSTEM: PC-DOS/MS-DOS OF SERVING SYSTEM: BW 7094/48,196A
| CORPUTER IN SPECIAL STANDARD STANDARD SYSTEM: BW 7094/48,196A
| CLASSIFICATION NUMBER: 18,757 |
| REPERENCE/DOCKET NUMBER: 18,757 |
| REDERMING/DOCKET NUMBER: 18,757 |
| RELEPANCE/DOCKET NUMBER: 18,757 |
| RELEPANCE OF SEGUENCE OF SEGUENC
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| Sequence 14, Application US/08153799 |
| Patent No. 576683 |
| GENERAL INFORMATION: | APPLICANT: Goodey, Andrew R |
| TITLE OF INVENTION: POlypeptides |
| VMMBER OF SEQUENCES: 23 |
| NUMBER OF SEQUENCES: 23 |
| NUMBER OF SEQUENCES: 23 |
| STREET: 100 Mountain Avenue |
| CITY: Murray Hill |
| STATE: New Jersey |
| COUNTRY: USA |
| COUNTRY: USA |
| COUNTRY: USA |
| STATE: New Jersey |
| COUNTRY: USA |
| COUNTR
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Best Local Similarity 100.
Matches 6; Conservative
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247 HGDLLE 252
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GENERAL INFORMATION:

APPLICANT: CARTER, DANIEL C
APPLICANT: CARTER, DANIEL C
APPLICANT: CARTER, FLORIAN
TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER
FILE REPERENCE: 08/984,176
CURRENT APPLICATION NUMBER: US/08/984,176
CURRENT PILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
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       Mismatches
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100.0%; Pred. No.
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US-08-702-572-2
; Sequence 2, Application US/08702572
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18-08-284-176-1
'Sequence 1, Application US/08984176
'Patent No. 5948609
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0
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CORGANISM: Homo sapiens
US-08-984-176-1
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Best Local Similarity
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Matches 6; Conserv
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ALABAMA
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LENGTH: 585
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

REFLICANT:

CONDUCTIVE OF INVALIDIATION:

CONDUCTIVE AND CONDUCTIVE AN
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APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Waright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
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Patent No. 6663485

GENERAL INFORMATION

APPLICANT: Ball et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

CURRENT APPLICATION NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SEQ ID NO 5

LENGTH: 585
                                          MBER: US/08/769,746
19-DEC-1996
APPLICATION NUMBER: US/08/76%, ...
FILING DATE: 19-DEC-1996
CLASSEFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: MRRI-(
; TELECOMMUNICATION INFORMATION: TELECHOME: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 585 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein
US-08-769-746-2
100.0%;
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Patent No. 5652352
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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CORGANISM: Homo Sapiens
US-10-153-064-5
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US-10-153-064-5
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICA DATE:
CLASSIFICATION: 08 / 08 / 222,619
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE: CHARACTERISTICS:
LENGING CHARACTERISTICS:
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OM protein - protein search, using sw model

Run on:

April 19, 2004, 11:37:59 ; Search time 1.4626 Seconds (without alignments) 789.208 Million cell updates/sec

US-09-832-929-18\_COPY\_266\_277 57 1 ENQDSISSKLKE 12 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: Pirl:\*
2: Pir2:\*
3: Pir3:\*
4: Pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	serum albumin prec	lbumin	in - dog	albumin		serum albumin prec	mannose-6-phosphat	afamin precursor -	serum albumin prec	ğ	albumin - Mongolia	hypothetical prote	afamin precursor -	hypothetical prote	hypothetical prote	hippurate hydrolas	serum albumin - mo	probable flagellar	cold acclimation p	۲,	hypothetical prote		hypothetical prote	serum albumin prec		$\sim$	prot	ran	transducer protein
SUMMARIES	ID	A47391	ABHUS	I46986	S57632	ABPGS	ABBOS	S41122	A54906	ABSHS	ABHOS	JC5838	H36812	A53195	T32033	T34107	E69640	A05139	F82123	831097	B82882	AH2975	C98307	F84657	ABRTS		B30305	T24693	2	4
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	Score	57	57	54	54	51	51	45	44	44	43	40	4.0	39	38	38	37	37	37	37	37	37	37	37	37	36	36	36	36	36
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C84298 C88924 S65668	D96786 S30010	T42977 G72392	B89761	T44137 A69173	T33614	G64453	AC1484	A11123	A48443	<b>S</b> 52075
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420 575 1011	1037	2471	79	06.4 8.4	264	296	314	314	317	416
63.2	63.2	63.2	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4
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30 31 32	33.5	. E &	37	38	0 4	4.	42	43	44	<b>4</b> ,

## ALIGNMENTS

Gaps . 0 Query Match
100.0%; Score 57; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 12; Conservative 0; Mismatches 0; Indels

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282 ENQDSISSKLKE 293 1 ENODSISSKLKE 12 g

RESULT 2

ABHUS

Startm albumin precursor [validated] - human

Nilternate names: preproalbumin

Nicontains: kinetensin

Cipecies: 190-11-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000

Cipecies: 190-311-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000

Cipate: 29-Jul-1981 #sequence of 13947; 159286; IS9313; GIN-7; SS5314; A91420; S06422; S3

Cipate: A. Fear and Start and A. S. C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seebu Nucleic Acids Res. 9, 6103-6114, 1981

A; Tatle: The sequence of human serum albumin menda A; Accession: A93743; MulD:82081882; PMID:6171778

A; Molecule type: menda Sci. U. S. A. 79, 71-75, 1982

R; Dugaiczyk, A.; Law, S. W.; Dennison, O.E.

R; Dugaiczyk, A.; Law, S. W.; Dennison, O.E.

P; Dugaiczyk, A.; Law, S. W.; Dennison, O.E.

P; Dugaiczyk, A.; Law, S. W.; Dennison, O.E.

P; Pugaiczyk, A.; Law, S. W.; Dennison, O.E.

R; Pugaiczyk, A.; Law, S. W.; Dennison, O.E.

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Aymotecule type: protein
A;Residues: 354-356, K',358-378 <MIN2>
A;Residues: 354-356, K',358-378 <MIN2>
A;Residues: 354-356, K',358-378 <MIN2>
A;Residues: 358, 201-215, 1992
A;Vete: this variant is designated albumin Sondrio; another variant Paris-2 is reported R;He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
A;Title: Atomic structure and chemistry of human serum albumin.
A;Reference number: A46756; MUID:92334427; PMID:1630489
A;Contents: annotation; X-ray crystallography, 2.8 angstroms
A;Reference number: A9442
In The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-40
A;Reference number: A9442
A;Contents: annotation; three-dimensional structure and disulfide bonds
B;Saber; M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A;Title: Disulfide bonds in human serum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A90930
A; Contents: annotation; disulfide bonds
R;Jacobsen, C.
Biochem. J. 171, 453-459, 1978
A;Title: Lysine residue 240 of human serum albumin is involved in high-affinity binding
A;Title: Lysine residue 240 of human serum albumin is involved in high-affinity binding
A;Reference number: A90299; MUID:78186630; PMID:656055
A;Contents: annotation; bilirubin-binding site
R;Peters, T.; Reed, R.G.
in Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjoholm, I., eds., 11-20
A;Title: Serum albumin: conformation and active sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 166-173 <CAR>
R;Mogard, M.H.; Kobayash; R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; W.
Blochem. Blophys. Res. Commun. 136, 983-988, 1986
A,Title: The anino acid sequence of kinetensin, a novel peptide isolated from pepsin-tr.
A,Reference number: A03239; MUID:86242180; PMID:3087352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wholecule type: protein (1984). W. 1984 albumin Torino (1984). M. 24. 437. 44. 1983 albumin Torino (1984). M. 1984 albumin Torino (1984). M. 1984 alliano, M.; Zapponi, M.C.; Tenni, R. Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R. M. 1984 albumin 214, 437-444, 1993 albumin delicite: The structural characterization and bilirubin-binding properties of albumin He. (1986). M. 1985 albumin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                peptides formed by the action of acid protea:
PMID:2474609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 166-173,'L' <MOG>
R;Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, R;Galliano, M.; Minchiotti, L.; 8721-8725, 1990
A;Title: Muttations in genetic variants of human serum albumin found in Italy.
A;Reference number: A38255; MUID:91062352; PMID:2247440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: 533298
.Molecule type: protein
.Residues: 255-263, Ev. 265-281 «MINI»
.Roteit this variant is designated albumin Herborn
.Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, iochim. Biophys. Acta 1119, 232-238, 1992
.Title: Two alloalbumins with identical electrophoretic mobility are produced .Reference number: $21078; MUID:92190239; PMID:1347703
                                                                                                                                                                                                                                                                                                                                           W.; Mitra, S.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,Molecule type: protein
.,Residues: 82-105, 'K', 107-110 <GAL2>
.,Note: this variant is designated albumin Vibo Valentia
.,Accession: A38255
                                       A; Reference number: S17599; MUID:92126241; PMID:1772598
                                                                                    A, Mccession: S17599
A, Molecule type: protein
A, Residues: 25-44,34-437,431-447 < KAU>
A, Note: 49-Leu was also found
R; Carraway, R.E.; Cochrane, D.E.; Boucher, W.
J. Immunol. 143, 1680-1684, 1989
A, Title: Structures of histamine-releasing per
A, Reference number: A45800, Muid: 83341406; PM
A, Accession: A45800
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A,Residues: 76-111 <GAL1>
A,Accession: B38255
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Ajectures translated from GS/EVEL/DBJ
Ajectures 
A;Accession: A93936
A;Accession: A93936
A;Accession: By A;
A;Accession: By A;
A;Accession: By A;
A;Accession: By A;
A;Coss-references: EMBL: V00494; NID: g28589; PIDN: CAA23753.1; PID: g28590
R;Cross-references: EMBL: V00494; NID: g28589; PIDN: CAA23753.1; PID: g28590
R;Crass-Core number: 139427; MUID: 86140099; PMID: 2419329
A;Accession: 139427
A;Accession: 139427
A;Accession: 139427
A;Accession: L79427
A;Accession: L79417
A;Accession: L79427
A;Accession: L79417
A;Accession: L79427
A;Accession: L79417
A;Accession: L79427
A;Accession: L79447
A;Accession: L79427
A;Accession: L79417
A;Accession: L79427
A;Accession: L79427
A;Accession: L79427
A;Accession: L79427
A;Accession: L79444
A;Accession: L79427
A;Accession: L7944
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D.; Porta

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Series: Felia silvestris catus (domestic cat)

C;Species: Felia silvestris catus (domestic cat)

C;Species: Felia silvestris catus (domestic cat)

C;Accession: UCct-1955 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999

C;Accession: UCcf660; S5732

R;Hilger, C.; Grigioni, F.; Hentges, F.

Genen 169, 295-296, 1996

A;Title: Sequence on the gene encoding cat (Felis domesticus) serum albumin.

A;Reference number: UC4660; NUID:96194824; PMID:8647469

A;Accession: UC4660

A;Molecule type: mRNA

A;Residues: 1608 #HIZ>

A;Accession: UC4660

A;Molecule type: mRNA

A;Residues: EMBL:X84842; NID:9886484; PIDN:CAA59279.1; PID:9886485

A;Cross-references: EMBL:X84842; NID:9886484; PIDN:CAA59279.1; PID:9886485

A;Cromment: This protein is the major protein component in plasma. It functions as a c;Comment: inver; plasma

C;Superfamily: serum albumin; serum albumin methat procein capat homology <SA1>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;21-394/Domain: serum albumin repeat homology <S
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: Sol382; Asionece_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: Sol382; Asionece_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: Sol382; Asionece_revision 31-Dec-1993 #text_change 22-Jun-1999
R;Weinstock, J; Baldwin, G.S.
Nucleic Acids Ree: 16, 9045, 1988
A;Title: Nucleotide sequence of porcine liver albumin.
A;Reference number: Sol382; MUID:89016582; PMID:3174440
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A; Status: translation not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-605 < WEI>
A; Cross-references: EMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
R; Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
Bone Miner: Res. 4, 235-241, 1989
A; Title: Serum albumin and its acid hydrolysis peptides dominate preparat
A; Reference number: A61006; MUID:89269769; PMID:2728927
A; Accession: A61006
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Pred. No. 0.034;
1; Mismatches 0; Indels
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Best Local Similarity 91.7%;
Matches 11; Conservative
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A; Contents: annotation; binding sites

R; Hater, Ms.; Dugaiczy, A.

M. J. Hum. Genet. 35, 565-72, 1983

A; Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
A; Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
A; Contents: annotation; gene position
A; Contents: annotation; gene position
R; Malker, J. E.
FEBS Lett. 66, 173-175, 1976
A; Title: Lysine residue 199 of human serum albumin is modified by acetylsalicyclic acid
A; Contents: annotation
A; Rocherence number: A46755; MUID:7627808; PMID:955075
A; Reference number: A46755; MUID:7627808; PMID:955075
A; Reference number: A46755; MUID:7627808; PMID:955075
A; Reference number: A46755; MUID:7627808; PMID:954076
A; Contents: annotation
C; Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
A; Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
C; Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
C; Comment: A large number of variants of human serum albumin have been described.
A; Comment: A large number of variants of human serum albumin have been described.
A; Comment: A large number of variants of human serum albumin have been described.
A; Comment: A large number of variants experimental c, RDO
A; Comment: Broad sequence Heature specimental c, RDO
A; MDD position: 4011-4013
A; Cross-references: GELIB; Serum albumin; serum albumin repeat homology
C; Keyvords: corrier protents; duplication; metals experimental c, RDO
A; MDD position: serum albumin repeat homology c$120;
C; Superfamily: serum albumin repeat homology c$120;
B; 113, Aponalin: serum albumin repeat homology c$120;
B; 114, 125, Aponalin: serum albumin repeat homology c$120;
B; 114, 120; Aponalin: serum albumin 
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94.7%; Score 54; DB 2; Length 265;
Best Local Similarity 91.7%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 0; Indels
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Matches 12, Conservative
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of mineral

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A,Molecule type: protein
A,Rolecule type: protein
A,Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,'1
A,Reference number: A94551
A,Accession: A94551
A,Molecule type: protein
A,Refidues: 190-195 < BR2>
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A/Status: prediminary
A/Status: protein
A/Molecule type: protein
A/Molecule: 529-536,569-572 <MER>
A/Molecule: 529-536,569-572 <MER>
C/Superfamily: serum albumin; serum albumin repeat homology
C/Superfamily: serum albumin; serum experimental <SIG>
F/19-24/Domain: serum albumin #status experimental <PRO>
F/25-607/Product: serum albumin repeat homology <SA1>
F/20-337/Domain: serum albumin repeat homology <SA2>
F/20-393/Domain: serum albumin repeat homology <SA2>
F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-393/Domain: serum albumin serum product homology <SA3>
F/27/Shnding site: copper (His) #status predicted
F/77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,3883-392,
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M.Alternate names: phosphomannose isomerase

C,Species: Homo sapiens (man)

C,Date: 07-599-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999

C,Accession: S41122; S38666

B,Froudfoot, A.E.I.; Turcatti, G.; Wells, T.N.C.; Payton, M.A.; Smith, D.J.

Eur. J. Blochem. 219, 415-421, 1994

A,Title: Purification, CDNA cloning and heterologous expression of human phosphomannose

A,Reference number: S41122; MUID:94139717; PMID:8307007
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribrown, J.R. 2004. 23, 1389, 1974
A;Reference number: A91457
A;Contents: amontation, disulfide bonds
A;Contents: amontation, disulfide bonds
Biochem. J. 302, 907-911, 1394
A;Title: Preparation and characterization of novel substrates of insulin proteinase A;Reference number: S55232; MJID:95031935; PMID:7945219
A;Reference number: S55232; MJID:95031935; PMID:7945219
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A;Residues: 1-423 <PRO>
A;Residues: Erferences: EMBL:X76057; NID:g416016; PIDN:CAA53657.1; PID:g416017
C;Genestics:
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Pred. No. 0.13;
2; Mismatches 0; Indels
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A,Cross-references: GDB:119397; OMIM:154550
A,Map position: 15q22-15qter
C,Superfamily: yeast mannose-6-phosphate isomerase
C,Superfamily: yeast mannose-6-phosphate isomerase
                                                                                                        serum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 DNODTISSKIKE 300
                                                                                         A;Reference number: A91458
A;Accession: A91458
A;Mocession: A91458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ENQDSISSKLKE 12
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402-433 <REE>
                                                                  Fed. Proc. 34, 591, 1975
A, Title: Structure of bov
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                                                                                                Gaps
                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                  Serum albumin precursor [validated] - bowine

Nalternate names: 67K protein; preproalbumin

C;Species: Bos primiganius teurus (cattle)

C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18:

C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18:

C;Date: 34-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18:

R;Hollowachuk, E.W.; Scollenborg, J.K.; Reed, K.G.; Peters Jr., T.

submitted to the EMBL Data Library, August 1991

A;Reference number: A18885

A;Accession: A38885
                          Score 51, DB 1, Length 605,
Pred. No. 0.13,
2, Mismatches 0, Indels
                                                                                                0; Indels
                          Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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Gaps

292 ODSISSKIKE 301

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77 ENQDSLGSKVKD 88

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AyRoceule type: mRNA
AyResidues: 1-607 cHOA>
AyRoceule type: mRNA
AyResidues: 1-607 cHOA>
AyResidues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
C;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: propeptide #status predicted <PRO>
F;2-607/Product: serum albumin #status predicted <AMAT>
F;2-607/Promain: serum albumin repeat homology <SA1>
F;20-037/Domain: serum albumin repeat homology <SA1>
F;20-037/Domain: serum albumin repeat homology <SA3>
F;20-037/Domain: serum albumin repeat homology <SA3>
F;20-1937/Domain: serum albumin repeat homology <SA3>
F;27/Dianding site: copper (His) #status predicted
F;77-86,99-115.114-125,147-192.191-200,223-266,288-276,288-302,301-312,339-384,383-392,*
F;263/Binding site: bilirubin (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Cross_references: EVBL:X17055; NID:g1386; PIDN:CAA34903.1; PID:g1387
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
teroid hormones (weak bonds with these hormones promote their transfer across the membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
Bur. J. Biochem. 215, 205-212, 1993
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
A;Reference number: 834053; MUID:93345495; PMID:8344282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
serum albumin precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: 806936
                                                                                                                                                                                                                                                                                               RjBrown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R. Mudleic Acids Res. 17, 10495, 1989
A; Title: Nucleotide and deduced amino acid sequence of sheep serum albumin. A; Reference number: S06936; MUID:90098888; PMID:2602160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1; Length 607;
Pred. No. 2.8;
4; Mismatches 0; Indels
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Best Local Similarity 66...
8: Conservative
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289 DHQDALSSKLKE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: S06936
Molecule type: mRNA
Residues: 1-607 <BRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S34053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
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A, Roldides: 1-29 kNN
A, Roldides: 1-59 kNN
A, Roldides: 1-50 
                               Astrono precureor - human
NyAlternate names: alpha-albumin
CSpecies: Homo sapiens (man)
CSPECIES: Lossp-1999 #sequence revision 10-Sep-1999 #text_change 17-Mar-2000
CSACCESSION: A54906; UC6143; S68554; S78082; I39425
RSitchenstein, H.S.; Lyons, D.E.; Wurfel, M.M.; Johnson, D.A.; McGinley, M.D.; Leidli, J. J. Biol. Chem. 269, 18149-18154, 1994
Astrices and mumber: A54906
Astrices and mumber: A54906
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Astrices and mumber: A54906
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Pred. No. 2.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Gaps

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Indels

DB 1; Length 607;

Query Match 75.4%; Score 43; DB 1 Best Local Similarity 81.8%; Pred. No. 4.3; Matches 9; Conservative 1; Mismatches

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Gaps

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Indels

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Reidues: 1-238 cADA;
A;Reidues: 1-238 cADA;
A;Cross-references: EMBL:AF016676; PIDN:AAC25902.1; GSPDB:GN00023; CBSP:F41B5.5
A;Experimental source: strain Bristol N2; clone F41B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1091 <GAT>
A;Cross.references: EMBL:U55369; PIDN:AAC25825.1; GSPDB:GN00023; CESP:C18C4.5
A;Experimental source: strain Bristol N2; clone C18C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypochetical protein F41B5.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Dete: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999 (Accession: T32033 R;Dante, M.; Kramer, J. Spante, M.; Reference number: 221115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C18C4.5 - Caenorhabditis elegans
C.Speciese: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Cct-1999 #text_change 29-Oct-1999
C;Accession: T34107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-608 <BEL>
A;Cross-references: GB:X76456; NID:g456358; PIDN:CAA53994.1; PID:g456359
C;Genetics:
J. Biol. Chem. 269, 5481-5484, 1994
A;Title: New albumin gene 3' adjacent to the alpha-1-fetoprotein locus. A;Reference number: A53195; MUID:94164881; PMID:7509788
A;Accession: A53195
A;Status: preliminary
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Pred. No. 14;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 2; Length 608;
Pred, No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Ajintrons: 30/1; 47/2; 91/3; 162/2
C;Superfamily: serum albumin; serum albumin repeat homology
C;Superfamily: serum albumin; serum
C;Reywords: glycoptotein
F;1-2,LOomain: serima albumin repeat homology csA1>
F;22-608/Pomain: serum albumin repeat homology csA2>
F;21-394/Domain: serum albumin repeat homology csA2>
F;21-394/Domain: serum albumin repeat homology csA3>
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submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C18C4
A;Reference number: Z21478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%;
88.9%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ENODSISSKIKE 12
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A; Introns: 77/1; 132/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Gene: CESP: F41B5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T34107
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R; Albrecht, J.
Submitted to the EMBL Data Library, January 1992
R; Albrecht, J.
Submitted to the EMBL Data Library, January 1992
R; Albrecht, J.
R; Albrecht, J.
A; Reference number: A36806
A; Reference number: A36806
A; Residues: 1-2469
ALB>
A; Cross-references: GBX4346; NID:g60320; PIDN:CAA45687.1; PID:g60385
B; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wi J.
J; Virol. 66, 5047-5058, 1992
B; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wi J.
A; Reference number: A37309; MUID:9233688; PMID:1321287
A; Contents: annotation; protein-coding frames
A; Rote ineither protein nor nucleotide sequence is given
C; Genetics:
                                                                                                                                                                                                albumin - Mongolian jird
CiSpecies: Meriones unguiculatus (Mongolian jird)
CiSpecies: Meriones unguiculatus (Mongolian jird)
CiSpecies: Meriones unguiculatus (Mongolian jird)
CiAccession: JC5838
R;Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.
B;Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.
A;Title: Sequencing of CDNA encoding serum albumin and its extrahepatic synthesis in the A;Reference number: JC5838, MJD:98116663; PMID:9455485
A;Accession: JC5838
A;Molecule type: mkNA
A;Residues: 1-609 exOs>
A;Cross-references: DDBJ:AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278
A;Cross-reference: liver
C;Superiamental source: liver
C;Superfamily: serum albumin; serum albumin repeat homology
F;222-395/Domain: serum albumin repeat homology eSA2>
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N;Alternate names: alpha-albumin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-2000
C;Accession: A53195
R;Belanger, L.; Roy, S.; Allard, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ORF64 - saimiriine herpesvirus 1 (strain 11)
C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
C;Accession: H36812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 75;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2; Length 609;
Pred. No. 16;
1; Mismatches 1; Indels
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81.8%;
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Best Local Similarity 58.3
Matches 7; Conservative
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A;Gene: CESP:C18C4.5
A;Map position: 5
A;Introns: 38/3; 95/3; 179/2; 259/3; 301/3; 419/2; 573/3; 613/1; 875/3; 920/2; 959/2; 98
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Query Match 66.7%; Score 38; DB 2; Length 1091; Best Local Similarity 58.3%; Pred. No. 74; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps

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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALBU BOVIN
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MEDLINE-86196112; PubMed=3009475;
Minghetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,
Beattie W.G., Dugaiczyk A.; Kuang W.J., Dennison O.E., Hawkins J.W.,
"Molecular structure of the human albumin gene is revealed by
nucleotide sequence within q11-22 of chromosome 4.";
J. Biol. Chem. 261:6747-6757(1986).
                                                                                                                                                                                                                                                           Gaps
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MEDIINE=82081882; PubMed=6171778;
Lawn R.M., Adelaman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;
"The sequence of human serum albumin cDNA and its expression in E.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              E45C871A670E740B CRC64;
  COPPER (BY SIMILARITY).
          (POTENTIAL)
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        BILINUBIN (POPER STRULARITY BY SINILARITY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 9:6103-6114(1981).
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12; Conservative 0
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The chemistry and physiology of the human plasma proteins, pp.23-40,
Pergamon Press, New York (1979).
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MEDLINE=86140099; PubMed=2419329;
Urano Y., Watanabe K., Sakai M., Tamaoki T.;
"The human albumin gene. Characterization of the 5' and 3' flanking regions and the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
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Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
1994.";
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                                                                                SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378. Huang M.C., Wu HT.; T.; The cDNA Sequences of human serum albumin."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDDINE=76187907; PubMed=1225573;
Meloun B., Moravek L., Koetka V.;
Meloun B., Moravek L., Koetka V.;
Formplete amino acid sequence of human serum albumin.";
FBS Lett. 58:134-137(1975).
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MEDLINE=76257808; PubMed=955075;
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TISSUE=Heart;
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?EBS Lett. 66:173-175(1976).
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MEDLINE-90115852; PubMed=2104980; Bremnan S.O., Myles T., Peach R.J., Donaldson D., George P.M.; "Albumin Redhill (-1 Arg. 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106. MEDLINE=91062352; PubMed=2247440; Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J. VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23; KOMAGOME-2 ARG-152 AND KOWAGOME-1 GLU-396.

KOMAGOME-2 ARG-152 AND KOWAGOME-1 GLU-396.

Madison J. Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsica Y.-I., Amaki I., Putnam F.W.;

"Genetic variants of serum albumin in Americans and Japanese.";

Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857 (1991). MEDLINE=87157744, PubMed=3828358;
Bennan S.C., Herbort P.;
"Albumin Canterbury (31 Lys-->Asn). A point mutation in the second domain of serum albumin."; VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M., Minchiotri L., Putnam F.W., "A donor splice mutation and a single-base deletion produce two carboxyl-terminal variants of human serum albumin.";
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MEDLINE=89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M., Neel J.V., Sakurabayashi I., Putnam F.W.;
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MEDLINE=80605523; PubMed=3479777;
Takshashi N., Takhashi Y., Isobe T., Putnam F.W., Fujita M., Satoh C., Neel J.V.;
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Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987). MEDLINE=90115905; PubMed=2404284; Arai K., Madison J., Shimuzu A., Putnam F.W.; "Point substitutions in albumin genetic variants from Asia."; Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990). Saber M.A., Stockbauer P., Moravek L., Meloun B.; "Disulfide bonds in human serum albumin."; Collect. Czech. Chem. Commun. 42:564-579(1977). Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990). Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990). Biochim. Biophys. Acta 912:191-197(1987). Electrophoresis 15:1459-1465(1994) MEDLINE=91296740; PubMed=2068071; BILIRUBIN-BINDING SITE. MEDLINE=78186630; PubMed=656055; DESCRIPTION OF VARIANT REDHILL VARIANT CANTERBURY ASN-337 VARIANT VENEZIA. cleavage site." SULFIDE BONDS Jacobsen C. Italy. REAR SEED OF THE SECOND 
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SEQUENCE OF 25-48.
MEDLINE=75011422; PubMed=4414013;
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J. Biol. Chem. 249:5872-5877(1974).
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Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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MEDLINE=94201492; PubMed=7512102;
Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,
Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
"Molecular characterization of dog albumin as a cross-reactive
allergen.";
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                                                                                                                                                                                                                                                                                                                  Milger C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                        PARSEZ, 7077705, Q9TSZ4; (10-0077-1996 (Rel. 34, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2003 (Rel. 42, Last annotation update) Serum albumin precursor (Allergen Can f 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20148667; PubMed=10669848;
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STRAIN-Beagle; TISSUE-Liver;
290 ENQDSISSKLKE 301
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Length 609;

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Query Match Best Local Similarity 100. Matches 12; Conservative

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VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
MEDLINE-22190239, PubMed=1347703;
Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.,
"Two alloalbumins with identical electrophoretic mobility are produced

VARIANT CASEBROOK ASN-518.

MEDLINE=91316157; PubMed=1859851;
Peach R.J., Brennan S.O.;
"Structural characterization of a glycoprotein variant of human serum albumin: albumin Casebrook (494 Asp-->Asn).";
Biochim. Biophys. Acta 1097;49-54(1991).

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SECURIOR FROM N.A.

SEQUENCE FROM N.A.

Higer C., Grigtoni F., Kohnen M., Hentges F.;

Comparison of the gene encoding cat (Felis domesticus) serum albumin.";

Green 169:295-296 (1996).

I comparison of the gene encoding cat (Felis domesticus) serum albumin.";

Comparison of the gene encoding cat (Felis domesticus) serum albumin.";

Comparison of the gene encoding to water, Ca(2+), Na(+), K(+), fatty acids, borndones, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bainformatics and the EMBL outstation the Buropean Beioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
J. Allergy Clin. Immunol. 93:614-627(1994).

-i- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. (24), Na(+), K(+), fatty acids, normones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-i- SUBCELLULAR LOCATION: Secreted.

-i- TISSUE SPECIFICITY: Plasma.

-i- ALERGEN: Causes an allergic reaction in human.

-i- SIMILARITY: Contains 3 albumin domains.
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07E629CACSF60ESF CRC64;
REBULT 4

ALD FELCA STANDARD; PRT; 608 AA.

ID ALBUTELOA

PASON CALLEBELSOS (Rel. 33, Created)

OI-FEBL-1996 (Rel. 33, Created)

ON OI-FEBL-1996 (Rel. 33, Created)

ON OI-FEBL-1996 (Rel. 33, Created)

ON ALD.

BRANCHCE STANDARD; PROCUREOR CALLETGEN Feld G2).

ON Mannellals Eucheria Catus (Cat)

Commellals Eucheria Catus (Cat)

NCDI TaxID-9685;

NCDI TaxID-9686;

NCDI Ta
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Gaps

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                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                   69410
                                                                                                                                                                     287 ENQDTISTKLKE 298
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                                                                                                                                                          1 ENQDSISSKLKE 12
         REVISIONS TO 190-195.
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SEQUENCE OF 402-433
                                                                         535
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605 AA;
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286
2399
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4413
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ALBU BOVIN
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Baldwin G.S., Weinstock J.;
Baldwin G.S., Weinstock J.;
Baldwin G.S., Weinstock J.;
Baldwin G.S., Weinstock J.;
Nucleic Acids Res. 16:9045-9045(1988).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SINGELIVIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Plasma.
-!- SIMILARITY: Contains 3 albumin domains.
                             Gaps
                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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         Score 54; DB 1; Length 608;
Pred. No. 0.028;
1; Mismatches 0; Indels
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ALBUMIN 2.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
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Metal-binding, Lipid-binding; Repeat, Signal, Copper.
                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-RED-2003 (Rel. 41, Last annotation update)
Serum albumin precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
SERUM ALBUMIN.
                                                                                                              605 AA
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EMBL; M36787; AAA30988.1; -.
PIR, 301382; ABPG8.
HSSP; P02768; 1E74.
InterPro; IPR000264; Serum_albumin.
Pfam; PP00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SWART; SM00103; ALBUMIN; 3.
                                                                                                              PRT;
          94.7%;
Ouery Match
Best Local Similarity 91...
Best Local 11, Conservative
                                                         290 ENQDSISTKLKE 301
                                               1 ENODSISSKIKE 12
                                                                                                              STANDARD;
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MEDLINE-80024278; PubMed=488109;
McGillivray R.T.A., Chung D.W., Davie E.W.;
"Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin.";
Eur. J. Biochem. 98:477-485(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea
Bovidae, Bovinae, Bos
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Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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BY SIMILARITY.
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Wu H.T., Huang M.C.;
"The complete cDNA sequence of bovine serum albumin.";
submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holowachuk E.W., Stoltenborg J.K., Reed R.G., Peters T. Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barry T., Power S., Gannon F.; Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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21-UUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 32, Last sequence update)
Serum albumin precursor (Allergen Bos d 6).
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Pred. No. 0.1;
2; Mismatches
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Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANT THR-214
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Homo sapiens (Human)
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493
607 AA;
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                                                                                                                                                                                                                                                                                                SEQUENCE OF 25-41.
MEDIATR=886267456; PubMed=3389500;
HEIGH D.C., Lin F.P., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical isochectroblotting gel: a preparative method for isolating proteins for N-terminal microsequencing.";
Anal. Biochem. 170:1-8(1988).
                                                                                                                           Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
Kapid confirmation and revision of the primary structure of bovine
serum albumin by BSIMS and Frit-FAB LC/MS.",
Biochem. Biophys. Res. Commun. 173:639-646(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M73993; AAA51411.1; --
EMBL; X58999; CAA41735.1; --
EMBL; X58999; CAA76847.1; --
EMBL; AF542068; AAN17824.1; --
HSSP; P02768; IE7B.
HSSP; P02768; IE7B.
HSSP; P00273; transport, prof.; 3.
PRINTS; PR00802; SERUMALEUMIN.
ProDom; P0002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
                                   [9]
SEQUENCE OF 19-28.
MEDLINE=7134075; PubMed=843354;
Patterson J.E., Geller D.M.;
Bovine microsomal albumin: amino terminal sequence of bovine microsomal albumin: amino terminal sequence of bovine microsomal albumin:
MEDLINE-82023364; PubMed=7283978; Reed KG., Putnam F.W., Peters T. Jr.; "Sequence of residues 400-403 of bovine serum albumin."; Ejochem. J. 191:867-868(1980).
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ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
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                                                                                                           SEQUENCE, AND REVISIONS TO 118-119 AND 180.
MEDLINE=91083649; PubMed=2260975;
                                                                                                                                                                                                                                                        Vilbois F.;
Submitted (AUG-1998) to Swiss-Prot.
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2007
3004
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403
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01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphomannose isomerase)
(PMI) (Phosphohexomutase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.J.;
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MEDLINE-20438347; PubMed=10980531;
MEDLINE-20438347; PubMed=10980531;
Hujjman B., Dorland L., de Koning T.J., Van Diggelen O.P.,
Hujjmane J.G.M., Marquardt T., Babovic-Vuksanovic D., Patterson M.,
Imtiaz F., Winchester B., Adamowicz M., Pronicka E., Freeze H.,
Matthijs G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic organization of the human phosphomannose isomerase (MPI) and mutation analysis in patients with congenital disorders of glycosylation type Ib (CDG-Ib).";
Hum. Mutat. 16:247-252(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Placente, and Teefis;
MEDILINE=Placente, and Teefis;
Proudfoot A.E.I., Turcatti G., Wells T.N.C., Payton M.A., Smith D Proudfoot A.E.I., Turcatti G., Wells T.N.C., Payton M.A., Smith D Phosphomannos, Edwardse.";
Phosphomannos isonerase.";
Eur. J. Biochem. 219:415-423 (1994).
                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                      Score 51; DB 1; Length 607;
Pred. No. 0.1;
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A -> T.

C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

N -> D (IN REF. 6).

ST -> TS (IN REF. 6).

K -> A (IN REF. 6).

K -> B (IN REF. 6).

X -> B (IN REF. 6).
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Matches 10; Conservative
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MIM; 154550; -...
MIM; 602579; -...
GO; GO:00044F: :mannose-6-phosphate isomerase activity; TAS.
GO; GO:0007150; Man6p isomerasel.
PEAM; PF01238; PMI typeI; I.
PRINTS; PROOT14; MAN6P ISOMERASE.
PECDOM; PD004499; Man6p isomerasel; 1.
TIGRRAMS; TIGRO0218; manA; 1.
PROSITE; PS00965; PMI I 1; 1.
PROSITE; PS00966; PMI I 2; 1.
PROSITE; PS00966; PMI I 2; 1.
PROSITE; PS00966; PMI I 2; 1.
PROBABLE.
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218 R > Q (In CDG-TIB).
/FTIG=VAR 012340.
422 AA, 46524 MW, A450ABEF53722605 CRC64;
   EMBL, AF227216, AAF37697.1; JOINED.
EMBL, AF272717, AAF37697.1; JOINED.
EMBL, BC046337; AAH46357.1; -.
PIR; S41122; S41122.
HSSP; P34948; IPMI.
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AFAM_HUMAN
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L., A Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalon D.K., Muzny D.M., Raden R.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: Zinc (By similarity).
-!- PATHWAY: Glycosylation, early steps of mannosylation.
-!- PATHWAY: Glycosylation, early steps of mannosylation.
-!- SUBCELULIAR LOCATION: Cytoplasmic (Probable).
-!- TISSUE SPECIFICITY: Expressed in all tissues, but more abundant in heart, brain and skeletal muscle.
-!- DISEASE: Defects in MPI are the cause of congenital disorder of glycosylation type ID (CDG-ID) [MIM:602579]; also known as carbohydrate-deficient glycoprotein syndrome type IB (CDG-IB).
CDG-ID is clinically characterized by protein-losing enteropathy, a gastrointestinal disorder. Biochemically it is characterized by hypoglycosylation of serum glycoproteins.
-!- SIMILARITY: Belongs to the mannose-6-phosphate isomerase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98192671; PubMed=9525984; Michues R., Hadalik M., Alton G., Koerner C., Schiebe-Sukumar M., Nichhues R., Hadalik M., Alton G., Koch H.G., Zimmer K.-P., Wu R., Harms E., Reiter K., von Figura K., Freeze H.H., Harms H.K., Marquardt T.; "Carbohydrater-deficient glycoprotein syndrome type Ib: phosphomannose isomerase deficiency and mannose therapy."; Clin. Invest. 101:1414-1420(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99254476; PubMed=9585601;
Jaeken J., Matthijs G., Saudubray J.-M., Dionisi-Vici C., Bertini E.,
de Lonlay P., Henri H., Carchon H., Schollen E., Van Schaffingen E.;
"Phosphomannose isomerase deficiency: a carbohydrate-deficient
glycoprotein syndrome with hepatic-intestinal presentation.";
Am. J. Hum. Genet. 62:1535-1539(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preeze H.H.;
"Genetic and metabolic analysis of the first adult with congenital
disorder of glycosylation type Ib: long-term outcome and effects of
mannose supplementation."
Mol. Genet. Metab. 73:77-85(2001).
-!- FUNCTION: Involved in the synthesis of the GDP-mannose and
dolichol-phosphate-mannose required for a number of critical
mannosyl transfer reactions.
-!- CATALYTIC ACTIVITY: D-mannose 6-phosphate = D-fructose 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS CDG-IB THR-139 AND GLN-218.
MEDLINE=21249093; PubMed=11350186;
Westphal V., Kjaergaard S., Davis J.A., Peterson S.M., Skovby F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS CDG-IB LEU-101 AND THR-137.
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FTId=VAR 012339.

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Nishio H., Heiskanen M., Palotie A., Belanger L., Dugaiczyk A.; "Tandem arrangement of the human serum albumin multigene family in the sub-centromeric region of 4q: evolution and chromosomal direction
                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94299534; PubMed=7517938;
Lichenstein H.S., Lyons D.B., Wurfel M.M., Johnson D.A.,
Lichenstein H.S., Lyons D.B., Wurfel M.M., Mayer J.P.,
Wright S.D., Zukowski M.M.;
"Afamin is a new member of the albumin, alpha-fetoprotein, and
Vitamin D-binding protein gene family.";
                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Afamin precursor (Alpha-albumin) (Alpha-Alb).
Homo sapiens (Human).
599 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96240683; PubMed=8648639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of transcription.";
J. Mol. Biol. 259:113-119(1996)
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EMBL; X76057; CAA53657.1; -. EMBL; AF227218; AAF37697.1;

292 QDSISSKIKE 301

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ALBUMIN 2.
ALBUMIN 3.
BY SIMILARITY.
BY 
                                                                                                                                                          ortholog.";
Gene 153:287-288(1995).
Gene 153:287-288(1995).
-!- FUNCTION: Possible role in the transport of yet unknown ligand.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: N-glycosylated.
-!- PTM: N-glycosylated.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                Allard D., Gilbert S., Lamontagne A., Hamel D., Belanger L.; "Identification of rat alpha-albumin and cDNA cloning of its human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 599;
Pred. No. 1.9;
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SEQUENCE OF 1-69; 105-207 AND 560-599 FROM N.A. TISSUE=Liver;
MEDLINE=95180738; PubMed=7875606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 132140; AAA21612.1; ---
EMBL; U51243; AAC50720.1; ---
EMBL; 135497; AAA68199.1; ---
EMBL; 135497; AAA68199.1; ---
EMBL; 135498; AAA68199.1; ---
EMBL; 135498; A34906.

PIR; A54906; A54906.

PIR; 139424; 139424.

PIR; 139426; 139426.

HSSP; PO2768; LE7B.

GO: GO: COS576; C: extracellular; TAS.

InterPro; IPROG0264; Serum albumin.

Pfam; PF0273; transport prot; 3.

PROS17; PROM0025 SERUMALEDMIN.

PRODOM; PE00034 ALBUMIN; 3.

PROS1TE; PS00212; ALBUMIN; 3.

Transport; Repeat; Glycoprotein; Signal.

SIGNAL
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Matches 9; Conservative
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MEDLINE=9009888; PubMed=2602160;

MEDLINE=9009888; PubMed=2602160;

MEDLINE=9009888; PubMed=2602160;

M. Dates PubMed=2602160;

M. Dates PubMed=2602160;

M. Dates PubMed=2602160;

M. Modleotide and deduced amino acid sequence of sheep serum albumin.";

M. Nucleot Acids Res. 17:10495-10495(1989).

M. Dates PubMed Res. 17:10495-10495(1989).

M. Hordrow Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

M. SUBCELDULAR LOCATION: Secreted.

M. SUBMEDITITY: Belongs to the ALB/APP/VDB family.

MILARITY: Belongs to the ALB/APP/VDB family.
                                                                                                                                                                                              Ovis aries (Sheep).

Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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By SIMILARITY.
BY SIMILARITY.
SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                           Serum albumin precursor. ALB.
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Gaps

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SEQUENCE FROM N.A.

STRAIN=MGS IDR; TISSUB=Liver;

NEDLINE=98116663; PubMed=9455485;

NEDLINE=98116663; PubMed=9455485;

NEDLINE=98116663; PubMed=9455485;

NA Yoshida K., Seto-Ohshima A., Sinohara H.;

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"Sequencing of cDNA encoding serum albumin and its extrahepatic

"I EUNCTION: Serum albumin, the main protein of plasma, has a good

"I EUNCTION: Serum albumin, the main protein of plasma, has a good

"I EUNCTION: Serum albumin, the main function is the regulation

of the colloidal osmotic pressure of blood.

"I SUBCELLUIAR LOCATION: Secreted.

"I ISSUE SPECIFICITY: Plasma.

"I ISSUE SPECIFICITY: Plasma.

"I SIMILARITY: Contains 3 albumin domains.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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                                                                                                                                                                                                                                                                                                                                                          75.4%; Score 43; DB 1; Length 607; 81.8%; Pred, No. 3;
                                                                                                                                                                                                                                                                                                                   68598 MW; 256F6E830A1B90C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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PIR; JC5838; JC5838.
HSSP; P02768; IE7B.
Interpro; IPRO0264; Serum_albumin.
Pfam; PR00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
PROMO; PD002486; Serum_albumin; 1.
SMART; SM0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                         Owery Match
Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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537
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607 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;

MEDLINE=93145495; PubMed=8344282;

MEDLINE=93145495; PubMed=8344282;

A DO 1X., Holowachurk E.W., Norton B.J., Twigg P.D., Carter D.C.;

A DO 1X., Holowachurk E.W., Norton B.J., Twigg P.D., Carter D.C.;

A DO 1X., and primary structure of horse serum albumin (Equus caballus)

at 0.27-nm resolution..;

at 0.27-nm resolution..;

but of 15:205-212(1993).

- I-FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

- I-SUNCELULAR LOCATION: Sercted.

- I-TISSUE SPECIFICITY: Plasma.

- I-TISSUES SPECIFICITY: Plasma.
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R PIR; S34053; ABHOS.

DR HSSP, P02768; IE7B.

DR InterPro; IR800264; Serum albumin.

DR PRINTS; PRO002465; SERUMALBUMIN.

DR RART; SM00103; ALBUMIN; 3.

DR PROSTIE; PS00212, ALBUMIN; 3.

DR PROSTIE; PS00212, ALBUMIN; 3.

DR PROSTIE; PS00212, LB BY SIMILARITY.

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19 2.7 SERUM ALBUMIN.
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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                                                                                                           77.2%; Score 44; DB 1; Length 607; llarity 66.7%; Pred, No. 2; Conservative 4; Mismatches 0; Indels
BY SIMILARITY.

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84979A87F8B86596 CRC64;
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ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                            PAGE HORSE STANDARD; PRT; 607 AA. 185747; 601 July 195747; 601 July 195747; 601 July 19574 (Rel. 29, Last sequence update) 10-0CT-2003 (Rel. 29, Last sequence update) 29cum albumin precursor (Allergen Equ c 3). Abrus caballus (Horse).
  510 BY
582 BY
590 BY
69188 MW;
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289 DHQDALSSKLKE 300
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Micholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
Micholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
Micholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
Manalysis of nucleotide sequence of the rightmost 43 kbp of
nerpesvirus sammiri (HVS) L-DNA: general conservation of genetic
representation between HVS and Epstein-Barr virus.";
Virology 188:296-310(1992).
I Virology 188:296-310(1992).
I VIROLOGY 188:296-310(1992).
I STAILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
C. ISTAILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
C. EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCWV UL48.
C. EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCWV UL48.
C. This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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MEDLINE=92333689; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B., Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 609;
Pred. No. 11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9CASF97F67EF1A48 CRC64;
Metal-binding, Lipid-binding, Repeat, Signal, Copper. SIGNAL 1 18 BY SIMILARITY. 19 24 BY SIMILARITY. CHAIN 25 609 SERUM ALBUMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
TEGU HSUSA STANDARD; PRT; 2469 AA.
AC 001056;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DF 01-APR-1993 (Rel. 25, Last sequence update)
DF 01-APR-1993 (Rel. 25, Last annotation update)
GN 64 OR EERP2.
                                                                                ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 2.
COPER.
EN SIMILARITY.
BY SIMILARITY.
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Best Local Similarity 81.8
Matches 9; Conservative
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3386
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539
583
609 AA;
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ALBUMIN 2.
ALBUMIN 3.
COPPER.
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                    290 EHQETISSHLKE 301
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Best Local Similarity 66.7
Matches 8, Conservative
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METAL
DISULATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALB.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus;
NOB_TaxID=9986;
BY SIMILARITY.
N-LINKED (GLONAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                  Score 39; DB 1; Length 608;
Pred. No. 16;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U18344; AABS8347.1; -.
HSSP, P02764; IETB.
InterPro; IPR000264; Serum_albumin.
Pfam; PP00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; P0002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROPEP 19 24 BY SIMILARITY.
CHAIN 25 608 SERUM ALBUMIN.
DOMAIN 25 608
ALBUMIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor.
                                                                                                                                                                                                              69335 MW;
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9%;
Matches 8, Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
      292 QDSISSKIK 300
                                                                                                                                                                                                                                                                                                3 QDSISSKLK 11
      DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseable.ch).
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TISSUE=Diaphragm;
TISSUE=Diaphragm;
TISSUE=Diaphragm;
TISSUE=Diaphragm;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possible role in the transport of yet unknown ligand.
-!- SUBCELIULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 608
BY SIMILARITY.
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HSSP, P02768; 1E7B.
MGD, MG1:4229409; Aku.
InterPro; 1PR00264; Serum albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERVIMLEBUMIN.
ProDom; P0002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSTIE; P800212; ALBUMIN; 3.
Transport; Repeat; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFAM MOUSE STANDARD; PRT; 611 AA.
AC 089020;
DT 15-UUL-1999 (Rel. 38, Created)
DT 15-UL-1999 (Rel. 38, Last sequence update)
DT 0-OCT-2003 (Rel. 42, Last annotation update)
DE Afamin precursor (Alpha-albumin) (Alpha-Alb).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1; Pred. No. 16; 3; Mismatches
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Score 39; DB 1; Length 611;
Pred. No. 16;
1; Mismatches 0; Indels
AFAMIN.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
BY SIMILARITY.
BY SIMILAR
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Best Local Similarity 88.9%;
Matches 8; Conservative
               CHAIN
DOMAIN
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DOMAIN
DOMAIN
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SCARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
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Search completed: April 19, 2004, 11:52:51 Job time : 1.87535 secs

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Gaps

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Ywyje uncultured

Ywys uncultured

Ywyke uncultured
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to alpha-fetoprotein.
Func saptens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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SECURENCE FROM N.A.

TISSUE-Liver;
Straubberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC041789; AAH41789.1; -..

Or) GO.0005615; C:extracellular space; IEA.

Or) GO.000516; F:carrier activity; IEA.

CO; GO.000510; P:transport; IEA.

R. TherPro; IPR00024; Serum albumin.

R. PYODOM; PR00273; Lransport; prot; 2.

R. RENTS; RR0062; SERUMALEUMIN.

R. PYODOM; PR00121; ALBUMIN; 2.

R. SWART; SM00103; ALBUMIN; 2.

R. PROSITE; PR00121; ALBUMIN; 2.

SEQUENCE 417 AA; 47360 MW; I6E764833EFF4EBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 417 AA
             07WVJ8

07WVJ6

07WVJ3

07WVJ3

07WVJ1

07WVJ1

07WVJ2

07WVJ3

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Q86YG0
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Q86YG0
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   homo sapien
homo sapien
macaca fasc
uncultured
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Q7ysg3 felis silve
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                                                                                                            April 19, 2004, 11:37:09 ; Search time 4.63158 Seconds (without alignments) 817.479 Million cell updates/sec
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Q8hbz6 h
Q8hbz2 n
Q8bbz2 n
Q7wvj9 v
Q7wvj9 v
Q7wvh6 v
Q7wvh4 v
Q7wvh3 v
Q7wvk7 v
Q7wk6 v
Q7wk6 v
Q7wk6 v
Q7wk6 v
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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57
1 ENQDSISSKLKE 12
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                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: sp_archea;*
2: sp_archea;*
3: sp_hungi:*
4: sp_hunan:*
5: sp_invantebrate:*
6: sp_nammal:*
7: sp_nto:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_ordanelle:*
12: sp_vordanelle:*
13: sp_vordanelle:*
14: sp_unclassified:*
15: sp_vortus:*
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07XSG3
07XSG3
06ABBC
096ABB
06HXX2
07WVJ9
07WVJ9
07WVH6
07WVH4
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07WVH6
07WVH6
07WWH6
07WWH6
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
                                                                                                                                                                                                                                       Scoring table:
                                                                                  OM protein
                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                  Run on:
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Gaps

(Mannose-6-

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MPI.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euceleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain cerebellum cortex;
Kusuda J., Osada N., Hida M., Sugano S., Hashimoto K.;
"Isolation and characterization of cDNA for macaque neurological
disease genes.";
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.9%; Score 45; DB 4; Length 362; 66.7%; Pred. No. 7.1; 1; ove 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AA; 39834 MW; 58CA9B39BF20C459 CRC64;
                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to mannose phosphate isomerase (EC 5.3.1.8)
(Phosphote isomerase) (Phosphomannose isomerase) (PMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 ENQDSLGSKVKD 88
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1 ENODSISSKLKE 12
                        |||||: ||:|:
57 ENQDSLGSKVKD 68
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Astrocytoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isomerase; Zinc
SEQUENCE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8HXX2;
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-:- STRILARITY: BELONGS TO THE NANNOSE-6-PHOSPHATE ISOMERASE FAMILY 1.
BMBL; AF504648; AMA2819-1; -- GO, GO:0016853; F:isomerase activity; IEA.
GO; GO:0004476; F:mannose-6-phosphate isomerase activity; IEA.
GO; GO:0008270; F:anno ion binding; IEA.
GO; GO:0008575; P:carbohydrate metabolism; IEA.
InterPro; IPR001250; Man6p_isomerase1.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                 Felis silvestris catus (Cat).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
NCBI_TaxID=9685,
                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
Refaininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P.,
Rumpold H., Valenta R., Spitzauer S.,
"Escherichia coli expression and purification of recombinant cat
albumin:19E recognition, induction of basophil activation and
lymphoproliferative responses in atopic patients.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ487677; CAD32275.1;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-MANNOSE 6-PHOSPHATE = D-FRUCTOSE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%; Score 45; DB 4; Length 267; 66.7%; Pred. No. 5.3; vative. 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 194.7%; Score 54; DB 6; Length 584; Local Similarity 91.7%; Pred. No. 0.27; or Indels les 11; Conservative 1; Mismatches 0; Indels
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                                                                                Last sequence update)
Last annotation update)
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          584 AA
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Prodom; PD004391; Manép isomerasel; 1.
PROSITE; PS00965; PMI_I_1; 1.
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
Albumin (Fragment).
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Matches 8; Conservative
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MEDLINE-22753450; Pubmed=12871235;
Steglino C., Post A.F., Hess W.R.;
"Analysis of natural populations of Prochlorococcus spp. in the northern Red Sea using phycoerythrin gene sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-22753450; PubMed=12871235; Stepline-22753450; PubMed=12871235; Stepline C. Nost A.F., Hess W.R.; Stepline C. Nost A.F., Hess W.R.; Analysis of natural populations of Prochlorococcus spp. in the northern Red Sea using phycocrythrin gene sequences."; Environ. Microbiol. 5:681-690 (2003). EMBL; AF438714; AAP97641.1; -... NON_TER 1 74 74 74 74 74 NON_TER 1 74 AA; 8252 NW; C8997CF7E18D139E CRC64;
                MEDLINE=27753450; PubMed=12871235; Steglich C., Post A.F., Hess W.R.; Steglich C., Post A.F., Hess W.R.; Manalysis of natural populations of Prochlorococcus spp. in the northern Red Sea using phycoerythrin gene sequences."; Environ. Microbiol. 5:681-690(2003).
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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Pred. No. 8;
3; Mismatches 0; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                        LE EMBL, AB063318 BAC20597.1;
R GO, GO:0016853; F:18comerase activity; IEA.
GO, GO:0004476; F:mannose-6-phosphate isomerase activity; IEA.
GO, GO:0008270; F:rainc ion binding; IEA.
R GO; GO:0008275; P:carbohydrate metabolism; IEA.
R InterPro; IPR001250; Man6p_isomerase1.
R PRINTS; PR00714; MAN6PISYRASE.
R PRODGN; PD004391; Man6p_isomerase1.
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MEDLINE=2273956; PubMed=12871235;
Steglich C., Post A.F., Hess W.R.;
"Analysis of natural populations of Prochlorococcus spp. in the northern Red Sea using physoerythrin gene sequences.";
ENBL; AF436694; AAP97621.1; -..
NON TER 74
SROÜENCE 74 AA; 8305 MW; CFD43CFDEB8B5B94 CRC64;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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        Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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Matches 8, Conservative
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NCBL_TaxID=159733;
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Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae,
Prochlorococcus.
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Pred, No. 8;
3; Mismatches 0; Indels
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Pred. No. 8;
                                    Length 74;
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Last annotation update)
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70.0%; Pred. No. 8;
iive 3; Mismatches
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ilarity 70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                    Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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Q7WRK7
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MEDLINE=22753450; PubMed=12871235;

Steglich C., Post A.F., Hees W.R.;

"Analysis of natural populations of Prochlorococcus spp. in the northern Red Sea using phycoerychirin gene sequences.";

Environ. Microbiol. 5.681-690(2003).

EMBL; AF438738; AAP97665.1;

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SEQÜENCE 74 AA, 8332 MW; 24A77CFDEB9B02F9 CRC64;
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Pred. No. 8;
3; Mismatches 0; Indels
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74 AA; 8362 MW; 27A46DE040E0B2F9 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Environ. Microbiol. 5:681-690 (2003)

EMBL, AF438734; AAP97661.1; -.

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SEQÜENCE 74 AA; 8327 MW; D7B9B5(
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70.08;
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Matches 7; Conservative
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Search completed: April 19, 2004, 12:00:07 Job time : 4.63158 secs
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MEDLINE=22753450; PubMed=12871235;
Steglinch C., Post A.F., Hess W.R.;
Steglinch C., Post A.F., Hess W.R.;
"Analysis of natural populations of Prochlorococcus spp. in the northern Red Sea using phycoerythrin gene sequences.";
Environ Microbiol. 5:681-690 (2003).
EMBL; AF438689; AAP97616.1; -.

EMBL; AF438736; AAP97663.1; -.
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BMBL; AF43863; AAP97649.1; -...

BMBL; AF438722; AAP97655.1; -...

BMBL; AF438722; AAP97655.1; -...

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acteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
NCBI_TaxID=159733;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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01-0CT-2003 (TEMBLrel. 25, Last seq
01-0CT-2003 (TEMBLrel. 25, Last ann
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Matches 7; Conservative
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Matches 7; Conservative
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                                                               3 ENQDSVNSKI 12
                                     ENODSISSKT 10
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CPEB.
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Q7WRK5
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1127, App 1129, App 1123, App 1123, App 1123, App 1124, App 116, App 116, App 116, App 116, App 116, App 117, App 118, A

US-10-153-064-129 US-10-153-064-125 US-10-153-064-123 US-10-153-064-92 US-10-153-064-101 US-08-256-938-4 US-08-256-938-4 US-08-994-186-16 US-08-994-186-16 US-08-994-186-16 US-08-994-186-18 US-08-994-186-18 US-08-994-0033-81 US-08-83-274B-81 US-08-453-274B-81 US-08-453-274B-81 US-08-453-274B-81 US-08-453-274B-81 US-08-453-274B-81

Sequence Sequence Sequence

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APPLICANT: Ballance, David J
APPLICANT: Ballance, David J
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 2
NUMBER OF SEQUENCES: 23
ADDESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 01974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 07/847975
FILING DATE: 06-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 29-OCT-1991
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INPORMATION:
NAME: SWODE, R HAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEFHONE: (908) 665 2400
TELEFAX: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08153799
Patent No. 5766883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 219484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
             RESULT 1
US-08-153-799-14
April 19, 2004, 11:40:29 ; Search time 1.07295 Seconds (without alignments) 336.813 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
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1. /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /ogn2_6/ptodata/2/iaa/5B_COMB.pep:*

3. /ogn2_6/ptodata/2/iaa/6A_COMB.pep:*

4. /ogn2_6/ptodata/2/iaa/6B_COMB.pep:*

5. /ogn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6. /ogn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6. /ogn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-944-196A-3
US-08-944-176-1
US-08-702-572-2
US-08-769-746-2
US-08-769-746-5
US-08-222-619-3
US-08-433-037-4
US-08-89-956A-2
US-09-976-594-977
US-09-976-594-977
PCT-US95-04075-3
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US-09-984-186-2
US-10-153-064-183
US-10-153-064-99
US-10-153-064-105
US-10-153-064-105
US-10-153-064-131
US-10-153-064-99
US-10-153-064-99
US-10-153-064-99
US-10-153-064-99
US-10-153-064-99
US-10-153-064-99
US-10-153-064-99
US-10-153-064-95
US-10-153-064-99
US-10-153-064-99
US-10-153-064-99
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                                                                                                                                                                                                                                                                                        389414 seqs, 51625971 residues
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                                                                                                                                                                             US-09-832-929-18_COPY_170_176
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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                                                                                                                                                                                                               Sequence:
                                                                                                               Run on:
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GENERAL INFORMATION:

APPLICANT: CARTER, DANIEL C
APPLICANT: HO, JOSEPH X
APPLICANT: HO, JOSEPH X
APPLICANT: HO, JOSEPH X
APPLICANT: HO, SYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REFLACEMENT
IITLE OF INVENTION: CONFOSTION AND BLOOD VOLUME EXPANDER
FILE REFERENCE: 08/984,176
CURRENT APPLICATION NUMBER: US/08/984,176
CURRENT APPLICATION NUMBER: US/08/984,176
SURBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NOS: 1
SOFTWARE: PATENTIN VER. 2.0
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US-08-702-572-2
US-08-702-572-2
US-08-702-572-2
Patent No. 5965386
Fatent No. 5966
Fatent No. 5965386
Fatent No. 5966
Fatent No. 5966386
Fatent No. 5
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REFERENCE/DOCKET NUMBER: CE0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610/878/4294
                                                                                                                                                                                    US-08-984-176-1
; Sequence 1, Application US/08984176
; Patent No. 5948609
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TELEFAX: 610/878/4221
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 585
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 QAADKAA 176
                                                                   170 QAADKAA 176
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US-08-702-572-2
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US-08-448-196A-3
US-08-448-196A-3
Sequence 3, Application US/08448196A
Setent No. 5780594
GENERAL INFORMATION:
TPILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
CORRESPONDENCES: 9
CORRESPONDENCES. 9
CORRESPONDENCES. 9
CORRESPONDENCES. 9
ADDRESSEE: NASA

ADDRESSEE: UASA
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100.0%; Score 32; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 32; DB 1; Length 585; 100.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Region
LOCATION: 369.419
OTHER INFORMATION: //note= "Alternative C-termini of
OTHER INFORMATION: HSA(1-n)"
FEATURE:
FEATURE:
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AUDESSES:
ALDESSES:
ALDESSES:
ALDESSES:
ALBAMA
COUNTRY: HUNTSVILLE
STATE: ALBAMA
ZIP: 3.881.2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: S30
ATTORNEY/AGRYT INFORMATION:
NAME: BROAD JR., ROBERT L.
REGISTRATION NUMBER: 18,757
REPRENONE: 205-544-023
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: ALLO ACID
                                                                                                                                                                                                                                                                                                                                                                            /note= "Amino acid sequence of natural HSA"
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Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                               MANE/KEY: Region
LOCATION: 1.585
OTHER INFORMATION: 0
US-08-153-799-14
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ANTI-SENSE: N
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Length 585;
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APPLICANT: Lyons, David
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
APPLICANT: Wurfel, Mark
APPLICANT: Wight, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES:
ADDRESSE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STREET: California
CCUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 609,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
FIYE: amino acids
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                    ; Score 32; DB 4;
; Pred. No. 33;
0; Mismatches 0;
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100.0%; Pred. No. 35;
cive 0; Mismatches 0
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PATENTIN VERSION 3:1
LENGTH. 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08433037; Patent No. 5707828
GENERAL INFORMATION: GENERAL INFORMATION: SAPPLICAMT: Sreekrishna, Kotikanyadan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08222619
Patent No. 5652352
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo Sapiens
US-10-153-064-5
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Patent No. 6274305
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: South And M.
TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 32; DB 3; Length 585; 100.0%; Pred. No. 33;
                                                                                                                                                                 Query Match
100.0%; Score 32; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,746
FILING DATE: 19-DEC-1996
CLASSIFICATION:
NAME: Carroll, Peter G
REGISTRATION NUMBER: MS1.03584
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 195-8410
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TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
COUNIRY: United States of America
ZIF: 94104
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Sequence 5. Application US/10153064
Patent No. 6663485
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 amino acids
amino acid
                              LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-572-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein
              SEQUENCE CHARACTERISTICS LENGTH: 585 amino acid
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Sequence 977, Application US/09976594

Sequence 977, Application US/09976594

Sequence 977, Application US/09976594

Sequence 977, Application US/09976594

GENERAL INFORMATION:
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REFERENCE: PA-0041 US.
CURRENT APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 1143

SEQ ID NO 977

LENGTH: 609

LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 32; DB 4; Length 609; 100.0%; Pred. No. 35;
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                                                                                                                                                                                                                               Sequence 7, Application US/10153064

Patent No. 6663485

GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REPRENCE: PESG
CURRENT APPLICATION NUMBER: US/10/153,064

CURRENT APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFFWARE: Patentin version 3.1

SEQ ID NO 7

LENGTH: 609
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 32; DB 100.0%; Pred. No. 35; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapiens
US-10-153-064-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 QAADKAA 200
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US-09-976-594-977
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PCT-US95-04075-3
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US-10-153-064-7
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APPLICANT: Barr, Kathryn A.
APPLICANT: Brieley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Tschopp, Uterg F.
APPLICANT: Tschopp, Uterg F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
TITLE OF INVENTION: BICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STREET: New York
COUNTRY: US.A.
ZIP: 11530-029
COMPUTER: IBM PC compatible
COMPUTER: BRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC compatible
COMPUTER: BR PATENTANION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 32; DB 4; Length 609; Best Local Similarity 100.0%; Pred. No. 35; Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE COF INVENTION: Fusion Polypeptides
TITLE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR PILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 2: SEQ ID NOS: 38
LENGTHREE: FastSEQ for Windows Version 4.0
SEQ ID NO 2: LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo Sapiens
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Fournier, Alain
Guitton, Jean-Dominique
Guitton, Jean-Adminique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
CORPATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-0ct-2001
CLASSIFICATION NUMBER: US/09/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1997
FILING DATE: 31-JAN-1997
FILING DATE: 31-JAN-1997
FILING DATE: 28-JAN-1993
FILING DATE: 28-JAN-1993
FILING DATE: 31-JAN-1997
FILING DATE: 31-JAN-1997
FILING DATE: 31-JAN-1997
FILING DATE: 31-JAN-1997
FILING DATE: 38-JAN-1993
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NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-88,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
RADRESSER: RADRE-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
               ATTURN DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3809
INFORMATION FOR ESQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
  APPLICATION NUMBER: PCT/FR93/00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09984186; Patent No. 6686719; Garent No. Applicantion: Applicant Reinhard
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                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-797-689-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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US-09-984-186-2
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APPLICANT: Fleer, Alain
APPLICANT: Fleer, Alain
APPLICANT: Fournier, Janain
APPLICANT: Fournier, Jean-Dominique
APPLICANT: Gutteon, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Jeh, Fatrice
TITLE OF INVENTION: OVUEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STREET: California
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE FORM:
MEDIUM TYPE FORMS: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
ATTING DAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
TT.ING DATE: A15.
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CLASCIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION UNBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08797689
Patent No. 5876969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acids
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
7; Conservative
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) MOLECULE TYPE: protein
PCT-US95-04075-3
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CLASSIFICATION:
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US-08-797-689-2
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                      Query Match 100.0%; Score 32; DB 4; Length 610; Best Local Similarity 100.0%; Pred. No. 35; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-153-064-133

Sequence 133, Application US/10153064

Patent No. 6663485

GENERAL INFORMATION:
APPLICANT: Bell t al.
ITILE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: FF556

CURRENT APPLICATION NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: Patentin version 3.1

LENGTH: 651
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-153-064-133
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Search completed: April 19, 2004, 12:05:19 Job time : 1.07295 secs

236 QAADKAA 242

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April 19, 2004, 11:37:59 ; Search time 0.731302 Seconds (without alignments) 789.208 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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1: Dirl:*
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3: Dir3:*
4: Dir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Descrip             | tical ) | albumin - dog (fra | potassium channel | serum albumin - mo | serum albumin prec | serum albumin prec | serum albumin prec | serum albumin prec | albumin | serum albumin prec |        | serum albumin prec | albumin - Mongolia | ATP-dependent DNA | hypothetical prote | phosphopantetheine | pyridoxal phosphat | conserved hypothet | hypothetical prote | probable protein k | ATP-dependent zinc | poly (3-hydroxyalka | d hypot | kinase | protein kinase C ( | _    |     | cal | hypothetical prote |
|---------------------|---------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------|--------------------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------------------|---------|--------|--------------------|------|-----|-----|--------------------|
| ID                  | . 0     | I46986             | A57477            | A05139             | A47391             | ABPGS              | ABBOS              | ABSHS              | ABHOS   | ABRTS              | S57632 | ABHUS              | JC5838             | AE3595            | G72774             | A83600             | D83750             | B75445             | T32042             | T08777             | H71952             | A38604              | B81723  | A53215 | 7                  | 0518 | 32  |     | 93                 |
| DB                  | . 4     | 7                  | 7                 | Ŋ                  | N                  | Н                  |                    | Н                  | ٦       | н                  | N      |                    | N                  | N                 | N                  | 7                  | C)                 | Ŋ                  | N                  | N                  | N                  | 7                   | N       | ч      | Н                  | N    | N   | N   | (1                 |
| Length              | 250     | 265                | 379               | 453                | 600                | 605                | 607                | 607                | 607     | 608                | 608    | 609                | 609                | 714               | 132                | 159                | 334                | 348                | 394                | 542                | 550                | 559                 | 601     | 912    | 918                | 06   | 346 | 406 | 409                |
| *<br>Query<br>Match | 100.0   | 100.0              | 100.0             | 100.0              | 00                 | 00                 | 00                 | 100.0              | 00      | 100.0              | 00     | 100.0              | 100.0              | 100.0             | 93.9               | 93.9               |                    | 93.9               |                    |                    |                    | 93.8                |         |        |                    | 90.9 |     |     |                    |
| Score               | 333     | 33                 | 33                | 33                 | 33                 | 33                 | 33                 | 33                 | 33      | 33                 | 33     | 33                 | 33                 | 33                | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                  | 31      | 31     | 31                 | 30   | 30  | 30  | 30                 |
| Result<br>No.       |         | 7                  | m                 | 4                  | ιŋ                 | 9                  | 7                  | œ                  | σι      | 10                 | 11     | 12                 | 13                 | 14                | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                  | 23      | 24     | 25                 | 26   | 27  | 28  | 29                 |

|        | hypothetical prote | monooxygenase Atu6 | conserved hypothet | poly (3-hydroxyalka | long chain fatty a | mic1 homolog - fis | fibroblast growth | hypothetical prote | hypothetical prote | DNA-directed RNA p | protein kinase lik | mRNA guanylyltrans | protein-tyrosine k | DNA-directed RNA p | DNA-directed RNA p |  |
|--------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| H84718 | F84083             | AC3237             | G75576             | C38604              | T02835             | T40900             | A49151            | AE0075             | T20891             | 807137.            | T49009             | RMXRR3             | 138185             | RNR2C2             | RNZMB2             |  |
| (7     | ~                  | 7                  | Ŋ                  | N                   | ~                  | N                  | ~                 | N                  | N                  | 7                  | ~                  | Н                  | Н                  | ~                  | Н                  |  |
| 415    | 435                | 495                | 554                | 260                 | 707                | 720                | 816               | 1117               | 1149               | 1163               | 1271               | 1289               | 1400               | 1513               | 1527               |  |
| 6.06   | 6.06               | 6.06               | 6.06               | 6.06                | 6.06               | 90.9               | 6.06              | 90.9               | 90.9               | 90.9               | 6.06               | 90.                | 6.06               | 6.06               | 6.06               |  |
| 30     | 30                 | 30.                | 30                 | 30                  | 30                 | 30                 | 30                | 30                 | 30                 | 30                 | 30                 | 30                 | 3.0                | 9                  | 30                 |  |
| 30     | 31                 | 32                 | E                  | 34                  | 3.5                | 36                 | 3.7               | 3.9                | 6                  | 40                 | 41                 | 24                 | 43                 | 44                 | 4.5                |  |

## ALIGNMENTS

| ain PAO1)<br>ec-2000 | S.D.; Warrener, P.; Hickey, M.;<br>lger, K.R.; Kas, A.; Larbig, K.; | Alitie: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor Alrice: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor Alrecession: R83009 Alfocession: R83009 Alfocesion: Preliminary Alfocuse: preliminary | A,Residues: 1-250 <sto><br/>A,Crose-references: GB:AE004466, GB:AE004091, NID:g9946120, PIDN:AAG03667.1, GSPDB:GN001<br/>A,Experimental source: strain PAO1<br/>C,Genetics:<br/>A,Gene: PAO278</sto> | Query Match<br>Best Local Similarity 100.0%; Pred. No. 13;<br>Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Oy 1 HGDLLE 6<br>  }   <br>Db 191 HGDLLE 196 | - dog (fragment) es: Canis lupus familiaris ( 04-Sep-1997 #sequence_revis sion: 146986 auter, S.; Schweiger, C.; Spe regy Clin. Immunol. 93, 614-6 : Molecular characterization ence number: 146986; MUID: 94 sion: 146986 si preliminary; translated f ule type: mRNA use: 1-265 sgpp. regiscences: GB: S72946; NID: family: serum albumin; serum /Domain: serum albumin repee | Best Local Similarity 100.0%; Pred. No. 14;<br>Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
|----------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|
|----------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|

ò D.

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A; Accession: Sulsa.

A; Accession: Sulsa.

A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mosides: 1-605 (WE).
A; Mosides: 1-605 (WE).
A; Mosides: 1-605 (WE).
A; Cross-references: EMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
B; Limeback, H.; Gakarya, H.; Chu, W.; Mackinnon, M.
J; Bone Miner. Res. 4, 235-241, 1989
A; Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mineral A; Reference number: A61006
A; Molecule type: protein
A; Residues: 22-51, XY; 53-54; XXXXXY, 146, E', 150-151, XXNY, 155 (LIM)
A; Residues: 22-51, XY; 53-54; XXXXXY, 146, E', 150-151, XXNY, 155 (LIM)
A; Residues: 22-51, XY; 53-54; XXXXY, 146, E', 150-151, XXNY, 155 (LIM)
A; Residues: 22-51, XY; 53-54; XXXXXY, 146, E', 150-151, XXNY, 155 (LIM)
A; Residues: 22-51, XY; 53-54; XXXXXY, 146, E', 150-151, XXNY, 155 (LIM)
A; Residues: 22-51, XY; 53-54; XXXXXY, 146, E', 148, E', 150-151, XXNY, 155 (LIM)
A; Residues: 22-51, XY; 53-54; XXXXXY, 146, E', 140-169; Preparation is serum albumin; serum albumin repeat homology
C; Superfamily: serum albumin repeat homology (SA1)
F; 21-16, Domain: serum albumin repeat homology (SA2)
F; 21-16, Domain: serum albumin repeat homology (SA2)
F; 21-16, Domain: serum albumin repeat homology (SA3)
F; 21-18, 21-113, 112-123, 145-190, 189-138, 221-267, 266-2300, 299-310, 337-382, 381-390, 4
F; 261/Binding site: bilirubin (Lys) #status predicted
F; 261/Binding site: bilirubin (Lys) #status predicted
                                                                                                                   Accession: A47391
A; Contents: B/B homozygote
A; Contents: B/B homozygy
A; Contents: B/B homozygy
A; Contents: Serum albumin; serum albumin repeat homology
F; 213-2186/Domain: serum albumin repeat homology <8A2>
F; 213-286/Domain: serum albumin repeat homology <8A3>
F; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerum albumin precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S01382, A61006
R;Weinstock, J; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Title: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:3174440
A;Accession: S01382
'Species: Macaca mulatta (rhesus macaque)
.Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 33; DB 1; Length 605; 100.0%; Pred. No. 35; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 HGDLLE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 HGDLLE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HGDLLE 6
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                                                                                              Accession: A47391
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C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: A05139; Is6838

Nol. 1861. Evol. 2, 347-358; Is6838

Nol. Biol. Evol. 2, 347-358; Is6838

Nol. Biol. Evol. 2, 347-358; Is6838

A;Title: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudog A;Reference number: A93055; MUID:88216123; PMID:2452956

A;Accession: A05139

A;Molecule type: mRNA

A;Reference number: A93055; MUID:88216123; PMID:2452956

A;Residues: 1448 AIN>

A;Residues: 1448 AIN>

A;Reference number: 1486, 1990

A;Title: Empty and occupied insertion site of the truncated LINE-1 repeat located in the A;Reference number: 148638; MUID:90268606; PMID:1971802

A;Reference number: 14838; MUID:90268606; PMID:1971802

A;Reference number: 148638; MUID:90268606; PMID:1971802

B;Stutus: preliminary: rerum albumin repeat homology (fragment)

F;1104/Domain: serum albumin repeat homology (fragment)

F;123-296/Domain: serum albumin repeat homology (fragment)
                                                                                                                                                                                                                                                                                A57477

pocassium channel K-AB-2 - rat

C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Sep-1999

C;Accession: A57477

K;Takumi, T.; Ishli, T.; Horio, Y.; Morishige, K.I.; Takahashi, N.; Yamaahit

J; Biol. Chem. 270, 16339-16346, 1995

A;Title: A novel ATP-dependent inward rectifier potassium channel expressed predominantl

A;Reference number: A57477; MUID:95332346; PMID:7608203

A;Accession: A57477

A;Accession: A57477

A;Accession: A57477

A;Residues: 1239 cTAK>

A;Residues: 1339 cTAK>

A;Residues: 1339 cTAK>

A;Esidues: 1339 cTAK>

A;Cross-references: GB:X86818; NID:g939969; PIDN:CAA60501.1; PID:g939970

C;Superfamily: G protein-activated pocassium channel protein

C;Keywords: ATP; transmembrane protein
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100.0%; Score 33; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 33; DB 2; Length 379; 100.0%; Pred. No. 21;
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Best Local Similarity 100..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 HGDLLE 98
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A.Roclecule type: MRNA
A.Rosldude: 1-607 <eB0>
A.Gross-references: EMBL:X17055, NID:g1386, PIDN:CAA34903.1; PID:g1387
A.Cross-references: EMBL:X17055, NID:g1386, PIDN:CAA34903.1; PID:g1387
A.Cross-references: EMBL:X17055, NID:g1386, PIDN:CAA34903.1; PID:g1387
A.Cross-references: EMBL:X17055, NID:g1386, PIDN:CAA34903.1; PID:g1387
C.Superfamily: Serum albumin, serum albumin repeat homology
C.Superfamily: Serum albumin metal binding; plasma
F.19-24/Domain: signal sequence #status predicted <eNG>
F.19-24/Domain: serum albumin #status predicted <MAT>
F.29-201/Domain: serum albumin repeat homology <SA2>
F.42-591/Domain: serum albumin repeat homology <SA2>
F.412-591/Domain: serum albumin repeat homology <SA3>
F.412-591/Domain: serum albumin repeat
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S06936
R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:9009888; PMID:2602160
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Pred. No. 35;
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100.0%; Pred. No.
R,Brown, J.R. submitted to the Atlas, April 1975 A,Reference number: A94551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                     A;Molecule type: protein
A;Residues: 190-195 <BR2>
R;Brown, J.R.
Ped. Proc. 33, 1389, 1974
A;Reference number: A91457
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Best Local Similarity
Matches 6; Conserv
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Matches
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AyAccession: A38888

AyAccession: A38888

AyAccession: A58888

AyCoss-references: EMEL:M73215

ByCothem. Biochhem. Biophyse. Res. Commun. 173, 639-646, 1990

AyItle: Rapid confirmation and revision of the primary structure of bovine serum albumin. AyReference number: A36401; MUID:91083649; PMID:2260975

AyAccession: A36401; MUID:91083649; PMID:2260975

AyAccession: AyAccession: A36401; MUID:91083649; PMID:326.393, TS',396-607 cHIR>

ByAccession: AyAccession: A91258; MUID:80024278; PMID:488109

AyAccession: A91258

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AyActering onto glass-fiber filter from an analytical iscelectrofocusing glass-fiber filter from an analytical scelectrofocusing glass-fiber filter from form and filter from an analytical filter from an analy
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A; Residues: 25-41, 'H', 43-57, 59-64 <STR>
B; Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
T. Immunol. 143, 1680-1684, 1989
A; Title: Structures of histamine-releasing peptides formed by the action of acid proteas A; Reference number: A45800; MUID: 89341406; PMID: 2474609
A; Reference number: A5800; MUID: 89341406; PMID: 2474609
A; Molecule type: protein
A; Residues: 163-172 <CAR>
B; Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A; Title: Structure of a biologically active neurotensin-related peptide obtained from pe A; Reference number: A26693; MUID: 87194805; PMID: 2437111
A; Rocession: A26693; MUID: 87194805; PMID: 2437111
A; Rocession: A26693; MUID: 870-403 of bovine serum albumin.
A; Reference number: A90309; MUID: 82023364; PMID: 7283978
A; Accession: A90309
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A;Title: Structure of bovine serum albumin.

A;Reference number: A91458

A;Accession: A94458

A;Molecule type: protein

A;Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,'B
                                                                                                                                                                         serum albumin precursor [validated] - bovine
NiAlternate names: 67K protein; preproalbumin
C;Species to so primigenius taurus (cattle)
C;Decies 24-Apr-1984 #sequence revision 30-Sep-1993 #text change 18-Aug-2000
C;Accession: A38885; A36401; A91258; B60808; S10780; D45800; A26693; A90309; A9458; A94
S;Holowachuk, E. M.; Sroltenborg, J.K.; Reed, R.G.; Peters Jr., T.
A;Description: Bovine serum albumin: oDNA sequence and expression.
A;Reference number: A38885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 402-433 <REE>
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 223-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 572-288; 57
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C, Comment: This protein is the major protein component in plasma. It functions as a mult
ein has 35 conserved cysteine residues.
C, Superfamily: serum albumin; serum albumin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Status: preliminary
A)Anolecule type: protein
A)Anolecule type: protein
A)Residues: 166-173 < CAR>
R)Heard, J.
R)Heard, J.
A)L Cell. Biol. 7, 2425-2434, 1987
A)Title: Determinants of rat albumin promoter tissue specificity analyzed by an improvec A)Reference number: 157621; MUID:87286876; PMID:3475566
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F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,4
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Cypecias: Fells silvestris catus (domestic cat)
Cypace: 19-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
Cylaccesion: 076660, 557632
R/Hilger, C.; Grigioni, F.; Hentges, F.
Gene 169, 295-296, 1996
A/Title: Sequence off the gene encoding cat (Felis domesticus) serum albumin.
A/Reference number: 074660, MUID:96194824; PMID:8647469
A/Accession: 076460
A/Accession: 1608 cHIZA
A/Residues: 1-608 cHIZA
A/COSS-references: EMBL:X84842; NID:9886484; PIDN:CAA59279.1; PID:9886485
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A, Residues: 1-5 <RBS>
A, Cross-references: GB:MI6825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C, Cross-references: GB:MI6825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C, Reywords: carrier protein; duplication; metal binding; plasma
C, Reywords: carrier protein; duplication; metal binding; plasma
F; 1-18 / Domain: signal sequence #status experimental <AGO-
F; 24 / Domain: propeptide #status experimental <ART>
F; 25 -608/Product: serum albumin #status experimental <AMT>
F; 29 -202/Domain: serum albumin repeat homology <ARI>
F; 21 -394/Domain: serum albumin repeat homology <ARI>
F; 41 -592/Domain: serum albumin repeat homology <ARI>
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;1-18/Domain: signal sequence #status predicted <SIG>
;19-24/Domain: propeptide #status predicted <PRP>
;25-608/Product: serum albumin #status predicted <WAT>
;29-202/Domain: serum albumin repeat homology <SAL>
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0;
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N.Alternate names: prepreablemin
(N.Alternate names: prepreablemin
(S.Species: Ratues norregious (Norway rat)
(S.Species: Ratues norregious (Norway rat)
(S.Species: Janay-1979 #sequence_revision 31-May-1979 #text_change 22-Jun-1999
(S.Spacession: A03872, A32211, A91946; A91940; C45800; I57621; A03233
(S.Ascossion: A03872, A32211, A91946; A91940; C45800; I57621; A03233

R.Sargent, T.D.; Yang, M.; Bonner, U.
A.Rocession: A39872, MUD:81223722; PMID:701712
A.Rocession: A39872; MUD:81223722; PMID:701712
A.Rocession: A39872; MUD:81223722; PMID:701712
A.Rocession: A39872; MUD:71249557; PMID:893447
A.Rocession: A3921; MUD:77249557; PMID:893447
A.Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analys
A.Rocession: A9221; MUD:77249557; PMID:893447
A.Rocession: A9221
A.Rocession: A9346
A.Rocession: A93146; MUD:78109429; PMID:564345
A.Rocession: A93146
A.Rocession: A93146
A.Rocession: A93146
A.Rocession: A93146
A.Rocession: A93146
A.Rocession: A93146
A.Rocession: A9346
A.Roc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: 834053
R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
R:Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
A;Reference number: 834053; MUID:93345495; PMID:8344282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local Similarity 100.
Matches 6; Conservative
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A/MCJecule type: protein
A/Roceule type: protein
A/Residues: 25-48 cRGs>
A/Residues: 25-48 cRGs>
A/Residues: 25-48 cRGs>
A/Residues: 25-48 cRGs>
Brinch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 595-599, 1993
A/Title: Mass spectrometric identification of modifications to human serum albumin treal
A/Reference number: 836882; MUID:99384321; PMID:8373198
A/Reference number: 836882
A/Residues: 45-67/141-1160/311-337;469-490/570-581 cFIN>
B/Residues: 45-67/141-1160/311-337;469-490/570-581 cFIN>
A/Reference number: 872, 849-855, 1991
A/Reference number: 87599; MUID:92126241; PMID:11772598
A/Accession: 817599; MUID:92126241; PMID:11772598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 166-173 <CAR>
R;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; W:
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A;Title: The anino acid sequence of kinetensin, a novel peptide isolated from pepsin-trans. A;Reference number: A03239; MUID:86242180; PMID:3087352
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                                                                                                                                         Riweloun, B.; Moravek, L.; Kostka, V.

BESE Lett. 158, 134-137, 1975
A;Title: Complete amino acid sequence of human serum albumin.
A;Reference number: A91420; MUID:76187907; PMID:1225573
A;Accession: A91420
A;Accession: A91420
A;Accession: A91420
A;Molecule type: protein
A;Residues: 25-117, EQ', 120-154, Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-38, A;Robiru, U, Spiteller, G', Triplère, D', Spiteller, G', Triplère, D', Spiteller, G', Triplère, D', Spiteller, G', Triplère, B', 1988
A;Title: Isolation and structure elucidation of middle-molecular weight peptides from un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides formed by the action of acid protes:
PMID:2474609
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A,Residues: 255-263,'E',265-281 <MINI>
A,Note: this variant is designated albumin Herborn
R;Minchiotti, L; Galliano, M; Stoppini, M; Ferri, G; Crespeau, H; Rochu,
Biochim. Biophys. Acta 1119, 232-238, 1992
A,Title: Two alloalbumins with identical electrophoretic mobility are produced
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A,Molecule type: protein
A,Residues: 166-173,'L'. <MOG>
A,Residues: 166-173,'L'. <MOG>
A,Residues: 166-173,'L'. <MOG>
A,Residues: 166-173,'L'. <MOG>
B,C. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A,Title: Mutations in genetic variants of human serum albumin found in Italy. A,Reference number: A38255; MUD:91062352; PMID:2247440
A,Accession: C38255
A,Molecule type: protein
A,Residues: 76-111 cGAL1>
A,Residues: 76-111 cGAL1>
A,Recession: B38255
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,Residues: 25-54,354,357,431-447 <KAU>
,Residues: 25-54,354,357,431-447 <KAU>
,Note: 49-Leu was also found
,Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
- Immunod. 144, 1680-1684, 1989
,filtle: Structures of histamine-releasing peptides formed
,Reference number: A45800; MUID:89341406; PMID:2474609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Isolation and structure elucidation of middle-mo'
A,Reference number: 806422
A,Note: this paper is in German, with an English abstract
A,Accession: 806422
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A;Residues: 82-105, K',107-110 <GAL2>
A;Note: this variant is designated albumin Vibo Valentia
A;Accession: A38255
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A; Residues: 76-83, K', 85-106 < GAL3>
A; Residues: 76-83, K', 85-106 < GAL3>
A; Note: this variant is designated albumin Torino
R; Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Blochem. 214, 437-444, 1993
A; Title: The structural characterization and bilirubin-b
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Ajrosteculer (February 1999 mRWA)

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ABHUS

Berum albumin precursor [validated] - human

NyAlternate names: preproalbumin

NyAlternate names: preproalbumin

NyContains: kinetensin

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: 199-011-1981

Asgemence revision 31-Jan-1997 #text change 17-Mar-2000

C.Saccession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422; S36

R.Jawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.B.; Houck, C.M.; Najarian, R.C.; Seebur

Nucleic Acids Res. 9, 6103-6114, 1981

A;Title: The sequence of human serum albumin cDNA and its expression in Escherichia coli

A;Reference number: A93743; MUID:82081882; PMID:6171778
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                                 Pred. No. 35; ; Mismatches
100.08; F1
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A; Molecule type: mRNA
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hypothetical protein APB0185 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: (72174 (72774 )
R;Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Takal awa, H; Takamiya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A;Reference number: A72450; MUID:99310339; PMID:10382966
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                                                                                                                                                                                                                                                         C.Species: Wariones unguiculatus (Mongolian jird)
C.Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
B.Yoshida, K.; Seto-Obshima, A.; Sinohara, H.
DNA Res. 4, 351-354, 1997
A.Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in the A; Reference number: UC5838
A.Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in the A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: DDBJ:AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278
A; Experimental source: liver
C. Superfimental source: liver
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iive 0; Mismatches 0
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C; Superfamily: DNA helicase recG
C; Keywords: hydrolase
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A, Accession: G72774
A, Status: preliminary
A, Status: preliminary
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A, Status: preliminary
A, Status: 1-13 cKAW>
A, Residues: 1-132 cKAW>
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A, Residues: 1-132 cKAW>
A, Cross-references: DDBJ: AP000058; NID: G5103388; PIDN: BAA79097.1; PID: d1042873; PID: g510
A, Experimental source: strain Kl
C, Genetics:
A, Gene: APE0185
C, Superfemily: Aeropyrum pernix hypothetical protein APE0185
C, Superfemily: Aeropyrum pernix hypothe
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Search completed: April 19, 2004, 12:02:27 Job time : 2.7313 secs

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April 19, 2004, 11:25:34 ; Search time 0.437673 Seconds (without alignments) 713.823 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 HGDLLE 6 **BLOSUM62** score: Scoring table: Sequence:

141681 segs, 52070155 residues Searched:

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length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 21            | 33     | 00    | ٠.   |    | CDAD HUMAN |             | homo sapien  |
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| 23            | 31     | m.    | •    |    | XRC2 HUMAN |             | homo sapien  |
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| 26            | 31     | w.    | •    |    | SET8 HUMAN |             | homo sapien  |
| 27            | 31     | m.    |      |    | 1 1        |             | pseudomonas  |
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| 32            | 31     | 93.9  |      | -  | -          | 2101        | mins musculu |
|               |        |       | 159  | -  | COAD_PSESM | 3ah3        | pseudomonas  |

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EMBL; U73192; AAC50923.1; -. EMBL; U73193; AAC50924.1; -.

| Q88cq7 pseudomonas<br>P26496 pseudomonas<br>P19297 niene sativ | P11079 recvirus (t<br>P56764 arabidopsis | O9thv5 sinapis alb<br>O9mtm3 oenothera h | P38550 nicotiana t<br>Q04912 homo sapien | P12093 oryza sativ<br>P16025 zea mays (m | Q88be2 pseudomonas |
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| COAD PSEPK PHAC PSEOL                                          | REOU FEA<br>MCE REOVD<br>RPOD ARATH      | RPOD_SINAL<br>RPOD_OENHO                 | RPOD_TOBAC<br>RON_HUMAN                  | RPOD ORYSA<br>RPOD MAIZE                 | KGUA_PSESM         |
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| 9.06                                                           | , o o                                    | 9.06                                     | 9.09<br>9.09                             | 90.9                                     | 87.9               |
| 000                                                            | 000                                      | 30 8                                     | 30                                       | 9 9                                      | 53                 |
| 3.5                                                            | 9 17 88                                  | 0 W 4                                    | 44                                       | 4. 4.<br>E. 4.                           | 45                 |

## ALIGNMENTS

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-!- SUBSULTY: SEEMS TO FORM HETERODIMER WITH KIRS.1/KCNJ16 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the inward rectifier-type potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Cerebellum;
Schoots O., van Tol H.H.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1996) to the EMBL FOR POTASIUM BUFFERING ACTION OF
-!-FUNCTION: MAY BE RESPONSIBLE FOR POTASIUM BUFFERING ACTION OF
-!-FUNCTION: ECELL RATHER THAN OUT OF ILL WPOTASIUM FOR FORM FOR INTO THE CELL RATHER THAN OUT OF IT. THEIR VOLITAGE DEPENDANCE IS
REGULATED BY THE CONCENTRATION OF EXTRACELLULAR POTASSIUM: AS
EXTERNAL K(+) IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING
SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS
MAINLY DUE TO THE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL
MAGNESIUM. CAN BE BLOCKED BY EXTRACELLULAR BA(2+) AND CS(+) (BY
                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of two K+ inward rectifier (Kir) 1.1 potassium channel homologs from human kidney (Kirl.2 and Kirl.3)."; J. Biol. Chem. 272:586-593(1997).
                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
IRKA HUMAN STANDARD; PRT; 379 AA.
P78508; 092808; 3.
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP-sensitive inward rectifier potassium channel 10 (Potassium channel, inwardly rectifying, subfamily J. member 10) (Inward rectifier K+ channel Kirl.2) (ATP-dependent inwardly rectifying potassium channel Kirl.1).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Kidney;
TISSUE-Kidney;
Shuck M.E., Piser T.M., Bock J.H., Slightom J.L., Lee K.S.,
Bienkowski M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family
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SUBUNIT: SEEMS TO FORM HETERODIMER WITH KIRS.1/KCNJ16 (BY
                                                  family
                                                                                                                                                                                                                                                                                                                                                                           NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRKA RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurachi
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                   MIN, 802.008; 7.

MIN, 802.0005887; C:integral to plasma membrane; TAS.

GO; GO:0005881; P:ATP-activated inward rectifier potassium ch. . .; TAS.

GO; GO:0005813; P:Potassium ion transport; TAS.

InterPro; IPR001638; K-channel_IR.

InterPro; IPR001622; K-channel_Dore.

Pram; PF001007; IRK; 1.

ProDom; PD001103; K-channel IR; 2.

Pronic channel; Ion transport; Voltage-gated channel; Transmembrane;

ATP-binding; Potassium transport.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                    INTRACELULAR MAGNESIUM (BY SIMILARITY).
ATP (POTENTIAL).
L -> P (IN REF. 2).
L -> Q (IN REF. 2).
R -> C (IN REF. 2).
R -> C (IN REF. 2).
W, D9DA013FF4003533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glia 33:57-71 (2001).

Glia 33:57-71 (2001).

-1. FUNCTION: MAY BE RESPONSIBLE FOR POTASSIUM BUFFERING ACTION OF GLIAL CELLS IN THE BRAIN. INWARD RECTIFIER K(+) CHANNELS ARE CHARACTERIZED BY A GREATER TENDANCY TO ALLOW POTASSIUM TO FLOW INTO THE CELL RATHER THAN ONT OF IT. THEIR VOLTAGE DEPENDANCE IS REGULATED BY THE CONCENTRATION OF EXTRACELLULAR POTASSIUM; AS EXTERNAL K(+) IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS MAINLY DUE TO THE BLOCKAGE OF COUTWARD CURRENT BY INTERNAL MAGNESIUM. CAN BE BLOCKED BY EXTRACELULAR BA (2+) AND CS(+) (BY SIMILARITY).
                                                                                                                                                                  MI (POTENTIAL).

H5 (PORE-PORMING) (POTENTIAL).

M2 (POTENTIAL).

M3 (POTENTIAL).

R01E IN THE CONTROL OF POLYAMINE-MEDIATED CHANNEL GATING AND IN THE BLOCKING BY
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
4TP-sensitive inward rectifier potassium channel 10 (Potassium channel, inwardly rectifiying, subfamily J, member 10) (Inward rectifier K+ channel Kir4.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Interpreted M., Fujita A., Kurachi Y.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
STRAIN-CD-1, and ICR, TISSUE-Brain;
MEDLINE-21100968; PubMed=11169792;
Li L., Head V., Timpe L.C.;
"Identification of an inward rectifier potassium channel gene expressed in mouse cortical astrocytes.";
                                                                                                                                                                                                                                                                                                                   100.0%; Score 33; DB 1; Length 379; 100.0%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 A.A.
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                 42508 MW;
                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.0%;
Matches 6; Conservative 0
      EMBL; US2155; AAB07046.1;
Genew; HGNC:6256; KCNJ10.
MIM; 602208; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                   217
50
166
271
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134
167
158
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50
166
166
379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRKA MOUSE
                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                   NP BIND
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB039879; BAA92432.1; -.

R EMBL; AR322631; AAG42845.1; -.

R MGD; MGI:1194564; Kchilo.

R InterPro; IPR001639; K-channel_IR.

InterPro; IPR001639; K-channel_Pore.

R Pfam; PF01007; IRK; 1.

R PFINTS; PR01320; KICCHANNEL.

R Propon; PD001103; K-channel; IR; 2.

I onic channel; Ion transport; Voltage-gated channel; Transmembrane;

M ATP-binding; Potassium transport; Voltage-gated channel; Transmembrane;

T TRANSMEM 70 92 MI (POTENTIAL).

T TRANSMEM 118 134 H5 (POTENTIAL).

T TRANSMEM 143 167 MC (POTENTIAL).

T DOMAIN 168 3167 MC (POTENTIAL).

T DOMAIN 168 159 ROLE IN THE CONTROL OF POLYAMINE-MEDIATED

T SITE 159 L59 ROLE IN THE CONTROL OF POLYAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MI (POTENTIAL).

H5 (PORE-FORMING) (POTENTIAL).

M2 (POTENTIAL).

M3 (POTENTIAL).

R0LF IN THE CONTROL OF POLYAMINE-MEDIATED CHANNEL GATING AND IN THE BLOCKING BY
SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the inward rectifier-type potassium channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTRACELLULAR MAGNESIUM (BY SIMILARITY)
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel ATP-dependent inward rectifier potassium channel expressed predominantly in glial cells."; U. Biol. Chem. 270:16339-16346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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MEDLINE=59322346; PubMed=7608203;
Takumi T., Ishii T., Horito Y., Morishige K.-I., Takahashi N.,
Yamada M., Yamashita T., Kiyama H., Sohmiya K., Nakanishi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 379;
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7FF08446B7F43453 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 AA.
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STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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379 AA;
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Best Local Similarity
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93 HGDLLE 98

1 HGDLLE 6

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potassium channels.";
Proc. Natl. Acad. Sci. U.S.A. 92:6753-6757(1995)

I. Proc. Natl. Acad. Sci. U.S.A. 92:6753-6757(1995)

C. I- FUNCTION: MAY BE RESPONSIBLE FOR POTASSIUM BUFFERING ACTION OF GLIAL CELLS IN THE BRAIN. INWARD RECTIFIER K(+) CHANNELS ARE CHARACTERIZED BY A GREATER TENDANCY TO ALLOW POTASSIUM TO FLOW INTO THE CELL RATHER THAN OUT OF IT. THEIR VOLTAGE DEPENDANCE IS REGULATED BY THE CONCENTRATION OF EXTRACELLULAR POTASSIUM; AS EXTERNAL K(+) IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS MAINLY DUE TO THE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL MAGNESIUM. CAN BE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL MAGNESIUM. CAN BE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL.

- SUBUNIT. SERMS TO FORM HETERODIMER WITH KIRS.1/KCNJ16.

- SUBUNIT. SERMS TO FORM HETERODIMER WITH KIRS.1/KCNJ16.

- TISSUE SPECIFICITY: Predominantly in glial cells of the cerebellum and forebrain. Expressed to a lesser extent in the kidney, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M1 (POTENTIAL).

HS (PORE-FORMING) (POTENTIAL).

M2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

ROLE IN THE CONTROL OF POLYAMINE-MEDIATED CHANNEL GATING AND IN THE BLOCKING BY INTRACELLULAR MAGNESIUM (BY SIMILARITY).

A -> P (IN REF. 3).

VQV -> GAGA (IN REF. 3).

LT -> YL (IN REF. 3).

V -> E (IN REF. 3).

H -> L (IN REF. 3).

H -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other peripheral tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A57477; A57477.
InterPro; IPR001623; K+channel_IR.
InterPro; IPR001622; K+channel_pore.
Pfam; PF01007; IRK; 1.
PRNTMS; PF01307; KIRCHANNEL.
PRODOM; PD001103; K+channel_IR; 2.
Ionic_channel_i Ion transport; Voltage-gated channel; Transmembrane;
                                         delman J.P.;
Cloning and expression of a family of inward rectifier potassium
                                                                                                                                                                         Bredt D.S., Wang T.L., Cohen N.A., Guggino W.B., Snyder S.H., "Cloning and expression of two brain-specific inwardly rectifying
MEDLINE=95179470; PubMed=7874445;
Bond C.T., Pessia M., Xia X.-M., Lagrutta A., Kavanaugh M.P.,
Adelman J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M -> D (IN REF. 3).

H -> L (IN REF. 3).

K -> Q (IN REF. 3).

K -> Q (IN REF. 3).

7733671907868C52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                         IISSUE=Brain;
MEDLINE~95350147; PubMed=7624316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propuls, 100 transport.
ATP-binding, Potassium transport.
                                                                                     Recept. Channels 2:183-191(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X86818; CAA60501.1; -. EMBL; X83585; CAA58568.1; -. EMBL; U27558; AAA87811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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1112
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379 AA;
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
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DOMAIN
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CONFLICT
                                                                      channels
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                         HIR, A47331, A47391.
HSSP, P02768, 1E7B.
InterPro, IPRO00264, Serum_albumin.
Pfam, PF00273, transport prot; 3.
PRINTS, PR00802; SERUMALEUMIN.
PRODOM; PD002486, Serum_albumin, 1.
SMARY, SM00103, ALBUMIN; 3.
PROSTITE, PS00212, ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
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                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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SERUM ALBUMIN.
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                                                             Serum albumin precursor (Fragment).
                                                                                Macaca mulatta (Rhesus macaque)
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         STANDARD;
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                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=9544;
       ALBU MACMU
Q285<u>2</u>2;
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DOMAIN
METAL
ALBU_MACMU
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Gaps

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0; Indels

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 6; Conservat

100.0%; Score 33; DB 1; Length 379; 100.0%; Pred. No. 9.4;

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RESULT 6
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                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                         E45C871A670E740B CRC64;
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InterPro; IPR000264; Serum albumin.
PR000273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
PR000m; P0002486; Serum albumin; 1.
PROSITE; PS00212; ALBUMIN; 3.
Metal.binding; Lipid-binding; Repeat; Signal; Copper.
SIGNAL CALL SIGNAL CALBUMIN; 3.
MON TER CALL CALBUMIN; 3.

SIGNAL CALL CALBUMIN; 3.

SIGNAL CALL CALBUMIN; 3.

SIGNAL CALBUMIN; 3.

SIGNAL CALBUMIN; 3.
                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-RDV-1988 (Rel. 09, Last sequence update)
Serum albumin precursor (Fragment).
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SERUM ALBUMIN.
ALBUMIN 1.
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202
302
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SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                  Best Local Similarity
Matches 6; Conser
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SEQUENCE OF 1-32.
MEDLINE=80024278; PubMed=488109;
MCGIllivray R.T.A., Chung D.W., Davie E.W.;
MIGOSILIVRON B. D. D. Davie E.W.;
MIGOSYNTHESIS Of bovine plasma proteins in a cell-free system. Amino-
terminal sequence of preproalbumin.";
Eur. J. Biochem. 98:477-485(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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B -> D (IN REF. 1; AAA30988).
3E556BODDIALF4FF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barry T., Power S., Gannon P.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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                          SIMILARITY)
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100.0%; Pred. No. 15;
ive 0; Mismatches 0;
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605 AA,
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TISSUBLIVE:

X MEDINE-93145495; PubMed-8314282;

X MEDINE-93145495; PubMed-8314282;

H. J.X., Holowachuk B.W., Norton E.J., Twigg P.D., Carter D.C.;

H. J.X., Holowachuk B.W., Norton E.J., Twigg P.D., Carter D.C.;

T. T.X. and primary structure of horse serum albumin (Equus caballus)

at 0.27-nm resolution...;

at 0.27-nm resolution...;

L. Strochem. 215:205-212 (1993).

-1. FUNCTION: Serum albumin, the main protein of plasma, has a good hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-1. FUNCTIONES SPECIFICITY: Secreted.

-1. TISSUBE SPECIFICITY: Plasma.

-1. TISSUBE SPECIFICITY: Plasma.

-1. SUMILARITY: Belongs to the ALB/AFF/VDB family.
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
Metal-binding, Lipid-binding, Repeat; Signal; Copper; Allergen;
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Pred. No. 16;
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3 -> ES (IN REF. 6).
39167DFE768585D4 CRC64;
                                                                                      SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
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C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

N -> D (IN REF. 6).

ST -> TS (IN REF. 6).

K -> R (IN REF. 6).

SE -> ES (IN REF. 6).
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Equ c 3).
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607 AA;
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Best Local Similarity
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                            Polymorphism.
SIGNAL
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P35747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of serum albumin: disulfide bridges.";
Fed. Proc. 33:189-189(1974).
-!- Proc. 33:1889-189(1974).
-!- PUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Canes an allergic reaction in human.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=88267456; PubMed=3389500;
Hsieh J.C., Lin F.P., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical
isoelectrofocusing gel: a preparative method for isolating proteins
for N-terminal microsequencing.";
Anal. Biochem. 170:1-8(1988).
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MEDLINE=91083649; PubMed=2260975;
Hirayama K., Akabhi S., Furuya M., Fukuhara K.-I.;
"Rapid confirmation and revision of the primary structure of bovine
serum albumin by ESIMS and Frit-FAB LC/MS.";
Biochem. Biophys. Res. Commun. 173:639-646(1990).
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 19-28.
MEDLINE=77134075; PubMed=843354;
Patterson J.E., Geller D.M.;
Bovine microsomal albumin: amino terminal sequence of bovine
                                                                                                                                                                                                        MEDLINE-82023364; PubMed-7283978;
Reed R.G., Putnam F.W., Peters T. Jr.;
"Sequence of residues 400-403 of bovine serum albumin.";
Biochem. J. 191:867-868(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem, Biophys. Res. Commun. 74:1220-1226(1977)
                                                                                                                             Brown J.R.;
Submitted (APR-1975) to the PIR data bank.
                               "Structure of bovine serum albumin."; Fed. Proc. 34:591-591(1975).
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PRINTS; PR00802; SERUMALBUMIN.
PRODOD, PD002486; Serum albumin; 1.
SMART; SM0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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InterPro; IPR000264; Serum_albumin.
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Submitted (AUG-1998) to Swiss-Prot
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                                                                                                     REVISIONS TO 190-195
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Similarity 100.0%;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                     modice entitles ...

EMBL; X74045; CAA52194.1,

R PIR; G34053; ABROS.

DR HSSP; PO2764; Serum albumin.

DR PERNO, IPRO0264; Serum albumin.

DR PERNO, PD002466; Serum albumin.

DR PRODON; PD002466; Serum albumin.

DR SMART; SM00103; ALBUMIN.

DR SMART; SM00103; ALBUMIN.

DR RACSTER; PS00212; ALBUMIN.

DR MART; SM00103; ALBUMIN.

DR SMART; SM00103; ALBUMIN.

DR SMART; SM00103; ALBUMIN.

DR SMART; SM00103; ALBUMIN.

DR SMART; SM00103; ALBUMIN.

SIGNAL

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25 607 SERUM 10.

ALBUMIN.

25 204 ALBUMIN.

COPPER (BY SIMILARITY).

COPPER (BY SIMILARITY).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 33; DB 1; Length 607; 100.0%; Pred. No. 16; ive 0; Mismatches 0; Indels
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01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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    -!- SIMILARITY: Contains 3 albumin domains.

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TISSUE=Liver;
MEDLINE=90098888; PubMed=2602160;
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Best Local Similarity 100.
Matches 6; Conservative
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ALBU SHEEP
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Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
"Nucleotide and deduced amino acid sequence of sheep serum albumin.";
Nucleotide Acids Res. 17.10499-10455(1989).

1. FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hormones, bilitubin and drugs. Its main function is the regulation
of the colloidal osmocito pressure of blood.

1. SIBCELLUIAR LOCATION: Secreted.
1. SINILARITY: Belongs to the ALB/AFP/VDB family.
1. SIMILARITY: Contains 3 albymin domains.
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R HSSP, PO2768; LBPB.
R InterPor; 1PR00264; Serum albumin.
R Pfam; PF00273; transport prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR PRODM; PE000486; SERUMALBUMIN.
DR SWART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
TWW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
TWM Metal-binding; Lipid-binding; Repeat; Signal; Copper.
TWM METAL-BINGING; Lipid-binding; Repeat; Signal; Copper.
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84979A87F8B86596 CRC64;
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COPPER (BY SIMILARITY).
BY SIMILARITY.
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; Pred. No. 16;
0; Mismatches 0;
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608 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Salivary gland;

MEDLINE-94201492; PubMed=7512102;

MEDLINE-94201492; PubMed=7512102;

Spirzauer S., Scheiner O., Kraft D., Rumpold H.;

Muchl S., Ebner C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;

Molecular characterization of dog albumin as a cross-reactive

T allergen...;

J Allergy Clin. Immunol. 93:614-627(1994).

-: FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, Corrence, binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, containes, bilitubin and drugs. Its main function is the regulation of the colloidal osmocic pressure of blood.

-: SUBCELLULAR LOCATION: Secreted.

-: SUBCELLULAR LOCATION: Secreted.

-: SUBCELLULAR Causes an allergic reaction in human.

-: Allergen:
-: SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        SEQUENCE OF 25-48.
MEDLINE=75011422; PubMed=4414013;
Dixon J.W., Sarkar B.;
"Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-24) of dog serum albumin.";
J. Blol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart;
MEDLINE=98163340; PubMed=9504812;
MDLINE=98163340; PubMed=9504812;
MUND M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
               Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                         TISSUB-Liver;
MEDINDE-20148667; PubMed=10669848;
Pandjaitan B., Swoda I., Brandejsky-Pichler F., Rumpold H., Valenta R., Spitzauer S.;
"Escherichia coli expression and purification of recombinant dog albumin, a cross-reactive animal allergen.";
J. Allergy Clin. Immunol. 105:279-285(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR000486; SERUMALBUMIN; 1.
PRODOM; PD002486; SERUMALBUMIN; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
                                                                                                          Hilger C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ133489; CAB64867.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 215-478 FROM N.A.
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EMBL; S72946; AAB30434.1; -.
HSSP; POZ768; 1E7B.
HSC-ZDPAGE; P49822; DOG.
                                                                             SEQUENCE FROM N.A.
STRAIN=Beagle, TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-38.
                                                                                                                                            SEQUENCE FROM N.A.
                                                    NCBI_TaxID=9615
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                                    Length 608;
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MKWVTFISLFFLFSSAYSRGLVRREA
                                                                                                                                                                                                                                                                                                                                                 D -> E (IN REF. 1).
3CF1C8FF7DD8FC06 CRC64;
                                                                                                                                                                                                                                                                             REF. 2).
A -> R (IN REF. 2).
I -> T (IN REF. 2).
V -> A (IN REF. 2).
S -> A (IN REF. 1).
V -> VV (IN REF. 5).
                                             SIMILARITY)
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0
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llarity 100.0%; Pred. No. 16;
Conservative 0; Mismatches 0;
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ALBU_FELCA STANDARD, PRT; 608 AA.

AC 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-CCT-2003 (Rel. 42, Last annotation update)

DE Serum albumin precursor (Allergen Fel d 2).
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SERUM ALBUMIN
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ALBUMIN 2.
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MEDLINE=21085660; PubMed=11217851;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                    R MSB, X86842; CAA59279.1; -.
R MSSP, PO2768, 1E78.
R InterPro; IPR000264; Serum albumin.
R Pfiam, PF000273; transport prot; 3.
R PRINTS; PR000213; transport prot; 3.
R PRINTS; PR00012; ALBUMIN.
R SMART; SM00103; ALBUMIN.; 1.
R PROSITE; PS00212; ALBUMIN.; 3.
R Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
I 1 B BY SIMILARITY.
I PROPEP 19 24 BY SIMILARITY.
I CHAIN 25 608 SERUM ALBUMIN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                           Length 608;
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01-APR-1988 (Rel. 07, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAZ-2004 (Rel. 43, Last annotation update)
ALB OR ALB-108 ALB-1.
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Pred. No. 16;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
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608 AA;
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Best Local Similarity
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As Reward T. Hears A. Minhera M. Yoshino M. Toh M. Ishin Y. Yashino M. Sawil J. Sainesawa A. Minhera M. Yoshino M. Adachi J. Pehutus S. As Markawa T. Hears A. Minhera M. Minhera M. Yoshino S. Yashino S. Yashino M. Mankawa T. Saito M. Minhi P. Lewis S. W. Nishini M. Minhi P. Lewis S. Washini M. Month P. Lewis S. Washini M. Monthi P. Mankawa T. Saito M. Minhi P. Lewis S. Washini M. Monthi P. Lewis S. Washini M. Monthi P. Lewis S. Washini M. Monthi M. M. Monthi
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                                                                      SEQUENCE FROM N.A.

STRAIN=New Zealand white, TISSUE=Liver;
STRAIN=New Zealand white, TISSUE=Liver;
Sheffiteld W.P., Syed S., Schuyler P.D.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin action from ain function is the regulation of the colloidal osmotic pressure of blood.

-I- SUBCELLULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Plasma.
-I- SIMILARITY: Belongs to the ALB/AFP/VDB family.
      Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordaca, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae; Oryctolagus.
   Serum albumin precursor.
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-:- SIMILARITY: Belongs to the ALB/AFP/VDB family.
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-:- SIMILARITY: Contains 3 albumin domains.
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--- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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292F7C7EED3A61B4 CRC64;
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RMBL; Ul83-1, 127B.
RASS; POC786; 1E7B.
R InterPro; IPRO0264; Serum albumin.
R Pfam; PF00273; transport prot; 3.
R PRINTS; PR00802; SERUMALBIDIAIN.
DR PROMOS; PR00804; Serum albumin; 1.
DR SMART; SM0103; ALBUMIN; 3.
DR ROSITE; PS00212; ALBUMIN; 3.
DR ROSITE; PS00212; ALBUMIN; 3.
REALL binding; Lipid-binding; Repeat; Signal; Copper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!-FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!-FUNCTION: NRP regulates fat digestion, lipid absorption, and blood flow (Potential).
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the ALB/APP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                           P02770; P11382; 21-7UL-1986 (Rel. 01, Created) 21-7UL-1986 (Rel. 01, Last sequence update) 21-5UL-1986 (Rel. 41, Last annotation update) Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
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MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.;
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-38, AND PROCESSING.
MEDLINE=77249657; PubMed=893447;
Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
"Rat liver pre-proalbumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
messenger RNA.";
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDDLINE=81223722; PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
Sargent T.D., Yang M., Bonner T.;
"Nucleotide sequence of cloned rat serum albumin messenger RNA.";
Proc. Natl. Acad. Sci. U.S.A. 78:243-246 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-222.
MEDLINE-7810429; PubMed=564345;
ISEMURA S., Ikenaka T.;
"Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage of rat serum albumin.";
J. Biochem. 83:35-48(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87194805, PubMed=2437111;

Carraway R.E., Mitra S.P., Cochrane D.E.;

Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPPER-BINDING.
MEDLINE=79001617; PubMed=80265;
AOyagi Y., Ikenaka T., Ichida F.;
"Copper(II)-binding ablility of human alpha-fetoprotein.";
Cancer Res. 38:3483-3486(1978).
                         608 AA.
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MEDLIFERSE619112; PubMed=3009475;
MIDDACTESE659112; PubMed=3009475;
MIDDACTI P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,
Beattie W.G., Dugaiczyk A.;
"Molecular structure of the human albumin gene is revealed by
nucleotide sequence within q11-22 of chromosome 4.";
J. Biol. Chem. 261:6747-6757(1986).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=82081882, PubMed=6171778;
Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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NEUROTENSIN-RELATED PEPTIDE
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P02768; 095574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0; 21-UUL-1986 (Rel. 01, Created) 61-APR-1990 (Rel. 14, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
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5BB497A282411AB7 CRC64;
EMBL, V01222; CAA24532.1; -..
PIR, A93872; ABRTS.
INTERPRO, IPRO00264; Serum_albumin.
InterPro; IPRO00264; Serum_albumin.
Prion, PRO0030; KRRUMALBUMIN.
PRINTS; PRO0080; SERUMALBUMIN.
PRODOM; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
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Q941Y7

RESULT 8 Q941Y7 SEQUENCE

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STRAIN=1021;

MEDLINE=21396509; PubMed=11481432;

MEDLINE=21396509; PubMed=11481432;

MEDLINE=21396509; PubMed=11481432;

MEDLINE=21396509; PubMed=11481432;

MEDLINE=21396509; PubMed=11481432;

MEDLINE=21396509; PubMed=11481432;

MEDLINE=21396509; PubMed=11, Komp C., Abola A.P.,

MEDLINE=21396509; PubMed=11, Komp C., Rahn M.L.,

MEDLINE=21396509; PubMed=11, Komp C., Rahn M.L.,

MEDLINE=2100009, MEDLINE M., Pederspiel D., Galibert F., Gouzy J.,

MEDLINE=2100009, Medline Medline Medgaplasmid.";

MEDLINE=2109609; MEDLINE MEDLINE MEGAPPLE MEDLINE M
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens CS8.";
                                                                                                                                                                                                                                                                                                                                          MEDLINE-2160851, PubMed=11743194; Miller N., Blanchard M., MEDLINE-2160851, PubMed=11743194; Miller N., Blanchard M., Qurollo B., Gattung S., Miller N., Balling C., Mullin L., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Eppa A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CS8.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative D-isomer specific 2-hydroxyacid.
RA0268 OR SMAOSIO.
RA0268 OR SMAOSIO.
Plasmid pSyma (megaplasmid 1).
Plasmid pSyma (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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EMBL, AE008217; AKE8759.1; -..
PIR, AG3133; AG3133.
PIR; E98154; E98154.
GO; GO:0016654; F: caxidoreductase activity, actir
GO; GO:0006564; P:-serine biosynthesis; IEA.
Interpro; IPRO06139; 2-Hacid_DH.
PEAM, PPC0389; 2-Hacid_DH.
PEAM; PPC0389; 2-Hacid_DH.C.
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MEDLINE=2160850; PubMed=11743193;
MODLINE=2160850; PubMed=11743193;
MODLINE=2160850;
MODLINE=2160850;
MODLINE=216081 J.C., Kaul R., Monks D.E., Kitajima J.P.,
MODLINE V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
                                                                                                                                                                                                                                   01-DEC-2001 (TREMBLrel. 19, Created)
01-DEC-2001 (TREMBLrel. 19, Last sequence update)
01-DEC-2001 (TREMBLrel. 24, Last annotation update)
01-JUN-2003 (TREMBLrel. 24, Last annotation update)
043.1G06.23 procein (B1139B11.1 protein).
043.1G06.23 OR B1139B11.1.
07.2a sativa (Rice), and
07.yas sativa (Rice), and
07.yas sativa (Apponica cultivar-group).
Enkaryota; Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
11 NCDI_TAXID=4530, 39947;
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AGRODACTERIUM TUMEfaciens (strain CS8 / ATCC 33970).

Agrobacterium tumefaciens (strain CS8 / ATCC 33970).

Ratceria, Proteobacteria, Alphaproteobacteria; Rhizobiales; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Nipponbare;
Sasaki T.; Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0431G06.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:B1139B11.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS I RING-TYPE ZINC FINGER.
EMBL; AP003683; BAB64711.1; -.
EMBL; AP004688; BAB90773.1; -.
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01-UJW-2002 (TrEMBLrel. 21, Created)
01-UJW-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pfam; PP00097; Zf-C3HC4; 1.
PR0SITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50089; ZF_RING_2; 1.
SROINGA; Zinc; Zinc; Zinc-finger.
SRQUENCE 280 AA; 30370 WW; 0971
                                                                                                                                                                 PRT;
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Matches 6, Conservative
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                                                                                                                                                                     PRELIMINARY;
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Query Match

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RESULT 9
Q8U6WS
ID Q8U6
DT 01-0
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Gaps

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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 23913 / NCPPB 528;

NEDIIME-2202145;

RADIIME-2202145;

RADIIME A.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RADIIME-2202145,

RADIIME A.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RADIIME A.M., Rishi L.T., Cursino-Santos J.R., El-Dorry H.,

RADIIME A.M., Rishi L.T., Caregio C.C., Gruber A.M.

RADIIME A.M., Rishi L.T., Lemos B.G.M., Lemos M.V.F.,

RADIIME A.M., Rishi L.T., Lemos R.G., do Souba M.A.,

Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RADIIME A.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RECTAR A.M., Rishi M.A., Tamira M.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

RADIIME A.M. SOUZA M. ANDERS M., Matthe P.F.,

NATH SOUZA M. SOU
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Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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acteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycinese, Streptomycinese, Streptomycinese, WCBI_TaxID=1902;
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Nagy I., Tamura T., Vanderleyden J., Baumeister W., de Mot "The 20S proteasome of Streptomyces coelicolor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE012229; AAM40593.1; -.
InterFro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR ITPOPROTETN; 1.
Hypothetial protein; Complete proteome;
SEQUENCE 111 AA; 11336 MW; D2301B0058BC5445 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SCO1650.
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STRAIN≈A3(2);
                                                                                          NCBI TaxID=340;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2) / M.45;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
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85.7%; Pred. No. 2.76+02;
M:mmatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.6%; Score 29; DB 16; Length 19
85.7%; Pred. No. 1.9e+02;
cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypotherical protein, Complete proteome.
SEQUENCE 196 AA; 20239 MW; 35E647F0EE6256C4 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OSJNBA0085110.13 protein.
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Best Local Similarity 85.7.,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coelicolor A3(2).";
Nature 417:141-147(2002).
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InterPro; IPR005545; YCII.
Pfam, PF03795; YCII; YCII, Hypothetical protein; Complete proteome.
SEQUENCE 96 AA; 10359 MW; 0A876F8F2BCB68F6 CRC64;
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STAIN=1330 / Biovar 1;

STRAIN=1330 / Biovar 1;

MEDLINE=22247741; PubMed=12271122;

MEDLINE=22247741; PubMed=12271122;

A Pauleen I.T., Seehadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Read T.D., Dodson R.J., Umayam L., Erinkac L.M., Beanan M.J.,

A Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madhup R.,

A Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

A Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

The Druce D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

I "The Brucella subs genome reveals fundamental similarities between an immal and plant pathogens and symbiones.";

II Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

R PIR; AH3273; AH3273.

R TIGR; BRL890; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STEATINGTON TACC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
DelVecchio 'G', Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI TaxID=29459;
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359 MW; 0A876F8F2BCB68F6 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                          01-MER-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical cytosolic protein BMEI0173.
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EMBL, AB009453, AAL51355.1;
- PIR, AH3273, AH3273
INCEPPRO, IPR005545; YCII.
Pfam; PF03795; YCII; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete Broteome.
96 AA, 10359 MW; 0A876F872BCB68F6 (
                                                                                                                                   96 AA
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                  450 QAADKAA 456
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56 EAADKAA 62
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Best Local Similarity
Matches 6; Conserv
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Q8FY14
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales;
Xanthomonadaceae, Xanthomonas.
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 Length 96;
                         Indela
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
11-0CT-2003 (TrEMBLrel. 25, Last annotation update)
XCC1295.
                                                                                                                                                         01-0cr-2002 (TrEMBLrel. 22, Created)
01-0cr-2002 (TrEMBLrel. 25, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein XAC1346.
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Score 29; DB 16;
Pred. No. 89;
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                         1; Mismatches
 Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                         EAADKAA 62
                                                1 QAADKAA 7
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Q8yjg2 brucella me Q8fyd8 brucella su Q8xrr8 ralstonia s Q82v52 nitrosomona

Q81iz6 plasmodium Q8f6p8 leptcopira Q8fd2 porphyromon Q7xzx2 oryza sativ Q8m102 porphyromon Q7xzx2 oryza sativ Q8m10 peudomonas Q9113 pseudomonas Q9113 pseudomonas Q913 vibrio para Q8a213 bacterpicomyce Q8a213 bacterpicomyce Q8A39 streptcomyce Q8A39 streptcomyce Q8A59 streptcomyce Q8A61 trypanosoma Q9460 oryctolagus Q7mvo rhodopirell Q28622 oryctolagus Q7miz2 bordetella Q7miz2 concus Q84611 myxococcus Q905144 toxoplasma Q26770 trypanosoma

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STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DAR Res. 9:1189-197(2002).
BMBL; AP005964; BAC59416.1; -.
GO; GO:0030693; F:capqase activity; IEA.
GO; GO:0005608; P:proteolyais and peptidolysis; IEA.
Interpro; PR001309; ICE_DO.
Pfam; PF00656; Peptidase Cut; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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100.0%; Score 32; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                         QBIIZG
QBKGFEPB
QBKGFEPB
QBXZXZ
QBNGCTUB
QBNZI3B
QBAZI3B
QBAZI3B
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QBAZI3
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Q9BJF4
Q26770
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                                                                                      667 AA;
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SEQUENCE FROM N.A.
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SEQUENCE 667 AA
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01-JUN-2003
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08fy14 brucella su

08fy16 brucella su

08pmt0 xanthomonas

087592 streptomyce

07xp13 oryza sativ

0941y7 oryza sativ

09406w5 agrobacteri

0930d0 rhizobium m

0700z1 mycobacteri

082pd6 streptomyce

08sxm8 drosophila

079937 felis silve

099327 drosophila
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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32
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Q8FYB3
Q8FYB3
Q8FWT0
Q8PWT1
Q8FB31
Q87F92
Q7XPL3
Q940W5
Q930DG
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Q8VENT
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sp_archea:*
sp_bacteria:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_plant:*
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sp_rodent:*
sp_virus:*
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Gaps

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Indels

Length 667;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Thyroid transcription factor 1 (Thyroid nuclear factor 1) (TTF-1)
(Homeobox protein Nkx-2.1) (Fragment).
TITP1 OR TFT.
Cavia porcellus (Guinea pig).
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NTB TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00389; HOX; 1.
SpoolTr; PS00027; HOMEDBOX 1; 1.
PROSITE; PS50071; HOMEDBOX 2; 1.
Transcription regulation; Activator; Homeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.4%; Score 27; DB 1; Length 112;
85.7%; Pred. No. 36;
ive 0; Mismatches 1; Indels
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SEQUENCE 112 AA; 12723 MW; AEEAEDF06905F9DB CRC64;
                         112 AA.
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                         PRT;
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InterPro; IPR001356; Homeobox. Pfam; PP00046; homeobox; 1. PRINTS; PR000246; HOWEGBOX.
ProDom; PD000010; Homeobox; 1. SWART; SM00389; HOX; 1.
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Best Local Similarity 85...
6, Conservative
                          STANDARD;
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P97273;
01-NOV-1997 (
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Search completed: April 19, 2004, 11:52:50 Job time: 1.51062 secs

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CHIB_ARAHY
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STRAIN=6715 / UAB66.

XM MEDLIN=94292401; PubMed=8021165;

XM Wanda S.-Y., Curtiss R. III;

A Wanda S.-Y., Curtiss R. II;

A Wan
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                                                                                                                                                                                                                                                                        403 403 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
1061 AA; 119467 MW; 7915DACC20578978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
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Cell wall; Peptidoglycan-anchor; Repeat;
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REMOVED BY SORTASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 1; Length 1061;
Pred. No. 1.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pYA902.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).
                                                                                                                      CYTOCHROME P450.
NADPH-P-450 REDUCTASE.
FLAVODOXIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus downei (Streptococcus sobrinus).
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                                                                                                                                                                                                                                   FAD-BINDING.
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Pfam; PF00746; Gram pos anchor; 1.
TIGRPAMS; TIGRO1167; IPXTG anchor; 1.
PROSITE; PS50847; GRAM POS ANCHORING; Hydrolase; Glycosidase; Cell wall; Pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M96978; AAA21772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          87.5%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                      474
1061
632
880
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464 QAAEKAA 470
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                                                                                 Complete proteome.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Herger T., Schell J., Schreier P.H.;
"Elicitor-specific induction of one member of the chitinase gene
family in Arachis hypogaea.";
Mol. Genet. 224.469-476(1990).
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
acetyl-D-glucosamine polymers of chitin.
-!- INDUCTION: By yeast extract and dilution. Slight induction by
glucon elicitor.
-!- INDUCTION: By Least Extract and dilution. Slight induction by
glucon elicitor.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA OR IB (BELONGS TO FAMILY
19 OF GLYCOSYL HYDROLASES).
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01-UTN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 29, Last annotation update)
10-OCT-1994 (Rel. 20, Last annotation update)
10-OCT-1994 (Rel. 20, Last annotation update)
10-OCT-1994 (Rel. 20, Last annotation update)
10-OCT-1994 (Rel. 29, Last annotation update)
10-OCT-1994 (Rel. 20, Last annotation update)
11-OCT-1994 (Rel. 29, Last annotation u
1305 1309 LEXTG SORTING SIGNAL (FOTENTIAL).
1308 1308 AMIDE-LINKED TO CELL WALL (FOTENTIAL).
1337 AA; 143298 MW; B494275A77A2E3D0 CRC64;
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HSSP; P23951; CAA40210.1; -.

InterPro; IPRO00726; Glyco_hydro_19.

Prom; PF00182; Glyco_hydro_19; 1.

Propon; P354900; Glyco_hydro_19; 1.

PROSITE; PS00773; CHITINASE_19_1; PARTIAL.

Hydrolaee; Glycosidase; Cnitin degradation; Chitin-binding; Multigene family.

NON TER 46 46
                                                                                                                                                                                                                Score 28; DB 1; Length 1337; Pred. No. 2.1e+02; 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 6; Conservative
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MEDLINE=98044033; PubMed=9384377;
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
protein synthesis. Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30s ribosomal subunits. Also involved in the hydrolysis of GTP during the formation of the 70s ribosomal complex (By similarity). SUBCELLULAR LOCATION: Cytoplasmic. SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJNE-39453479; PubNed-9308178;
Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
Duesterhoeft A., Ehrlich S.D.;
"Sequence of the Bacillus subtilis genome region in the vicinity of
the law operon reveals two new extracytoplasmic function RNA
polymerase sigma factors SigV and SigZ.";
Microbiology 143:2939-2943(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 839;
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85.7%; Pred. No. 1.3e+02;
ive 1; Mismatches 0; Indels
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
BDFF37BB8B1046ID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO0487; IP-2; 1,
TIGREAMS; TIGRO0221; small_GTP; 1.
PROSTIE; PS01176; IF2; 1.
Initiation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                     HAMAP; MF_00100; -; 1.
InterPro; IPR004161; BFTU_D2.
InterPro; IPR0001795; BF GTPbind.
InterPro; IPR000178; IFZ.
InterPro; IPR006847; IFZ.N.
InterPro; IPR006225; Small_GTP.
Pfam; PF00009; GTP_BFTU; 1.
Pfam; PF04760; IFZ_N; 1.
Pfam; PF04760; IFZ_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91846 MW;
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SEQUENCE FROM N.A.
STRAIN=168;
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                                                                                                                                                                                                                                                                                             MEDIATR=59370159; PubMed=7642507; MEDIATR=59370159; PubMed=7642507; MEDIATR=59370159; PubMed=7642507; MEDIATR=59370159; MEDIATR=59370159; MEDIATROWELLY TO BIOSYNTHESS IN ASPERGILLS NICHOSS IN DOLYKETIGE SYNTHESS IN ASPERGILL 17774792-4800(1995).

-I- FUNCTION: Involved in the synthesis of the polyketide nucleus of sterigmatocystin from hexanoyl-CoA and seven malonates.
-I- COFACTOR: Contains 2 covalently bound phosphopantetheines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA-KETOACYL SYNTHASE.
ACYL/MALONYI TRANSFERASS.
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
THIOESTERASE.
THIOESTERASE (BY SIMILARITY).
ACYL/MALONYL TRANSFERASES (BY
                                                                                                                          STRAIN=FGSC 26;

MDDLINE=FGSC 226;

Brown D.W., Yu J.-H., Kelkar H.S., Fernandes M., Nesbitt T.C.,

Keller N.P., Adams T.H., Leonard T.J.;

Frenty-fave coregulated transcripts define a sterigmatocystin gene

cluster in Aspergillus nidulans.";

Proc. Natl. Acad. Sci. U.S.A. 93:1418-1422(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1738 1738 PHOSPHOPANTETHEINE (BY SIMILARITY)

1652 1862 PHOSPHOPANTETHEINE (BY SIMILARITY)

2028 2028 THOSETERASE (BY SIMILARITY)

2181 AA; 238831 MW; SABEST12AA9AD942 CRC64;
                Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Acyltransferase; Phosphopantetheine; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Sterigmatocystin biosynthesis; first step. -!- SIMILARITY: Contains 2 acyl carrier domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008918; S.3 exo_C.
InterPro; IPR0012913; Ac_Lrans.
InterPro; IPR001294; Kercacyl_synth.
InterPro; IPR006163; Pp. bind.
InterPro; IPR006163; Pp. bind.
InterPro; IPR0061031; Phioesterase.
Pfam; Pr00698; Acyl_transf; 1.
Pfam; Pr02801; kercacyl_synt; 1.
Pfam; Pr02801; kercacyl-synt C; 1.
Pfam; Pr0550; pp.binding; 2.
Pfam; Pr0550; pp.binding; 2.
Pfam; Pr0550; Pp.binding; 2.
ProsiTis; Ps0075; Thioesterase; 1.
PROSITIS; PS00012; PHOSPHOPANIETHEINE; FALSE_NEG.
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Best Local Similarity 85...
6; Conservative
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                                                                      NCBI_TaxID=162425;
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SEQUENCE
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                                                                                                                                                                                                                                                 Robrer J., Rawlings D.B., "Sequence analysis and characterization of the mobilization region of a broad-host range plasmid, pTF-FC2, isolated from Thiobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
Munson L., Nguyen D., Wang J., Forst C., Bood L.;
The complete genome sequence of Haemophilus durreyl.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: One of the essential components for the initiation of
                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobācteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.5%; Score 28; DB 1; Length 409;
85.7%; Pred. No. 70;
sive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 AA; 46836 MW; 27C6S93202572FE2 CRC64;
                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Translation initiation factor IF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         839 AA.
                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 174:6230-6237(1992).
                                                                                                                                                                                                                                    MEDLINE=93015664; PubMed=1400173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A43256; A43256.
InterPro; IPR005094; Relaxase.
Pfam; PF03432; Relaxase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M57717; AAA27389.1; -.
                                                                                                                  hiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                  MOBA protein (Fragment).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 QAAEKAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus ducreyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OAADKAA 7
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                    Plasmid pTF-FC2
                                                                                                                                                                                    NCBI_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFB OR HD1461
                                                                                                                                                                                                                                                                                                        ferrooxidans."
THIFE
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SEQUENCE
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0; Gaps

Length 2181;

Score 29; DB 1; Length 218: Pred. No. 1.9e+02; 1; Mismatches 0; Indels

90.6%;

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  encoding cat (Felis domesticus) serum albumin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X84442; CAA55979.1; -..

R HSRS; POZ7660; S57632.

R HSRS; POZ768; LERB.

R RSS; POZ768; LERB.

R RSS; POZ768; LERB.

R RSS; POZ768; LERB.

R PFO0273; transport pro; 3.

R PRODOM; PRO00264; SERUMALBUMIN.

R PRODOM; PRO00265; SERUMALBUMIN.

R RART; SMO0103; ALBUMIN; 3.

R SMART; SMO0103; ALBUMIN; 3.

R SIGNAL

T DOWAIN 212 397 ALBUMIN 1.

DOWAIN 212 397 ALBUMIN 2.

DOWAIN 212 397 ALBUMIN 3.

PT DOWAIN 212 397 ALBUMIN 3.

DOWAIN 212 397 ALBUMIN 3.

T DISULPID 399 115 BY SIMILARITY.

PT DISULPID 114 125 BY SIMILARITY.

PT DISULPID 192 201 BY SIMILARITY.

PT DISULPID 224 270 BY SIMILARITY.

PT DISULPID 269 303 BY SIMILARITY.

PT DISULFID 302 313 BY SIMILARITY.

PT DISULFID 344 395 BY SIMILARITY.

PT DISULFID 346 462 BY SIMILARITY.

PT DISULFID 346 395 BY SIMILARITY.

PT DISULFID 360 313 BY SIMILARITY.

PT DISULFID 500 511 BY SIMILARITY.

PT DISULFID 558 591 BY SIMILARITY.

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28-FEB-2003 (Rel. 41, Last annotation update)
Putative sterigmatocystin biosynthesis polyketide synthase (PKS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07E629CAC5F60E5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%; Score 29; DB 1;
85.7%; Pred. No. 61;
cive 1; Mismatches
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01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68659 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 EAADKAA 200
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608 A
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Q12397;
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28-FEB-2003
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            SHAPAG
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                                                                                                              STRAIN=CDC 1551 / Oshkosh,
MEDLINE=2220649; PubMed=1218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Alland D., Eisen J.A., Eaft D., Hickey E.,
Kolonay J.F., Delson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                            laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta
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0
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-i- SUBUNIT: Composed of an alpha chain and a beta chain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 387;
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TIGRFAMs; TIGR1016; sucCoAbeta; 1.
PROSITE; PS01217; SUCCINYL_COA_LIG_3; 1.
Ligase; Tricarboxylic acid CyCle; Complete proteome.
SEQUENCE 387 AA; 40925 MW; C3155A7CCAF98FDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96194824; PubMed=8647469;
Hilger C., Grigioni F., Kohnen M., Hentges F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 1;
Pred. No. 40;
1; Mismatches (
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01-FEB-1996 (Rel. 33, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Pel d 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 AA
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HAWAP; MF 00558; -; 1.
InterPro; IPR003135; ATP-grasp.
InterPro; IPR05809; CoA_lig_beta.
InterPro; IPR05811; CoA_ligase.
Pfam; PP00222; ATP-grasp; 1.
Pfam; PF00549; ligase-CoA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Local Similarity 85.7%;
hes 6; Conservative 1
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                    complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P07460; 1SCU.
TIGR; MT0978; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit family.
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SEQUENCE FROM N.A.
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01-FEB-1996
10-OCT-2003
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P49064;
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Best Loc Matches

Length 608; Indels

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RESULT 5 RL7\_STRVG

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Cole ST., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole ST., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole ST., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamiln N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seborne J., Quall M.A., Rajandream M.A., Rogers J.,
Stutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitchead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                            MEDLINE-92380478; PubMed=1511874; Parkin Mendez C., Salas J.A.; Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.A.; "Cloning and sequence of a gene encoding the L7/L12 ribosomal protein equivalent of Streptomyces antibioticus."; Gene 118:127-129(1992).
                                                                                                                                                                                                                                                                                 -:- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
-:- SIMILARITY: Belongs to the bi2P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Succinyl-CoA synthetase beta chain (EC 6.2.1.5) (SCS-beta).
SUCC OR RV0351 OR MT0978 OR MTCY10D7.23C.
MyCobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
COTYDEDACTERINES:
NGBL TAXID=1773;
                                             Streptomyces antibioticus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match
Local Similarity 85.7%; Pred. No. 15;
Local Similarity 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA; 13272 MW; F5C3EE4F45D606E8 CRC64;
                                                                                Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M89911; AAA26811.1; -.
PIR; JC1273; JC1273.
HSSP; PO2392; JCTF.
HAMAP; MF 00368; -; 1.
InterPro; IPR008932; Ribos_L12/7_olig.
InterPro; IPR001056; Ribosomal_L12:
Probom; PD001326; Ribosomal_L12: 1.
Probom; PD001326; Ribosomal_L12: 1.
50S ribosomal protein L7/L12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                        NCBI_TaxID=1890,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=9257210; PubMed=8675024;
MEDILINE=9257210; Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.;
Katayama M., Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.;
"Gene organization in the ada-rpli region of Streptomyces virginiae.";
Gene 171:135-136(1996).

-1- FUNCTION: Seems to be the binding site for several of the factors
involved in protein synthesis and appears to be essential for
accurate translation (By similarity).

-1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                            Rochu D., Porta F.; "Two alloalbumins with identical electrophoretic mobility are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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    Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces virginiae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                            Length 609;
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                                                                                          100.0%; Score 32; DB 1;
100.0%; Pred. No. 13;
ive 0; Mismatches 0;
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(Rel. 24, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
505 ribosomal protein L7/L12 (SA1).
                                                                                                                                                                                                                                                                                                                                          126 AA
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InterPro; IPR008932; Ribos L12/7 olig.

R InterPro; IPR008932; Ribos L12/7 olig.

R Pfam; PP00542; Ribosomal L12.

R ProDom; PD001326; Ribosomal L12; 1.

Ribosomal profein.

Ribosomal profein.
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Similarity 85.7%; Pred. No. 1
6; Conservative 1; Mismatch
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Best Local Similarity
7; Conserva
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Matches 6; Conserv
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RL7 STRAT
ID RL7 STRAT
AC P29342;
DT 01-DEC-1992 (
DT 28-FEB-2003 (
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P48936;
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The chemistry and physiology of the human plasma proteins, pp.23-40,
Pergamon Press, New York (1979).
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Urano Y., Watanabe K., Sakai M., Tamaoki T.;
The human albumin gene. Characterization of the 5' and 3' flanking
regions and the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
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Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walker J.E.,
"Lysine residue 199 of human serum albumin is modified by
acetylsalicylic acid.";
FEBS Lett. 66:173-175(1976),
                                                                                                                                                                                                                                                                                                                                                                                                                      Menaya J., Parrilla R., Ayuso M.S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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"Complete amino acid sequence of human serum albumin.";
FRBS Lett. 58:134-137(1975).
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                                                                                                                                                                                                                                                                       SEQUENCE OF 25-609.
MEDLINE=76187907; PubMed=1225573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BILIRUBIN-BINDING SITE,
MEDLINE=78186630, PubMed=656055,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=76257808; PubMed=955075;
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Peach R.J., Brennan S.O.;
"Structural characterization of a glycoprotein variant of human serum albumin: albumin casebrook (494 Asp--Asn).";
Biochim. Biophys. Acta 1097:49-54(1991).
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MEDDLINE-91063352; PubMed=2247440;
Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
Walkins S., Putnam F.W.;
"Mutations in genetic variants of human serum albumin found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION OF VARIANT REDHILL.
MEDLINE=90115852; Pubmed=2104980;
MEDLINE=90115852; Pubmed=2104980;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
"Albumin Redhill (-1 Arg. 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23; KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.

MEDLINE=92052189; PubMed=1946412;

Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Mataison J., Arai K., Peld R.D., Kyle R.A., Watkins S., Davis E., Mateuda Y.-I., Amaki I., Putnam F.W.;

"Genetic variants of serum albumin in Americans and Japanese.";

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MEDLINE-90115905; PubMed-2404284;
Arai K., Madison J., Shimmuzu A., Putnam F.W.;
"Point substitutions in albumin genetic variants from Asia.";
Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
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Minchiotti L., Putnam F.W.;
A donor splice mutation and a single-base deletion produce two carboxyl-terminal variants of human serum albumin.";
Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
"Lysine residue 240 of human serum albumin is involved in high-affinity binding of bilirubin.";
Biochem. J. 171:453-459(1978).
                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS NAG-1, HIR-1, HIR-2 AND TOCHIGI.
MEDLINE=89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M., Neel J.V., Sakurabayashi I., Putnam F.W.;
Potnt gubstitutions in Japanese alloalbumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
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Takehashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
Satoh C., Neel J.V.,
"Amino acid substitutions in inherited albumin variants from
                                                                                                                                                                                                                                                                                                                                            Amerindian and Japanese populations.";
Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cleavage site.";
Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
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VARTANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
MEDLINE=92190239; PubMed=1347703;
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MEDLINE=91296740; PubMed≥2068071;
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                                                                                     VARIANT CANTERBURY ASN-337
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                                                                                                                                                                                                                                                                   allergen.";
J. Allergy Clin. Immunol. 93:614-627(1994).
J. Allergy Clin. Immunol. 93:614-627(1994).
J. PUNCTION: Serum albumin, the anin protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

SUBCELLUIAR LOCATION: Secreted.

-IT TRSUE SPECIFICITY: Plasma.

-IT ALLERGEN: Causes an allergic reaction in human.

-I SIMILARITY: Belongs to the ALB/AFP/VDB family.
"Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-24) of dog serum albumin."; J. Biol. Chem. 249:5872-5877(1974).
                                                                                       MEDLINE=98163340; PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R EMBL; Y17737; CAA76841.1; -.
R EMBL; Y17737; CAA76841.1; -.
R EMBL; S72946; AAB30434.1; -.
R HSSP; P02768; 1R7B.
R HSC2DPAGE; P4982.2; DOG.
R HSC2DPAGE; P4982.2; DOG.
R HSC2DPAGE; P8000264; Serum albumin.
Pfam; PF000273; transport prot; 3.
R PRODOM; PD002466; Serum albumin.
R PRODOM; PD002466; Serum albumin.
R SMART; EM00103; ALBUMIN; 3.
R PROSTIE; PS00212; ALBUMIN; 3.
R MAATI-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
R SIGNAL
PROPEP 19
                                                                                                                                                                                              TISSUE=Salivary gland;
BDDLINE=94201492;
Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,
Muchl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
"Molecular characterization of dog albumin as a cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                  Electrophoresis 18:2795-2802(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ133489; CAB64867.1; -.
                                                                                                                                                                               SEQUENCE OF 215-478 FROM N.A.
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SEQUENCE FROM N.A.
MEDINESSISSILE, PubMed=3009475,
MIGHNESSISSILE, Studence D.B., Kuang W.J., Dennison O.E., Hawkins J.W.,
Beartie W.G., Dugaiczyk A.;
"Molecular structure of the human albumin gene is revealed by
muclecular structure within q11.22 of chromosome 4.";
J. Biol. Chem. 261:6747-6757(1986).
                                                                                                                                                                                                                                       Gaps
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Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Luo L.,
K. W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.,
"Punctional prediction of the coding sequences of 121 new genes
deduced by analysis of cDNA clones from human fetal liver.",
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
BY SIMILARITY.
MXWVTFISLFFLFSSAYSRGLVRREA -> MDT (IN
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MEDLINE-82081382; PubMed-6171778;
Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;
"The sequence of human serum albumin cDNA and its expression in E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT GLY-121.
MEDIJURE-82105994; PubMed=6275391;
Dugaiczyk A., Law S.W., Dennison O.E.;
Nucleotide sequence and the encoded amino acids of human serum
                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                             Score 32; DB 1; Length 608; Pred. No. 13; 0; Indels
                               REF. 2).
A -> R (IN REF. 2).
T -> T (IN REF. 2).
V -> A (IN REF. 2).
S -> A (IN REF. 1).
C -> V (IN REF. 1).
D -> E (IN REF. 1).
W, 3CFICSFFIDD8FC06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 ALBU HUMAN STANDARD; PRT; 609 AA.
PO2768; O95574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0;
21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378. Huang M.C., Wu H.T.; "The cDNA sequences of human serum albumin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982)
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                                                 146
206
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349
V
359
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478
V
474
D
68606 MW;
                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serum albumin precursor.
                                                                                                                                                                                                                                                                                                            194 QAADKAA 200
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                                                                                                                                                            608 AA;
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TISSUE=Liver;
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CONFLICT
SEQUENCE
DISULFID
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PRINTS; PRO0802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSTTE; PRO0212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
NON TER 1 1 1 22 BY SIMILARITY.
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DOMAIN 209 394 ALBUMIN 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1011 TaxID=9823,
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               COPPER (BY SIMILARITY).
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InterPro, IPR000264; Serum albumin.
Pfam; PF00273; transport_prot; 3.
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Best Local Similarity 100.
Matches 7; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
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"Escherichia coli expression and purification of recombinant dog abunin, a cross-reactive animal allergen.";
J. Allergy Clin. Immunol. 105:279-285(2000).
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3ESSGBODDIA1F4FF CRC64;
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COPER (98 SIMILARITY).
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AC P49822, 077705, 09T8Z4,

BT 16-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DF Serum albumin precursor (Allergen Can f 3).
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MEDLINE=20148667; PubMed=10669848;
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MEDLINE=75011422; PubMed=4414013;
Dixon J.W., Sarkar B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69410 MW;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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RL7_STRAT
SUCC_MYCTU
ALBU FELCA
STCA_EMENI
MOBA_THIFE
IF2 HAEDU
CYPD_BACSU
DEXT_STRDO
CYPD_BACSU
TTFI_CAVPO
RSB_ECOLI
OMPH_SALTY
OMPH_TERPE
PTNC_CCOLI
PTRC_KLEPN
TIST_VIBCH
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Listing first 45 summaries
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| Q9ky56 streptomyce P13119 rhizobium m P77304 escherichia P54541 bacillus su Q8byk5 mus musculu Q96kr7 homo sapien P48679 mus musculu P48679 strus norv P52157 streptomyce Q9kgw3 pseudomonas P34712 caenorhabdi Q62504 mus musculu |
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| SUC1_STRCO<br>F1B2_RHIME<br>YDGR_BCCUI<br>BCCB_BACSU<br>SCPN_MOUSE<br>LAWA_RALI<br>RHO STRLI<br>NUOG_PSEFL<br>MDRI_CAEEL                                                                                                           |
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OC Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales,
OX NCBI TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STAIN=MR-1;
RA Heidelberg J.F., Paulsen I.T., Nalbon K.E., Gaidos E.J., Nelson W.C.,
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Heidelberg J.F., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madpu R., Peterson J.D., Unayam L.A., Mate D.H., Kolonay J.F.,
RA Vamachevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Wadpu R., Peterson J.D., Unayam L.A., Mate D.H., Kolonay J.F.,
RA Vamachevan J., Khouri H., Gill J., Utterback T.R., McDonay J.F.,
RA Wadpu R.V. Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
RA Heldblyum T.V. Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
RA Material aneidensis.",
REDBL; AE015709; AAN55728.1; -.
DR TIGRI SOZYON; -.
DR TIGRI SOZYON; -.
COMPLETE Z15 AA, Z3197 MW, BACPDA22355AD55E CRC64;
SEQUENCE Z15 AA, Z3197 MW, BACPDA22355AD55E CRC64;
Best Local Similarity 85.7%; Pred. No. 1.18+02;
Best Local Similarity 85.7%; Pred. No. 1.18+02;
Batches G, Conservative I; Mismatches 0; Indels 0, Gaps 0;
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Search completed: April 19, 2004, 11:59:59 Job time : 5.08772 secs

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MEDLINE=21537279; PubMed=11679669;

REDLINE=21537279; PubMed=11679669;

Rales F., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Faihi H., Garcia-del Portillo F., Carrido P.,

Rantian K.-D., Faihi H., Garcia-del Portillo F., Marker G.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitcurnam A., Mata Vicence J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,

Narquez-Ebland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.";

Science 294:849-852 (2001).

BENEL, ALSI91979, CAC99489-1, -.
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                           2; Length 75
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ListiList: LMOO1411; -.
O.; GO:0003677; F:DNA binding; IEA.
InterPro; IPRO01387; HTH 3.
SMART; SMO0530; HTH XRE; 1.
            EMBL; AJ012114; CAC13962.1; -.
GO; GO:0003677; F:DNA binding; IBA.
InterPro; IPR001387; HTH 3.
SMART; SM00530; HTH 3; 1.
SMART; SM00530; HTH XRB; 1.
SEQUENCE 75 AA; 8192 MW; 5F1899
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                                                                    Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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84.2%; Score 32; DB 5; Length 1702;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                 Score 32; DB 5; Length 1128;
Pred. No. 3.9e+02;
2; Mismatches 0; Indels
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Bacteria, Firmicutes; Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Briston N.A.
STRAIN-Briston N.;
Waterston R.;
"Direct Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U39653; AAL56623.1; -.
WormPep; T13H2.4a; CE30179.
Hypothetical protein.
SEQUENCE 1702 AA; 190617 MW; IF5CAC942100FEB5 CRC64;
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Perez-Diaz J.C.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid T13H2.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T13H2.4.
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Last annotation update)
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                      84.2%;
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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Query Match
Best Local Similarity
6, Conserv?
                                                                                                                 1 VADESAEN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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09F428;
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Q9F428
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08990C9
10 0890C9
10 01-MA
DT 01-MA
RX MEDLI
RX MA
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Caenoriabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NOBL_TaxID=6239;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Tillar. 4.
Caenorhabditis elegans.
Caenorhabditis elegans.
Rhabditidae, Metazoa, Nematoda, Chromadorea; Rhabditidae, Rhabditoidea,
NUBL TAXID-6239;
                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%; Score 32; DB 5; Length 649; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cottage A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 281532; CAB04326.3; --
Hypothetial protein.
SEQUENCE 1128 AA; 130372 WW; 6445EE26D7D4775D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
"Direct Submission.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U39653; AAL56624.1;
"NormPep; T13H2.4b; CE30180.
Hypothetical protein.
BROUENCE 649 AA; 72873 MW; 598733DFFF63A506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of C. elegans cosmid T13H2.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-2003 (TrEMBLrel. 25, Last Sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F36F2.3.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
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Best Local Similarity 100.
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SEQUENCE FROM N.A.
MEDLINE=223546683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AKO50248; BAC34145.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                          Length 576;
                                                                                                                                                                                                                                                                                                        Query Match

Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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SEQUENCE 608 AA, 68722 MW; 292F600EED3A61B4 CRC64;
                                                                                                                                                                                                                                                            NON TER 1 1 SEQUENCE 576 AA, 65002 MW, P85733E99AE37F04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin 1.
                 60,770 full-length cDNAs.";
Nature 420:652-573 (2002).
EMEL, AK050644; BAC34360.1; --
MGD; MG:187991; Alb1.
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005816; F:carrier activity; IEA.
GO; GO:0005810; P:transport; IEA.
InterPro; IRRO00264; Serum albumin.
PFMN; PRO0802; SERUMALEUMIN.
PRODRIE; PRO013; Albumin; 1.
SMART; SMO0103; Albumin; 3.
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GO; GO:000586; P:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000264; Serum albumin.
Pfam; PF00273; transport pro; 3.
PRINTS; PR00802; SERUMLEBUMIN.
SPRODO: PECOOM: PECOOM: ALBUMIN.
SMART; SM00103; ALBUMIN. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                        46 VADESAAN 53
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Q8WQC7
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RESULT 9 Q8C7H3

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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; IISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANNE Consortium.
the RINEN Genome Exploration Research Group Phase I & II Team;
the RINEN Genome Exploration Research Group Phase I annotation of "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Kalicki J.,
Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
       DB 10; Length 306;
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                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopais sequencing project;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AL137189; CAB69854.1; -.
PIK; T45966; T45966.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005975; P:catalytic activity; IEA.
GLITEPPCO; IRRO02044; CBD_4.
PEDMI, PF00686; CBM_20; I.
Prodon; P0001568; CBD_4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mayer K.F.X.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. –
SEQUENCE 385 AA; 43573 MW; B5B1AC3741836475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Last annotation update)
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Score 32; DB 1
Pred. No. 93;
2; Mismatches
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       84.2%;
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les 6; Conservative
           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
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Q8C7C7;
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Q8C7C7
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Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
Chan W.M., Chang C.H., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
Pana K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Hayashizaki Y.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
   A 110.05 (2000) 100.0899; F:DNA-directed RNA polymerase activity; IEA.

GO; GO:0001899; F:Sigma factor activity; IEA.

GO; GO:0001809; F:Sigma factor activity; IEA.

R GO; GO:000635; F:regularingform factor activity; IEA.

R GO; GO:000635; P:regularingform factor activity; IEA.

R GO; GO:000635; P:regularingform factor activity; IEA.

R GO; GO:000635; P:regularingform factor; IEA.

R InterPro; IPR00943; RNA pol_sigma.

R InterPro; IPR00963; Sigma70_r3.

R InterPro; IPR00963; Sigma70_r3.

R InterPro; IPR00943; Sigma70_r3.

R Pfam; PF04545; sigma70_r3; 1.

R Pfam; PF04545; sigma70_r3; 1.

R Pfam; PF04545; sigma70_r4; 1.

R RINTS; RR00046; SIGMA70_r4;

M NA-binding; DNA-directed RNA polymerase; Sigma factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arsgiols60/F708 240.
Arabidopsis thāliana (Mouse-ear cress).
Arabidopsis thāliana (Mouse-ear cress).
Arabidopsis thāliana; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Radbidopsis ORP clones.";

Scher (Aug-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AXOS7624; AAL15255.1;

R EMBL; AXOS7624; AAL15255.1;

R GO; GO:0003824; F:catalyric activity; IEA.

R GO; GO:0005975; P:catalyric activity; IEA.

DR InterPro; IPR002044; CBD, 4.

DR Pfam; PF00686; CBM 20; 1.

DR Probom; PD001568; CBM 20; 1.

DR Probom; PD001568; CBM 20; 1.

DR Probom; PD001568; CBM 20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Complete protecme.
SEQUENCE 253 AA: 28962 MW; 8365F50D21929538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 16;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.v.
Andrea 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Q8CG74;
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                                                                                                                                                                                                                                                                               RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
Component in murine infection with Schistosoma mansoni.";
Component in murine infection with Schistosoma mansoni.";
Submitted (SEP-2001) to the MEL/GenBank/DDBJ databases.

EMBL; AF418550; AAL08579.1;
EMBL; AF418550; AAL08579.1;
R GO; GO:0005386; F:carrier activity; IEA.

RO; GO:0005386; F:carrier activity; IEA.

RO; GO:0005386; F:carrier ablumin.

Pfam; PF00273; transport; IEA.

R PRINTS; PR00802; SERUMALBUMIN.

PRINTS; PR00802; SERUMALBUMIN.

R PRODOR; PD002486; Serum albumin, 1.

SMART; SM00103; ALBUMIN; 2.

SRQUENCE 608 AA; 68225 MW; ESEABB26EIC66E54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=SB1;
MEDLINE=2023653; PubMed=10760168;
Holmes M.L., Dyall-Smith M.L.;
"Sequence and expression of a halobacterial beta-galactosidase gene.";
Mol. Microbiol. 36:114-122(2000).
                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida,
Schistosomatoidea, Schistosomatidae, Schistosoma.
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100.0%; Score 38; DB 5; Length 608;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels
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84.2%; Score 32; DB 1; Length 157;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 1; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: U70664; AAB40124.1; -.
PIR; T44794; T44794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; JR003961; FN III.
InterPro; IPR003957; FN III-like.
Pfam; PF00041; fn3; 1.
SMART; SM0060; FN3; 1.
Hypothetical protein.
SEQUENCE 157 Aa; 17392 MW; 65445110P57407FD CRC64;
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Haloferax sp. (strain Aa 2.2).
Archaea; Euryarchaecta; Halobacteriaces; Halobacteriaces; Haloferax.
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q95VB7 PRELIMINARY; PRT; 608 AA.
Q95VB7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-UN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                     Schistosoma mansoni (Blood fluke).
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6183;
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                                                                                                                                                                                                                                   Albumin.
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P94805
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SEQUENCE FROM N.A.

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MEDLINE=20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

Mite O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

Gwinn M., Nelson W., Peboy R., Kolonay J., McClarty G., Salzberg S.L.,

Li Genome sequences of Chlamydia trachomatis MoPn and Chlamydia

preumoniae AR39:",

Nucleic Acids Res. 28:1397-1406(2000).

IN Uncleic Acids Res. 28:1397-1406(2000).

THEN IS RELEASED (BY SIMILARITY).

-: FUNCTION: THE BELONGS TO THE SIGMA-70 FACTOR FAMILY.

REMBL, ABDO2301; AAR39124.1; -.

REMBL, ABSO2301; AAR39124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/SvevTACfBr;
C STRAIN=129/SvevTACfBr;
A Van Reeth T., Gabant P., Szpirer J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
B Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AJ277794; CAC81993.1; -...
R GO; GO:0005615; C:extracellular space; IEA.
R GO; GO:0005615; C:extracellular space; IEA.
R GO; GO:0006810; P:transport; IEA.
R GO; GO:0006810; P:transport; IEA.
R InterPro; IRRO0264; Serum albumin.
R Fam; PF00273; transport prof; 1.
R PRINTS; PR00802; SERUMALEUMIN.
R SMART; SM0103; ALBUMIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%; Score 32; DB 11; Length 205;
87.5%; Pred. No. 60;
artive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA; 23624 MW; 0A982E85C7474BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
RNA polymerase sigma factor.
                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                       205 AA
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                    PRELIMINARY;
                                             102 VADEIAEN 109
                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 VADESAAN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VADESAEN 8
1 VADESAEN 8
                                                                                                                                                                                                                                                                                              Albumin (Fragment)
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VADESAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBIUK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
Q95VB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SO ON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q81uk7 homo sapien
Q95vb7 schistosoma
P94805 haloferax s
Q86g74 mus musculu
Q95kx9 chlamydia m
Q91f80 arabidopsis
Q91f80 arabidopsis
Q8777 mus musculu
Q8773 caenorhabdi
Q8xg27 caenorhabdi
Q8xg28 caenorhabdi
Q8xg28 caenorhabdi
Q8y28 listeria mo
Q8y784 listeria mo
Q8y784 listeria mo
Q8y784 seenorhabdi
Q9f428 seenorhabdi
Q9f428 seenorhabdi
Q9f428 seenorhabdi
Q9f438 seewanella
                                                                                                                                                       April 19, 2004, 11:37:09 ; Search time 3.08772 Seconds (without alignments) 817.479 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                    US-09-832-929-18_COPY_54_61
38
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Q95VB7
Q95VB7
Q8CG74
Q9EX29
Q91ZD1
Q8C7C7
Q8C7C7
Q8C7C3
Q8WQC7
Q6C735
Q6Z35
Q9F428
Q9F428
Q9F428
Q9F7384
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sp_rodent: *
sp_vortebrate: *
sp_vortebrate: *
sp_unclassified: *
sp_rvirus: *
sp_rvirus: *
                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_fungl:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Bp_bacteria:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>B</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
                                                                                                                                                                                                                                                                                                                    1 VADESAEN 8
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                  Run on:
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| 17 | 31 | 81.6 | 236 | 16 | QBE684 | QBE684 | Streptococcoccoccolors | 18 | 31 | 81.6 | 236 | 16 | QBE011 | QPSe011 | CONSCREENIS | CONSCREE
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## ALLGNMEN

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DESCRIPTION OF TRELIMINARY; PRT; 396 AA.

CORDING;
CORDING;
CORDING;
CORDING;
CORDING;
CORDING;
COLOCT-2003 (TrEMBLrel. 23, Last sequence update)
COLOCT-2003 (TrEMBLrel. 25, Last annotation update)
COLOCT-2003 (TrEMBLrel. 25, Last annotation update)
E Similar to serum albumin precursor.

SHOWD Sapiens (Human)
COLOCT-2003 (TrEMBLrel. 25, Last annotation update)
E Similar to serum albumin precursor.

COLOCT-2003 (TrEMBLrel. 25, Last annotation update)
E Homo sapiens (Human)
COLOCT-2003 (TrEMBLrel. 25, Last annotation update)
COLOCT-2004
COLOCT-2005
COLOC
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 114 6 X 5 AA TANDEM REPEATS OF G-P-E-E-T.
48 85 GPI-anchor amidated glycine.
114 AA, 11611 MW, FFF2690DAAAE445E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

Dest Local Similarity 85.7%; Pred, No. 29;

Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                        R EMBL, M25787; AAA53283.1; -.
R EMBL, M3129; AAA30224.1; -.
R EMBL, X5584; CAA36014.1; -.
PIT, A30229; A30229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPID
SEQUENCE
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DOMAIN
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28 ADESASN 34

2 ADESAEN 8

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0; Gaps

Search completed: April 19, 2004, 11:52:46 Job time: 1.58356 secs

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-!- SIMILARITY: Contains 1 acyl carrier domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
tes 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha) (PARI
PARPA-ALPHA.
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Matches
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When Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Name and C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Latorre A., Valencia C., Moya A.;

Tamames J., Viguera E., Jatorre A., Valencia A., Moran F., Moya A.;

Tamames J., Viguera E., Jatorre A., Moya A.;

Tamames J., Viguera E., Jatorre A., Valencia C., Moya A.;

Tamames J., Viguera E., Jatorre A., Moya A.;

Tamames J., Viguera E., Jatorre A., Jatorre A., Moya A.;

Tamames J., Viguera E., Jatorre A., Moya A.;

Tamames J., Viguera E., Jatorre A., Moya A.;

Tamames J., Viguera E., Jatorre A., Moya A.;

Tamames J., Voya M., Jatorre A., Moya A.;

Tamames J., Moya M., Jatorre A., Moya A.;

Tamames J., Moya M., Jatorre A., Moya A.;

Tamames J., Moya A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R PROSITE; PS000255; ZINC_FINNER_C2H2_1; 6.

R PROSITE; PS000255; ZINC_FINNER_C2H2_2; 6.

W PROSITE; PS000257; ZINC_FINNER_C2H2_2; 6.

W Developmental protein; Zinc_FINGE; Metal-binding; DNA-binding; Transcription regulation; Repeat; Nuclear protein.

F DOMAIN 115 162 SER/THR-RICH.

I DOMAIN 115 162 SER/THR-RICH.

I DOMAIN 169 186 GIN-RICH.

I ZN FING 268 292 C2H2-TYPE.

I ZN FING 268 320 C2H2-TYPE.

I ZN FING 330 351 C2H2-TYPE.

I ZN FING 357 379 C2H2-TYPE.

I ZN FING 411 463 C2H3-TYPE.

I ZN FING 441 463 C2H3-TYPE.

I ZN FING 441 463 C2H3-TYPE.

I ZN FING 441 463 C2H3-TYPE.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0234DD17F0F2BF20 CRC64;
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Acyl carrier protein (ACP).
ACPP OR BBP322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH
                                                                                                                                                                                                                                                                                          PIR, A30817; A30817.
TRANSFAC: T007689: --
Flyames, FBGD0005642; wdn.
InterPro; IPR007087; Znf C2H2.
Pfam; PS00096; Znf C2H2.
ProDom; PD000003; Znf C2H2.
SWART; SM00355; Znf C2H2.1.
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NCBI TaxID=135842;
                                                                                                                                                                                                                                                 EMBL; M23391; AAA28487.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 VLDESAQN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VADESAEN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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P59449;
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DOMAIN
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                                                SOLUTION SOL
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NCBI_TaxID=5702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vijayasarathy S., Ernest I., Itzhaki J., Sherman D., Mowatt M.R., Michels P.A.M., Clayton C.E., Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases. -: FUNCTION: Major surface antigen of procyclic forms. -:- SUBGELLULAR LOCATION: Attached to the membrane by a GPI-anchor. -:- DEVELOPMENTAL STAGE: Expressed only at a certain stage during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
U-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Procyclic form specific polypeptide A-alpha precursor (Procyclin A-
                                                                                                                                                                                                                                                                                                             R MBL, AE014017; AA027044.1;
R HAMAR, MF 01217; J. 1.
R InterPor, IPR00313; Acyl carrier.
R InterPor, IPR006163; Pp.bind.
R InterPor, IPR006163; Pp.bind.
R InterPor, IPR006162; Ppatne.
R InterPor, IPR006162; Ppatne.
R InterPor, IPR006162; Ppatne.
R InterPor, IPR006163; Pp.binding; 1.
R PR0SITE; PS00715; Acyl DoWAIN, 1.
R PR0SITE; PS00012; PHOSPHOPANTETHEINE; 1.
M Lipid synthesis; Ratty acid blosynthesis; Phosphopantetheine;
Complete proteome. PHOSPHOPANTETHEINE (BY SIMILARITY).
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MOWALT M.R., Wisdom G.S., Clayton C.E.;
Mowatt M.R., Wisdom G.S., Clayton C.E.;
Wariation of tandem repeats in the developmentally regulated
"Variation of tandem repeats in the developmentally regulated
procyclic acidic repetitive proteins of Trypanosoma brucei.";
Mol. Cell. Biol. 9:1332-1335(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.3%; Score 29; DB 1; Length 78;
llarity 62.5%; Pred. No. 20;
Conservative 1; Mismatches 2; Indels
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Mol. Cell. Biol. 10:3036-3047(1990)
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78 AA; 9031 MW;
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Cell 79:245-258(1994).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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be the effector of Sec4 function in exocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                           EMBL; AB006197; BAA21765.1; -.
PIR; JC5838; JC5838.
HSSP; PO2768; IEFD.
InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERUM_BUMIN; 1.
PROMORD; PROMO1286; SERUM_albumin; 1.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
PROPER SERUM_ALBUMIN; 2.
PROPER SERUM_ALBUMIN; 2.
PROPER SERUM_ALBUMIN; 2.
PROPER SERUM_ALBUMIN; 3.
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Brennwald P., Kearns B., Champion K., Keraenen S.,
Bankaitis V., Novick P.;
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01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
SEC9 OR HSS7 OR YGR009C.
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ALBUMIN 2.
ALBUMIN 3.
COPPER.
BY SINILARITY.
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Pred. No.
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539
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609 AA;
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                                                  Hebling U., Hofmann B., Delius H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

FUNCTION: COMPONENT OF A SNARE COMPLEX THAT MAY BE THE EFFECTOR OF SEC4 FUNCTION IN EXOCYTOSIS.

SEC4 FUNCTION IN EXOCYTOSIS to the SNAP-25 family.

SIMILARITY: TO YEAST WRR017W.

SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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Lepesant J.-A.;
Lepesant J.-A.;
Binwing maternal and zygotic expression.";
Mol. Cell. Biol. 8:4459-4468(1988).
I. FUNCTION: THIS MATERNAL AND ZYGOTIC FINGER PROTEIN MAY BELONG TO A COMPLEX SET OF MULTELNGERED PROTEINS WHICH PLAY AN IMPORTANT ROLE IN GENE ACTIVATION OR REGULATION AT EARLY EMBRYONIC STAGES THROUGH A MAXIMAL ACCUMULATION OF THEIR TRANSCRIPTS (OR PROTEIN PRODUCT) IN THE MAINTE GOCYTE.

-: SUBCELLULAR LOCATION: Nuclear.
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R GOTMONINE; 141321,
R GOTMONINE; SU003241; SEC.
R SCHART; SM00337; T SNARE.
DR SNART; SM00397; T SNARE; 2.
DR PROSITE; PSCO192; T SNARE; 2.
DR PROLEIN transport; Repeat; Coiled coil.
FT DOMAIN 434 496 T-SNARE COILED-COIL HOWOLOGY 1.
FT DOMAIN 588 650 T-SNARE COILED-COIL HOWOLOGY 2.
FT AA; 73623 MW; EA314D73D20A10C7 CRC64;
FT AAA; 73623 MW; EA314D73D20A10C7 CRC64;
FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAA FT AAAA FT AAA  FT AAA 
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10-CCT-2003 (Rel. 42, Last amnotation update)
25 serendipity locus protein H-1 (Wings-down protein).
SRY-C ON WDN.
Drosophila melanogaster (Fruit fly).

    -!- SUBCELLULAR LOCATION: Nuclear.
    -!- DEVELOPMENTAL STAGE: Blastoderm specific.

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10-OCT-2003 (Rel. 42, Last anno
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Conservative
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NCBI_TaxID=10047;
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SEQUENCE 478 AA
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035090;
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MEDLINE=22022145; PubMed=12024217;

A Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A los aractic G., Cannavan F., Cardozo U., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Greggio C.C., Gruber A.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
                                            MEDLINE=97382443; PubMed=9240447; Augustus M., Fan P., Zhang X., Zeng Z., Kyaw H., Gakenheimer K.R., Augustus M., Fan P., Zhang X., Zeng Z., Kyaw H., Gakenheimer K.R., Li Y.; Zu K., Carter K.C., Li Y.; Carter K.C., and tissue distribution of a human homologue of the mouse jerky gene product."; 236:389-395(1997).

-I TISSUE SPECIFICITY: Abundantly expressed in the majority of tissues examined, including brain and skeletal muscle.
-I SIMILARITY: Contains 1 CENPB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amocation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.6%; Score 31; DB 1; Length 442;
85.7%; Pred. No. 42;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 314 CENP-B.
442 AA; 50710 MW; 5EE5430FC54CE488 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF004715; AAB65833.1; -.
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Q8PLH2;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINEMGS IDR; TISSUB-Liver;

X MEDLINE-9811665; PubMed-9455485;

XY Setc-Ohshima A., Sinohara H.;

Yoshida K., Setc-Ohshima A., Sinohara H.;

Topical and the Mongolian gerum albumin and its extrahepatic

Topical and the Mongolian gerbil, Meriones unguiculatus.";

Topical and the main protein of plasma, has a good

Topical and the main function is the regulation of the colloidal osmotic pressure of blood.

Topical and the main function is the regulation of the colloidal osmotic pressure of blood.

Topical and the main function is the regulation of the colloidal osmotic plasma.

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Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
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InterPro; IPR004516; His6.
InterPro; IPR0051314; tRNA-synt_2b.
InterPro; IPR0061319; tRNA-synt_2b.
Pfam; PF00139; HGTP_anticocion; 1.
Pfam; PF00587; tRNA-synt_2b; 1.
TIGRRAMS; TIGR00442; his6; 1.
PR051TE; PS50662; AA TRNA_LIGASE II; 1.
Aminoacy1-tRNA synthētase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                   Nature 417:459-463 (2002).
-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidyl-tRNA(His).
diphosphate + Homodimer (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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HAMAP, MF_00127; -, 1.
InterPro, IPR004154; HGTP_anticodon.
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397 SDESAEN 403
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URKL HUMAN
LD COV4AI
DT 28-FEB-DT 28-
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STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
MODINESON M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
Kucaba T., Hillier L., W. Jier M., Johnston L., Langston Y.,
Latreille P., Louis B.J., Marri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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MEDLLINE-94253121; PubMed=8195187;
D'Mello N-9., Childress A.M., Franklin D.S., Kale S.P.,
Pinswasdi C., Jazwinski S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF5E92647AAFE9A2 CRC64;
                                                                                                                                                             Repeat; Signal; Copper. BY SIMILARITY. BY SIMILARITY. SERUM ALBUMIN.
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Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 0; Mismatcher
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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ALBUMIN 3.
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InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport prot; 3.
PRINTS; PR00020; SERUMALEUMIN.
Probom; PD002486; Serum albumin; 1.
SMART; SM0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; SIGNAL
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J. Biol. Chem. 269:15451-15459(1994)
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582
608 AA;
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P38703;
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F -> C (IN REF. 2).

VETPERPREADENTINGVITERRHEGNYUL

NEATOGYKEMISLEIVEVILIAALOLUNILYMELIIRILKRIL

IWQGIQKDERSDSDSDSBARNESKEKCE -> TEISGIWE

KQBIDSNNNPTERALSPWITSKQYKEDLILVYLNPTENRAL

LEARSROPPITAIDTDSESSLYFYPIPGNDSLRSKWFLL

GVARAGOGGLQNRLARNNEK (IN REF. 1).

M, 91676D56ACOS3F3C CRC64;
                                                                                                                 Science 265:2077-2082(1994).
-!- FUNCTION: Involved in the aging process. Deletion of LAG1 results
in a pronounced increase (approximately 50%) in mean and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome \operatorname{VIII."}_i;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                    protein (Potential).
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Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U08133; AAA21579.1; -.
EMBL; U18555; AAB68429.1; -.
PIR; S46800; AA6800.
Germonline; 139270; -.
SGD) S0000095; LAGI.
GO; GO:000578; D:cell aging (sensu Saccharomyces); IMP.
GO; GO:000578; P:cell aging (sensu Saccharomyces); IMP.
GO; GO:0005547; Excamide blosynthesis; IMP.
InterPro; IPR006634; TLC.
FRA; PR09798; LAGI.
FRA; SMO724; TLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
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                                                                                                                                                                                            maximum life span.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Poi-
-!- SIMILARITY: Contains 1 TLC (TRAM/LAGI/CLN8) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 1;
Pred. No. 39;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JRKL HUMAN STANDARD; PRT; 442 AA. 09Y4AO. 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) JRKL.
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ilarity 85.7%;
Conservative
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Read Stableton W. Sorges M. Bonnido M. P., Casavarth T.L. Schefert T.B., Raha S.S., Loguellano N. N., Peters G. J., Abramon R.D., Millany S. J., Brownido M. S. J., McHellano N. P., Peters G. J., Abramon R.D., Millany S. J., Bonnis S.S., Loguellano N. N., Peters G. J., Abramon R.D., Millany S. J., Bonnis S. S., Loguellano N. N., Peters G. J., Abramon R.D., Millany S. J., Bonnis S. S., Loguellano N. N., Peters G. J., Abramon R.D., Millany S. S., McHellano S., Morey R.D., Statistica A., Gunzathe P.H., S. M., McCharles S., Morey R.D., Statistica A., J., Statista U., Smallano B.E., Statistica A., Johnson A., A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Liver;
STRAIN=New Zealand white; TISSUE=Liver;
Sheffield W.P., Syed St., Schuyler P.D.;
Scheffield W.P., Syed St., Schuyler P.D.;
Submitted (DEC-1994) to the EMBJ/Genbank/DDBJ databases.

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPRECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the ALB/APP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
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Local Similarity 87.5%; Pred. No. 35;
1. Conservative 0; Mismatches 1; Indels
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Q -> I (IN REF. 6)

Q -> I (IN REF. 6)
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ID ALBU RABIT STANDARD; PRT; 608 AA.

AC P49065;
DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
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ALBUMIN 2.
ALBUMIN 3.
COPPER.
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TISSUB-Liver,

MEDLINE-9345495, PubMed-8344282;

MEDLINE-9345495, PubMed-8344282;

MEDLINE-9345495, PubMed-8344282;

MY-ray and primary structure of horse serum albumin (Equus caballus)

RT at 0.27-nm resolution.";

RT at 0.27-nm resolution.";

LD 15:205-212 (1993).

Butt. J. Blochem. 215:205-212 (1993).

C I- FUNCTION: Serum albumin, the main protein of plasma, has a good hormones, bilintubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

C I- SUBCELLULAR LOCATION: Secreted.

C I- SUBCELLULAR LOCATION: Secreted.

C I- ALLERGEN: Causes an allergic reaction in human. Binds IgE.

C I- SIMILARITY: Belongs to the ALB/AFF/VDB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; X74045; CAA52194.1,

EMBL; X74045; CAA52194.1,

EMBL; X74045; CAA52194.1,

ERR; S34053; ABHOS.

A HSSP; POCO73; Lransport prot; 3.

DR PRINTS; PRO00024; SERUMLEUNIN.

DR PRODOR, PRO0013; ALBUMIN, 3.

DR PROSITE; PS00012; ALBUMIN; 3.

DR PROSITE; PS00012; ALBUMIN; 3.

ENGART; SMO0103; ALBUMIN; 3.

ENGART; SMO0103; ALBUMIN; 3.

SIGNAL 1 1 18 BY SIMILARITY.

""OPEP 19 24 BY SIMILARITY.

25 204 ALBUMIN 1.

COPPER (BY SIMILARITY).

COPPER (BY SIMILARITY).
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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                                                Query Match 92.1%; Score 35; DB 1; Length 608; Best Local Similarity 87.5%; Pred. No. 8; Matches 7; Conservative 1; Mismatches 0; Indels
5BB497A282411AB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            193747, 01-JUN-1994 (Rel. 29, Created) 101-JUN-1994 (Rel. 29, Last sequence update) 101-JUN-1994 (Rel. 29, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Serum albumin precursor (Allergen Equ c 3).
                                                                                                                                                                                                                                                                                                                                                                       607 AA
68718 MW;
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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78 VADENAEN 85
                                                                                                                                                                    1 VADESAEN 8
608 AA;
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CREALME-CSTEL/64). TISSUE=TONGUE;

KRAMING-CSTEL/64). TISSUE=TONGUE;

KRAMI JU. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWA JU., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Bronstein M.J., Bult C., Fletcher C., Fullia J., Mombaerts P.,

Rousincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Saxamcto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Baris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.; F., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nature 409:685-690(2001).
                                                                                                                                                         Gaps
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STRAIN=FVB/N; TISSUE=Liver;
STRAIN=FVB/N; TISSUE=Liver;
MEDLINE=22386257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altechul S.F., Joordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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                                                                        89.5%; Score 34; DB 1; Length 607; 100.0%; Pred. No. 13; ive 0; Mismatches 0; Indels
68598 MW; 256F6E830A1B90C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 608 AA. P07724, Q61802; Created) 1-APR-1988 (Rel. 07, Created) 15-JUJ-1999 (Rel. 38, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Serum albumin precursor. ALB OR ALB1 OR ALB-1. Mus musculus (Mouse).
                                  Query Match
Best Local Similarity 10...
7; Conservative
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DISULFID
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"Two alloalbumins with identical electrophoretic mobility are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P02770; P11382;
21-ULL-1986 (Rel. 01, Created)
21-ULL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
                                                                                                                                                                                                                                                                 VARIANT CASEBROOK ASN-518.
MEDLINE=91316157; PubMed=1859851;
Peach R.J., Brennan S.O.;
"Structural characterization of a glycoprotein variant of human serum albumin: albumin Casebrook (494 Asp-->Asn).";
Biochim. Biophys. Acta 1097:49-54(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=77249657; PubMed=893447;
Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
"Rat liver pre-proalbumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23; KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.

MEDLINE=92052189; PubMed=1946412;

Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsida Y.-I., Amaki I., Putnam F.W.;

"Genetic variants of serum albumin in Americans and Japanese.";

Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81223722; PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
"Nucleotide sequence of cloned rat serum albumin messenger RNA.";
Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=78109429; PubMed=564145; Isemura S., Ikenaka T.; Anino acid sequences of fragments I and II obtained by cyanogen bromide cleavage of rat serum albumin."; J. Biochem. 83:35-48(1978).
                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
MEDLINE=92190239; PubMed=1347703;
Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Minchiotti L., Putnam F.W.; A donor splice muteation and a single-base deletion produce carboxyl-terminal variants of human serum albumin."; Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 38; DB 1; Length 609; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels
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J. Biol. Chem. 252:6846-6855(1977)
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MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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Matches 8; Conserv
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RI 'Fragmentation of rat serum albumin by cyanogen bromide cleavage and mino acid eaquences of four fragments.'

RE SEQUENCE OF 166-174.

RE TISSUPERENCE OF 166-174.

RE TISSUPERENCE OF 166-174.

RETURNING THE SPINSON THE
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MEDLINE=76257808; PubMed=955075;

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TISSUE=Liver, and Skeletal muscle;

MEDLINE=22388257; PubMed=12477932,

Riausher R.D., Collins F.G., Magner L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L.H., Schaefer G.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer G.F., Bhat N.K.,

Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Heich F.,

Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Heich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramoon R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevincholo, V., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Schlaka U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Salska U., Smailus D.E.,

Rodersation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=82105994; PubMed=6275391; Dugalczyk A., Law S.W., Dennison O.E.; "Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.";
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).
                                                                                                                                                       TISSUE-Liver;
Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;
Submitted (2EP-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=86140099; PubMed=2419329;
Urano Y., Watanabe K., Sakai M., Tamaoki T.;
Urhe human albumin gene. Characterization of the regions and the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
                                                                                    Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982)
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(In) Bing D.H. (eds.);
The chemistry and physiology of the hum
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Meloun B., Moravek L., Kostka V.;
"Complete amino acid sequence of F
FEBS Lett. 58:134-137(1975).
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SEQUENCE OF 222-229.
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VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106. MEDLINE-91062352; PubMed=2247440; Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J., Watkins S., Putnam F.W.; "Matkins S., Putnam F.W.; "Mutations in genetic variants of human serum albumin found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION OF VARIANT REDHILL.
MEDLINE=90115852; Pubmed=2104980;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
Brennan S.O., Myles T., Peach 3.20 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
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MEDLINE=87157744; PubMed=3828358;

Brennan S.O., Herbert P.;

"Albumin Canterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin.";

Biochim. Biophys. Acta 912:191-197(1987).
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MOEDLINE=95203287; PubMed=7895732;
COEDELT J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
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MEDLINE-90115905; PubMed-2404284;
Arai K., Madison J., Shimuzu A., Putnam F.W.;
"Point substitutions in albumin genetic variants from Asia.";
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Biochem. J. 171:453-459(1978).
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MEDIATE-88068523; PubMed=3479777;
Takehashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M., Satoh C., Neel J.V.;
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proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
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Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.
             Walker J.E., ""Invain to modified by ""Inysine residue 199 of human serum albumin is modified by acetylaalicylic acid."; PEBS Lett. 66:173-175(1976).
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MEDLINE=89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satoh C.,
Neel J.V., Sakurabayashi I., Putnam F.W.;
Potne substitutions in Japanese alloalbumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
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Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
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MEDLINE=78186630; PubMed=656055;
                                                                                                         SEQUENCE OF 25-44 AND 480-499
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MEDLINE-89016582; PubMed=3174440;

MEDLINE-89016582; PubMed=3174440;

MEDLINE-89016582; PubMed=3174440;

Mucleotide sequence of porcine liver albumin.";

Nucleotide sequence of porcine liver albumin.";

Nucleotide Res. 16:3045-304551988).

Incleic Acida Res. 16:3045-304551988.

Incleic Acida Res. 16:3045-30451988.

Incleic Acida Res. 16:3045-3045198.

Incleic Acida Res. 16:3045-3048.

Incleic Acida Res. 16:3045-3048.

Incleic Acida Capacity for water, Ca(2+), Na(+), K(+), fatty acids, hordeness, blintubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1918 TaxID=9823;
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, last sequence update)
08-PEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor (Fragment).
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InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
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EMBL; M36787; AAA30988.1; --
PIR; S01382; ABPGS.
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SECURINCE FROM N.A.
MEDLINE=86196112; PubMed=3009475;
Minghetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,
Beattie W.G., Dugaiczyk A.;
"Molecular structure of the human albumin gene is revealed by
nuclectide sequence within g11-22 of chromosome 4.";
J. Biol. Chem. 261:6747-6757(1986).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A., AND VARIANT LYS-420.
MEDLINE-82081882; PubMed-6171778;
Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;
"The sequence of human serum albumin cDNA and its expression in
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3E556BODD1A1F4FF CRC64;
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ProDom; PD002486; Serum albumin; 1.
SMRRT; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
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SEQUENCE FROM N.A., AND VARIANT GLY-121.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SECS YEBAST
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                           US-09-832-929-18_COPY_54_61
38
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                           1 VADESAEN 8
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                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                           Run on:
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No.
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|   | P29571 methanobact | Q889m3 pseudomonas | P52350 human herpe | P34292 caenorhabdi | Q830u2 enterococcu | 059626 pyrococcus | Q9ptm4 xenopus lae | P44001 haemophilus | P30183 arabidopsis | Q8pzr8 methanosarc | P09099 escherichia | Q92q12 rhizobium m |   |
|---|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---|
|   | YPV2_METTF         | BUTC PSBSM         | VP23 HSV7J         | YKO4 CAEEL         | SYW ENTFA          | HISX PYRFU        | KVB3 XENLA         | HISX HAEIN         | CG2B_ARATH         | HISX METMA         | XYLB ECOLI         | TIG_RHIME          |   |
|   | 284 1              | 287 1              | 293 1              | 315 1              | 336 1              | 375 1             | 401 1              | 427 1              | 428 1              | 433 1              | 484                | 491 1              |   |
|   | 73.7               | 73.7               | 73.7               | 73.7               | 73.7               | 73.7              | 73.7               | 73.7               | 73.7               | 73.7               | 73.7               | 73.7               |   |
| • | 28                 | 28                 | 28                 | 28                 | 28                 | 28                | 28                 | 28                 | 28                 | 28                 | 28                 | 28                 | - |
|   | 34                 | 35                 | 36                 | 37                 | 38                 | 39                | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |   |

## ALIGNMENTS

| MACHU MACHU STANDARD; PRT; 600 AA.  02852; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) ALB. MACHI STAND-1997 (Rel. 41, Last annotation update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PASSP, POZZ68; 1E7B. InterPro; IPRO0264; Serum_albumin. Pfam; PF00273; transport_pro; 3. Profine; PF002486; Serum_albumin; 1. ProDom; PD002486; Serum_albumin; 1. ProDom; PD002486; Serum_albumin; 1. ProDom; PD002486; Serum_albumin; 1. PROSITE; PS00212; ALBUMIN; 3. Metal-binding; Lipid-binding; Repeat; Signal; Copper. NON TER 1 1 B SIMILARITY. PROPEP 11 16 BY SIMILARITY. PROPEP 17 600 SERUM ALBUMIN. DOMAIN 17 197 ALBUMIN 1. DOMAIN 204 389 ALBUMIN 2. DOMAIN 396 587 ALBUMIN 3. |
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| RESULT 1 ALBU MACMU S ALBU OVV-1997 (Rel DT 01-NOV-1997 (Rel DT 28-FEB-2003 (Rel DE Serum albumin pr GN MALB. GN MACACA mulatta ( GN MALB. GN MALB. GN MALB. GN MALB. GN MALB. ALB. GN MALB. AND LITES 9244; RP MEDLIFES 932.1971 RP GN MALB. GN MAL | HESP, PO206 HILLERPO; II PEAM, PO009 PRINTS; PRO0 PRODOM; PD00 PROSTE; PS0 Metal-bindis MCTAIN PROPEP PROPEP PROPEP PROPEP PROPED                                                                                                                                                                                                                                                                  |
| HACOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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2 ADESAEN 8

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Jerky gene protein homolog - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo Sapiens (man) C;Species: Homo JCSS94 Rsequence_revision 23-Sep-1997 #text_change 05-Nov-1999 C;Accession: JCSS94 Rsequence_revision X.; Kyaw, H.; Gakenheimer, K.R.; Augustus, M.; Fan, P.; Zhang, X.; Su, K.; Carté Biochem. Biophys. Res. Commun. 236, 389-395, 1997 A;Title: Cloning, mapping, and tissue distribution of a human homologue of the mouse jer A;Reference number: JCS594; MUID:97382443; PMID:9240447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residuse: 1-172, TV,,175-219, C',221-300,'TBISGI',314,'EKQE',315,'DSNDNPTE',324,'A',32
A;7.381,'AGQR',386,'L',388,'NRLARNNEK' <DAM>
A;Cross-references: GB:U08133
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A) Residues: 1-442 < ZENA
A) Cross-references: DDBJ-AP004715; NID:g2314828; PIDN:AAB65833.1; PID:g2314829
A) Cross-references: DDBJ-AP004715; NID:g2314829
A) Note: it is uncertain whether Met-1 or Met-33 is the initiator
C; Comment: This protein functions as a nuclear regulatory protein.
C; Genetics:
C; Genetics:
A; Gene: hunig
A; Map position: 11g21
                                                                                                                                                                                                                                                                                 LAGI protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YHL003c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 23-Mar-2001
C;Accession: $46800; A54012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.6%; Score 31; DB 2; Length 411;
85.7%; Pred. No. 53;
tive 1; Mismatches 0; Indels
                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: involved in dertermination of longevity C; Superfamily: hypothetical protein YKL008c C; Keywords: transmembrane protein
Best Local Similarity 87.5%; Pred. No. 36; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SGD:LAG1
A;Cross-references: SGD:S0000995; MIPS:YHL003c
A;Map position: 8L
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Matches 6; Conservative
                                                                                                                                        176 VADGSAEN 183
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                                                                                   1 VADESAEN 8
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Search completed: April 19, 2004, 12:02:22 Job time : 2.97507 secs
                375 ADESSEN 381
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hypothetical protein - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Dates: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C;Accession: D71442
C;Accession: D71442
C;Accession: D71442
B;Bevan, M; Bancroft, I; Bent, E; Love, K; Goodman, H; Dean, C; Bergkamp, R; Dir R; Bevan, M; Bancroft, I; Medler, E; Wambutt, R; Wedler, T; Pohl, T.M.; Terryn, N; Gie avanagh, T; Hempel, S; Kotter, P; Entian, K.D; Rieger, M; Schaeffer, M; Funk, B. avanagh, T; Hempel, S; Kotter, P; Entian, K.D; Rieger, M; Schaeffer, M; Funk, B. Ayathors: Mueller-Auer, S.; Silvey, M; James, R.; Montfort, A; Moores, T; Jones, J.D.G; Eneva, T; Palme, K.; Benes, V; Rechman, S; Ar.C.; Chalwattis, N.
A; Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis the A; Reference number: A71400; MolD:98121113; PMID:9461215
A; Accession: D71442
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A, Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Reference number: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-75 < GLA>
A; Coss-references: GB:NC_003210; PIDN:CAC99489.1; PID:g16410840; GSPDB:GN00177
A; Residues: 1-75 < GLA>
A; Reperimental source: strain EGD-e
C; Generics: A; GPDB:GN00177
A; GPDB:GN00177
A; GPDB:GN00177
A; GPDB:GN00177
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C;Species: Streptomyces coelicolor
C;Decies: Streptomyces coelicolor
C;Decies: Deci-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T6578
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z21575
A;Reference number: Z21575
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A;Experimental source: strain A3(2)
C;Genetics:
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A;Cross-references: GB:Z97343; NID:G2245073; PID:e327054; PID:G2245091
C;Genetics:
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85.7%; Pred. No. 29;
tive 1; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-282 <OLI>
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Pred. No. 8.8;
1; Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Swim, X.

Submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid T13H2.

A;Accession: T16871

A;Accession: A;Accession: T16871

A;Accession: T16871

A;Accession: T16871

A;Accession: X

A;
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C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession AG1251
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                                                                                                                                                                            hypothetical protein F36F2.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T21861
B.Cottage, A.
submitted to the EMB1 Data Library, November 1996
A.Roctage: Drainmary; Lranslated from GB/EMBL/DDBJ
A.Roctagion: T21861
A.Roctagion: T21861
A.Roctagion: T21861
A.Roctagion: T21861
A.Roctagion: T21861
A.Roctagion: Data Library, November 1996
A.Roctagion: T21861
A.Roctagion: T21861
A.Roctagion: T21861
A.Roctagion: L1877 < WILL>
A.Roctagion: L1877 < WIL
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16871
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Pred. No. 1.6e+02;
2; Mismatches 0; Indels
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100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0; Indels
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 100.v
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714 VADENAQN 721
                                        231 VSDESAQN 238
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Score 32; DB 2; Length 157;
Pred. No. 12;
0; Mismatches 1; Indels
                                        A;Accession: T44794
A;Status: preliminary; translated from GB/EMBL/DDBJ.
A;Molecule type: DDF.
A;Residues: 1-157 cHOL>
A;Cross-references: EMBL:U70664; PIDN:AAB40124.1
A;Experimental source: strain SB1
                                                                                                                                                                                                                                                                                                                           84.2%;
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A;Note: F7J8.240
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Best Local Similarity 87.5
Matches 7; Conservative
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A; Reference number: Z22843
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Best Local Similarity
Matches 6; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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A, Map position: 5
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Mol. Cell. Biol. 7, 2425-2434, 1987

A,Title: Determinants of rat albumin promoter tissue specificity analyzed by an improved A,Reference number: 157621; MUID:87286876; PMID:347556
A,Accession: 157621; MUID:87286876; PMID:347556
A,Accession: 157621; MUID:87286876; PMID:347556
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-5 KES>
A,Cross-references: GB:M16825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C,Superfamily: serum albumin; serum albumin repeat homology
C,Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>F;19-24/Domain: serum albumin #status experimental <RO>F;29-202/Domain: serum albumin repeat homology <SA1>F;21-394/Domain: serum albumin repeat homology <SA2>F;21-394/Domain: serum albumin repeat homology <SA3>F;27/Binding site: copper (His) #status experimental
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-383,4
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A, Molecule type: miNA
A, Residues: 1-607 < HOAD.
A, Residues: 1-607 < HOAD.
A, Cross-references: GB.X74045; NID:g399671; PIDN:CAA52194.1; PID:g399672
A, Cross-references: GB.X74045; NID:g399671; PIDN:CAA52194.1; PID:g399672
C, Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper.
C, Comment: Serum albumin; serum albumin repeat homology
C, Superfamily: serum albumin; serum albumin repeat homology
C, Reywords: carrier protein; duplication; metal binding; plasma
C, Romain: signal sequence #status predicted < SIG>
F; 1-18, Domain: serum albumin #status predicted < NRO>
F; 25-607/Porduct: serum albumin repeat homology < SA1>
F; 25-607/Domain: serum albumin repeat homology < SA3>
F; 25-607/Domain: serum albumin repeat homology < SA3>
F; 25-107/Domain: serum albumin repeat hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S34053
Fylo, Jx.; Holowachuk, E.W.; Nortcn, E.J.; Twigg, P.D.; Carter, D.C.
Bur. J. Biochem. 215, 205-212, 1993
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
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C;Species: Haloferax alicantei
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T44794
S;Holmes, M.L.; Dyall-Smith, M.L.
submitted to the EMBL Data Library, May 1999
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92.1%; Score 35; DB 1; Length 608;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 0; Indels
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Matches 7; Conservative
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Cjaccession: T45966
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Le RiBevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Le R; Bevan, M.; Zimmermann, W.; Gruence Database, January 2000
A;Reference number: Z23018
A;Reference number: Z23018
A;Reference number: Z33018
A;Reference number: Z33018
A;Refidues: I-385 <BEV>
A;Refidues: I-385 <BEV>
A;Cross-references: EMBL:ALJ37189
                                                                                                  C, Accession: G81713
R, Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A, Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A, Reference number: A81500; MUID: 20150255; PMID: 10684935
                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: TC0331
C,Superfamily: transcription initiation factor sigmaD; transcription initiation factor
RNA polymerase sigma factor, sigma-70 family TC0331 [imported] - Chlamydia muridarum
C,Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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84.2%; Score 32; DB
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches
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A; Regidues: 25-22 <1S1>
A; Residues: 25-22 <1S1>
A; Residues: 25-22 <1S1>
A; Residues: 25-22 <1S1>
B; Residues: 35-126 <1S1>
A; Tisemura. 3.; Itsenaka. 7.
B; Description of rat serum albumin by cyanogen bromide cleavage and the amino A; Reference number: A91940; MUID: 76260153; PMID: 956149
A; Reference number: A91940
A; Residues: 223-288:572-608 <1S2>
A; Residues: 222-288:572-608 <1S2>
A; Residues: 222-288:572-608 <1S2>
A; Residues: 223-288:572-608 <1S2>
A; Residues: 283-3486, 1978
A; Title: Copper(II) binding ability of human alpha-fetoprotein.
A; Reference number: A90758; MUID: 9001617; PMID: 80265
A; Contents: annotation; copper binding
R; Carraway, R. B.; Cochtane, D. E.; Boucher, W.; Mitra, S. P.
J; Immunol. 143, 1680-1684, 1989
A; Title: Structures of histamine-releasing peptides formed by the action of acid protes
A,Molecule type: protein
A,Residues: 1-38 <STR>
K,Isemura, S.; Ikenaka, T.
J. Biochem. 83, 35-48, 1978
A,Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleave
A,Reference number: A91946; MUID:78109429; PMID:564345
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C;Species: Rattus norvegicus (Norway rat)
C;Dacession: 31-May-1979 #sequence_revision 31-May-1979 #text_change 22-Jun-1999
C;Accession: A93872; A92211; A1946; A91940; C45800; I57621; A03233
R;Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981
A;Itle: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUID:81223722; PMID:7017712
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A,Molecule type: protein
A,Residues: 166-173 <CAR>
R,Heard, J.
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Matches 8; Conserv
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                                                                                                                      A,Molecule type: procein
A,Residues: 76-83,'K',85-106 cGAL3>
A,Note: Lhis variant is designated albumin Torino
R,Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A;Title: The structural characterization and bilirubin-binding properties of albumin Her
A;Reference number: S33298; MUID:9329504; PMID:8513793
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A;Residues: 255-263, 'E', 265-281 <MINI>
B;Note: this variant is designated albumin Herborn
R;Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Porta, Biochim. Biophys. Acta 1119, 232-238, 1992
A;Title: Two alloabumins with identical electrophoretic mobility are produced by differ A;Reference number: S21078; MUD:92190239; PMID:1347703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized trubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak Comment: A large number of variants of human serum albumin have been described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:118990; OMIM:103600
A;Map position: 4q11-4q13
C;Superfamily: serum albumin; serum albumin repeat homology
                                        A;Residues: $2-105,'K',107-110 <GAL2>
A;Note: this variant is designated albumin Vibo Valentia
A;Accession: A38255
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A; Accession: 15913.
A; Accession: 15913.
A; Accession: Logic translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Mesidues: 589-590, 'AlperkVKILLQVKLP, «MAD>
A; Cross-references: 681-570799; NID:9547231; PIDN:AAB31177.1; PID:9547232
A; Note: this frame-shift variant is designated albumin Bazzano; four additional variant R; Manaya, ".; Partilla, R.; Ayuso, M.S.
A; Menaya, ".; Partilla, R.; Ayuso, M.S.
A; Reference number: G08292
A; Reference number: G08292
A; Residues from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Meseidues [1-120, 'G', 122-455 «MEN>
A; Molecule type: mRNA
A; Meseidues [1-120, 'G', 122-455 «MEN>
A; Cross-references: EMBL:U22061; NID:9763428; PIDN:AAA64922.1; PID:9763431
B; Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
B; Molecule type: processing of recombinant proalbumin variants by the yeast Ke; A; Reference number: S53114; MUID:95275251; PMID:775581
A; Molecule type: protein
A; Residues: 19-27 4LED>
B; Molecule type: protein
A; Reference number: A; Kostka, V.
R; Reference number: A; MulD:701701; PMID:1225573
A; Title: Complete amino acid sequence of human serum albumin.
A; Reference number: A; MulD:701701; PMID:725573
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A. Molecule type: protein

B. R. Biochem. Blochem. Blochem. Biochem. Blochem. Blochem
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A;Molecule type: protein
A;Reaidues: 166-173 <CAR>
R;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; V
Blochem. Blopkys. Res. Commun. 136, 983-988, 198 and A;Attle: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-t: A;Reference number: A03239; MUID:86242180; PMID:3087352
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A,Residues: 166-173, L' <MOG>
K,Ralallano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, R,Galllano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A,Title: Mutations in genetic variants of human serum albumin found in Italy.
A,Reference number: A38255, MUID:91062352; PMID:2247440
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A;Molecule type: protein
A;Residues: 25-54;354;31-447 <KAU>
A;Note: 49-Leu was also found
R;Carraway, R:E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the A;Title: Atsono, MUID:89341406; PMID:2474609
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A,Accession: $06422
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A, Residues: 76-111 <GAL1:
A, Accession: B38255
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A.A
A; Molecule type: protein
A; Residues: 23-51, 'X', 23-54; 'XXXGY', 146,'E', 148,'E', 150-151,'XVN', 155 < LIM>
A; Residues: 23-51,'X', 23-54; 'XXXGY', 146,'E', 148,'E', 150-151,'XVN', 155 < LIM>
A; Bxperimental source: dental enamel enamel enamel enamel source: dental enamel enamel source: dental enamel source: dental enamel en enamel c'superfamily: serum albumin serum albumin metal binding; plasma
F;17-22/Domain: signal sequence (fragment) #status predicted < RRO>
F;27-109/Domain: serum albumin repeat homology < SA1>
F;218-391/Domain: serum albumin repeat homology < SA2>
F;410-895/Domain: serum albumin repeat homology < SA3>
F;410-895/Domain: serum albumin repeat homology < SA3>
F;410-895/Domain: serum albumin repeat homology < SA3>
F;75-84,957/Domain: serum albumin repeat homology < SA3>
F;710-84,97-113,112-123,145-190,189-198,221-267,266-274,286-300,299-310,337-382,381-390,4
F;75-84,97-113,112-123,145-190,189-198,221-267,266-274
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C;Date: 29-U11-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000
C;Date: 29-U11-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000
C;Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422; S36
S;Lawn, R.M.; Adehman, R. S., Adehman, R. C.; Franke, A. E.; Houck, C. M.; Najarian, R. C.; Seebur Nucleic Acids Res 9, 6103-6114, 1981
A;Title: The sequence of human serum albumin cDNA and its expression in Escherichia coli
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Best Local 8; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        | Description | serum albumin prec |       |       |       | ij    | 144    | g      | ద      |        |        | hypothetical prote |        | Д      | LAG1 protein - yea | jerky gene protein | hypothetical prote | _      | _      |        | (I)    |        |        | -4     | othetical | B. subtilis YueK p | Ξ.  | hypothetical prote | Mon | SEC9 protein - yea |
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|        | ΩI          | A47391             | ABPGS | ABHUS | ABRTS | ABHOS | T44794 | G81713 | T45966 | T21861 | T16871 | AC1251             | D71442 | T36578 | S46800             | JC5594             | T00474             | T25421 | S32886 | C84899 | D84198 | F86393 | D84885 | T22141 | D84593    | ᅼ                  | 26  | 295                | C58 | 510                |
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|        | Length      | 909                | 605   | 609   | 608   | 607   | 157    | 253    | 385    | 1877   | 2215   | 75                 | 232    | 282    | 411                | 442                | 785                | 1657   | 109    | 221    | 265    | 309    | 387    | 466    | 475       | 496                | 496 | 508                | 609 | 651                |
|        | Match       | 00                 | 100.0 | 00    | ď     | φ.    | 4.     | 4.     | 4.     | 4.     | 4.     | H                  | H      | ÷.     |                    | Η.                 | ä                  | ÷.     | ω.     | œ.     | œ      | æ,     | œ.     |        | ω.        | æ                  | œ,  | 78.9               | œ   | 78.9               |
|        | Score       | 38                 | 38    | 38    | 32    | 34    | 32     | 32     | 32,    | 32     | 32     | 31                 | 31     | 31     | 31                 | 31                 | 31                 | 31     | 30     | 30     | 30     | 30     | 30     | 30     | 30        | 30                 | 30  | 30                 | 30  | 30                 |
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| serendipity (sry h procyclic acidic r conserved hypothet probable RNA 2-ph transcription regumand protein E - human histidinol dehydroprotein protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ALIGNMENTS | RESULT 1  Serum albumin precursor - rhesus macaque  G.Yspecies and Addition albumin precursor - rhesus macaque  G.Yspecies and Addition and Addition and Addition  G.Yspecies and Addition and Addition  G.Yspecies and Addition and Addition  G.Yspecies and Addition  G.Yspecies and Addition  G.Yspecies and Addition  M.Yspecies and M.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |        |
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| A30817<br>A30229<br>A20229<br>A202299<br>A65060<br>A63203<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A63209<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A6320<br>A63 | ALIG       | SULT 1  Tun albumin precursor - rhesus macaque Species: Macaca mulatta (rhesus macaque) Species: Macaca mulatta (rhesus macaque) Accession: A47391 Watkins, S.; Sakamoto, Y.; Madison, J.; Davi Matkins, S.; Sakamoto, Y.; Madison, J.; Davi Title: cDNA and protein sequence of polymorp Reference number: A47391; MUID:93211971; PMI Contents: B/B homozygote Accession: A47391 Reference number: A47391 Robertus: preliminary Note: sequence extracted from NCBI backbone Superimental source: liver Note: sequence extracted from NCBI backbone Superimental serum albumin; serum albumin repeat homolog 405-S84/Domain: serum albumin; serum albumin repeat homolog 405-S84/Domain: serum albumin repeat homolog 58coression: 8; Conservative 0; Mismatche 8; Ill                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |        |
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| 868<br>1114<br>1186<br>1186<br>1263<br>1395<br>1395<br>1471<br>1467<br>168<br>171<br>171<br>171<br>171<br>171<br>171<br>171<br>171<br>171<br>17                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            | r - 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; Patent No. 6663485
; GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR APPLICATION NUMBER: 501-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 2068; DB 4; Best Local Similarity 100.0%; Pred. No. 2.1e-203; Matches 387; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-153-064-105
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US-10-153-064-105
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LENGTH: 652
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                                             1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
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US-10-153-064-99
is Sequence 99. Application US/10153064
is Patent No. 666345.
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT APPLICATION NUMBER: 60/293,212
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
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    0; Mismatches
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      Matches 387, Conservative
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CAGANISM: Homo sapiens
US-10-153-064-99
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Sequence 133, Application US/10153064
FREERI NO. 6665485
FREERI NO. 6665485
FREERI INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT APPLICATION NUMBER: 60/293,212
FROR APPLICATION NUMBER: 60/293,212
FROR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 133
LENGTH: 651
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Patent No. 6663485
GENERAL INFORMATION:
APPLICANT Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 96
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100.0%; Score 2068; DB 4;
Best Local Similarity 100.0%; Pred. No. 2e-203;
Matches 387; Conservative 0; Mismatches 0;
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Pred. No. 2.1e-203;
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ORGANISM: Homo sapiens
US-10-153-064-96
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Best Local Similarity
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US-10-153-064-96
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100.0%; Score 2068; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.9e-203;
Matches 387; Conservative 0; Mismatches 0;
                                                                                                                              CUBLACUT AIRE: FLOUEY GIBN
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: BY 201064
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: SG-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH Ph. D., Julie K.
REGISTRATION UNMBER: P-38,619
REGISTRATION UNMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2
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(610) 454-3808
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                                                                  ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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SEQUENCE CHARACTERISTICS:
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US-10-153-064-133
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TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
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ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA: 920
APPLICATION WAMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY, AGENT INPORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-39,619
REFERENCE/DOCKT NUMBER: ST92006-US
REFERENCE/DOCKT NUMBER: ST92006-US
REFERENCE/DOCKT NUMBER: ST92006-US
TELEPHONE: (610) 454-3809
INFORMATION FOR SBQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LINGTH: 610 amino acids
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Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
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amino acid
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US-09-984-186-2
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Patent No. 587696
GENERAL INFORMATION
APPLICANT: Fleer, Reinhard
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Veh, Patrice
TITE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: OUTPAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
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                                                                                                                                                                                                                           Length 609;
                                                                                                                                                                                                                        100.0%; Score 2068; DB 5; 100.0%; Pred. No. 1.9e-203;
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Mismatches
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Macintosh
                                                                       LENGTH: 609 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                Similarity 100.
37; Conservative
         CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
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ADDRESSEE: Rhone-Pou
STREET: 500 Arcola R
CITY: Collegeville
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Matches 387; C
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COUNTRY:
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PCT-US95-04075-3
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US-08-797-689-2
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TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 977
LENGTH: 609
TYPE: PRI
ORGANISM: Homo sapiens
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Sequence 3, Application PC/TUS9504075
Sequence 3, Application PC/TUS9504075
GENERAL HORMATION:
GENERAL AMGEN INC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2068; DB 4;
100.0%; Pred. No. 1.9e-203;
iive 0; Mismatches 0;
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Drive
                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
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STREET: 1840 DeHavilland Di
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.
ZIP: 91320-1789
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APPLICATION NUMBER: PCT
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Best Local Similarity
Matches 387; Conserv
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Patent No. 6663485

GENERAL INFORMATION (ACCOUNTY OF TITLE OF INVENTION) Chemokine Beta-1 Fusion Proteins

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REPRENCE: PFFS6

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR RILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 1.9e-203;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 387; Conservative
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APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: 105/8/897,956A
CURRENT FILING DATE: 1997-07.21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
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Sequence 2, Application US/08897956A
Patent No. 6423512
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Best Local Similarity 100.
Matches 387; Conservative
 387; Conservative
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ORGANISM: Homo Sapiens
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                                                             Length 585;
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APPLICANT: Lichenstein, Henri
APPLICANT: Wurfel, Mark
APPLICANT: Wurfel, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
                                                     Query Match 100.0%; Score 2068; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-203; Matches 387; Conservative 0; Mismatches 0;
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Patent No. 5652352
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STREET: 1840 DeHavilland
CITY: Thousand Oaks
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 annino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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COUNTRY: U.S.
ZIP: 91320-1789
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Best Local Similarity
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Patent No. 6663485
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
CURRENT APPLICATION WIMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
FRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 5
LENGTH: 585
MANNEL PATENTING PATES DATE: 2011-05-25
MANNEL PATENTING PATENTING PATES DATE: 2011-05-25
MANNEL PATENTING PATES DATES DATES DATES DATES DATE
                                                 SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,746
FILING DATE: 19-DEC-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: CARTOLL' Peter G.
REGISTRATION NUMBER: 32,837
REFRENCE/POCKET NUMBER: 32,837
RELEPAR: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: Amino acids
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1.8e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 387; Conservative 0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1 n
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; ORGANISM: Homo Sapiens
US-10-153-064-5
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Sequence 2. Application US/08702572

Patent No. 5965386

GENERAL INFORMATION:
APPLICANT: Ribert, Sarah C
TITLE OF INVENTION: Yeast Strains and Modified Albumins
ITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
STATE: Pennsylvania
COUVERY: USA
                                                                                                                                                                                                                                                                                                   Length 585;
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                                                                                                                      /note= "Alternative C-termini of
HSA(1-n)"
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natural HSA"
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MicroSoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,572
FILING DATE: 11-NOV-1996
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
                                                                                          NAME/KEY: Region
LOCATION: 369.419
OTHER INFORMATION: /
OTHER INFORMATION: H
FEATURE:
NAME/KEY: Region
LOCATION: 1.585
OTHER INFORMATION: /
OTHER INFORMATION: n
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Patent No. 6274305

Patent No. 6274305

GENERAL INFORMATION:

APPLICANT: Soneneschein, Carlos

APPLICANT: Socto, Ana M.

TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

CONTRY: United States of America

SIP: 94104

COMPUTER: READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
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Pred. No. 1.8e-203;
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100.0%; Pred. No. ...
0; Mismatches
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Query Match
Best Local Similarity 100.
Matches 387; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-572-2
                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Sequence 123, App Sequence 92, Appl Sequence 2, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 3, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 1, Appli

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PER PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE: 06-MR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 16-MR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
FILING DATE: 29-APR-1989
PRIOR APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION NUMBER: US 07/775952
FILING DATE: 26-APR-1990
PRIOR APPLICATION NUMBER: US 07/775952
FILING DATE: 29-CCT-1991
APPLICATION NUMBER: US 07/775952
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APPLICATION NUMBER: US 07/775952
FILING DATE: 29-CCT-1991
APPLICATION NUMBER: US 07/775952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
                                                            US-08-256-938-2
US-08-256-938-4
US-08-98-1689-16
US-09-984-186-16
US-09-987-956A-3
US-10-133-064-89
US-08-433-064-89
US-08-448-196A-3
                 US-10-153-064-92
US-10-153-064-101
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US-08-448-196A-5
US-08-448-196A-4
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US-08-448-196A-7
US-08-134-638-1
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92H832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08153799;
Patent No. 5766883;
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Heal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Swope, R Hain
REGISTRATION WUMBER: 24864
REFERENCE/DOCKET NUMBER: 9218:
TELECOMMUNICATION INFORMATION:
TELEFAX: (908) 771 6159
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 animo acids
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TOPOLOGY: linear
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Sequence 5, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 77, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 96, Appli
Sequence 165, Appli
Sequence 113, Appli
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                                                                                                                                                                    April 19, 2004, 11:40:29 ; Search time 59.3186 Seconds (without alignments) 336.813 Million cell updates/sec
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Sequence 2,
Sequence 5,
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// Cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
// Cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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2068
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Best Local Similarity 100.0%; Score 70; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels 0
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100.0%; Score 70; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels (
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human derived fusion protein
US-10-425-000-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15

US-10-433-108-34

US-10-433-108-34

SEQUENCE 34, Application US/10433108

PUBLICATION No. US20040053370A1

GENERAL INFORMATION:

TITLE OF INVENTION: GLP-1 FUSION PROTEINS

FILE REPERENCE: K-13991

CURRENT APPLICATION NUMBER: US/10/433,108

CURRENT FILING DATE: 2003-05-29

PRIOR FILING DATE: 2000-06-12

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PATENT NOS: 35

TERNOTH: 585

TERNOTH: 585

TYPE: RRI HOMO SAPIENS

USGANISM: HOMO SAPIENS

USGANISM: HOMO SAPIENS

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US-10-424-999-11

Sequence 11, Application US/10424999

Publication No. US20040052810A1

GENERAL INFORMATION:
APPLICANT: Nesbit, Mark

APPLICANT: Nesbit, Mark

APPLICANT: Blanche, Francis

TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for INVENTION: Using Them to Inhibit Anglogenesis

TITLE OF INVENTION: Using Them to Inhibit Anglogenesis

FILE REFERENCE: ST01027-A

CURRENT APPLICATION NUMBER: US/10/424,999

CURRENT APPLICATION NUMBER: 10/233,675

PRIOR APPLICATION NUMBER: 10/233,675

PRIOR APPLICATION NUMBER: 10/233,675

WUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin version 3.2

SEQ ID NO 11

LENGTH: 585
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Sequence 31, Application US/10425000
Sequence 31, Application Wo. US20040052777A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neabit, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Stancis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
TITLE OF INVENTION: Anglogenesis
TITLE OF INVENTION: Anglogenesis
CURRENT PILING DATE: 2003-04
CURRENT FILING DATE: 2003-04-29
RECORD PRIOR PARILY NUMBER: 10/233,675
FRICK FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 105
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100.0%; Score 70; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0;
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                 | PRIOR APPLICATION NUMBER: 60/229, 358 |
| PRIOR FILING DATE: 2000-04-12 |
| PRIOR FILING DATE: 2000-12-21 |
| PRIOR FILING DATE: 2000-12-21 |
| PRIOR PEPLICATION NUMBER: 60/199, 384 |
| PRIOR FILING DATE: 2000-04-25 |
| NUMBER OF SEQ ID NOS: 2267 |
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| SEQ ID NO 18 |
| LENGTH: 585 |
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| PRIOR APPLICATION NUMBER: 60/199, 384 |
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100.0%; Score 70; DB 11; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels C
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100.0%; Score 70; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels 0
APPLICANT: Sadeghi, Homa
APPLICANT: Prior, Christopher P.
ITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF542
CURRENT APPLICATION NUMBER: US/09/832,501
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.1
SED ID NO 18
LENGTH: 585
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US-09-833-118-18
Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
SERBRAL INFORMATION:
APPLICANT: Haseltine, William A.
TITE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF544
CURRENT APPLICATION NUMBER: US/09/833,118
CURRENT APPLICATION NUMBER: G0/229,358
PRIOR APPLICATION NUMBER: G0/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE PARENTIN VOICE: 2.1
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Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PFS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
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US-09-833-118-18
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US-09-832-501-18
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Gaps

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Sequence 445, Application US/09932322
Publication No. US20030194743A1
Publication No. US20030194743A1
Publication No. US20030194743A1
APPLICANT: Dyax Corp.
APPLICANT: Beltzer, Uames P.
APPLICANT: Petter, M. Daniel
APPLICANT: Petter, M. Daniel
APPLICANT: Petter, M. Daniel
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REPERENCE: Dyx-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT PILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 4455
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 70; DB 10; Length 585; Best Local Similarity 100.0%; Pred. No. 0.00018; Matches 14; Conservative 0; Mismatches 0; Indels (
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Sequence 18, Application US/09833117
Publication No. US20030171267A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Sadeghi, Homa
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Abbumin Fusion Proteins
FILE REFERENCE: PF543
CURRENT APPLICATION NUMBER: US/09/833,117
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PARENT VET. S85
LENGTH: 585
LENGTH: 585
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US-09-832-501-18
Sequence 18, Application US/09832501
Publication No. US20030199043A1
GENERAL INFORMATION:
APPLICANT: Ballance, David J.
APPLICANT: Sleep, Darrell
APPLICANT: Turner, Andrew J.
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Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-833-117-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT CORGANISM: HomoSapiens US-09-932-322-445
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US-09-932-322-445
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                                                           COMPUTER READABLE

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Pacentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/984,010

FILING DATE: 21-May-2002

PRIOR APPLICATION NUMBER: US 09/091,873

FILING DATE: 19-DEC-1996

APPLICATION NUMBER: PCT/GB96/03164

FILING DATE: 19-DEC-1996

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: SS amino acid

STRANDEDNESS: cUnknown>

MOLECTLE TYPE: protein

HYPOTHETICAL: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-984-010-26

100.08; SCOME 70; Inear

US-09-984-010-26

100.08; Pred. NO. 0.00018;

100.09; Pred. NO. 0.00018;
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100.0%; Score 70; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels
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Publication No. US20030125247A1

GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Reselvine, William A.
ITILE OF INVENTION: Albumin Fusion Proteins
FILE REFRENCE: PF545
CURRENT FILING DATE: 2001-04-12
FRIOR APPLICATION NUMBER: US/09/833,041
CURRENT FILING DATE: 2000-04-12
FRIOR PILING DATE: 2000-04-12
FRIOR APPLICATION NUMBER: 60/199,384
FRIOR APPLICATION NUMBER: 60/199,384
FRIOR APPLICATION NUMBER: 60/199,384
FRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 585
                     COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; ORGANISM: Homo Sapiens
US-09-833-041-18
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US-09-833-117-18
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RESULT 5
US-09-932-613-445
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US-09-984-010-26
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TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF SECUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/10074956
| Publication No. US20020193332A1
| GENERAL INFORMATION:
| APPLICANT: Hedley, Mary Lynne
| TILLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
| FILE REPERENCE: 08191-02201,
| CURRENT APPLICATION NUMBER: US/10/074,956
| PRIOR APPLICATION NUMBER: 06/268,175
| PRIOR PILING DATE: 2001-02-12
| NUMBER OF SEQ ID NOS: 29
| SOFTMARE: FastSEQ for Windows Version 4.0
| ENGTH: 268
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100.0%; Score 70; DB 13;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 241
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US-09-929-552-2
Sequence 2, Application US/09929552
Patent No. US20020123080A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 14; Conservative
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US-10-074-956-27
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US-10-074-956-28
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Publication No. US20030091565A1
Publication No. US20030091565A1
Publication No. US20030091565A1
Publication No. US20030091565A1
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Pleming Tony J.
APPLICANT: Fleming Tony J.
APPLICANT: Fleming Tony J.
APPLICANT: Rosen, Craig A.
ITILE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON FILE REFERENCE: Dyx-025.1 US
CURRENT APPLICATION NUMBER: US/09/9922,613
MINDING DATE: 2001-08-17
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Publication No. US20030104578A1
GENERAL INFORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 585;
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100.0%; Pred. No. 0.00018;
ive 0; Mismatches 0;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/769,746
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: MBRI-02584
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                       TELEFAX: (415) 397-8338
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Best Local Similarity 100.0
Matches 14, Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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; ORGANISM: HomoSapiens
US-09-932-613-445
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April 19, 2004, 12:00:25; Search time 5.89474 Seconds (without alignments) 654.724 Million cell updates/sec
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2: / cgr2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
3: / cgr2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
4: / cgr2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
5: / cgr2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
6: / cgr2_6/ptodata/2/pubpaa/PCTUS_NEW_PUB.ppp:*
7: / cgr2_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
8: / cgr2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
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13: / cgr2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
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17: / cgr2_6/ptodata/2/pubpaa/USO0_PUBCOMB.ppp:*
18: / cgr2_6/ptodata/2/pubpaa/USO0_NEW_PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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70
1 TVATLRETYGEMAD 14
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                | Sequence 24, Appl | Sequence 27, Appl | Sequence 28, Appl | Sequence 2, Appli | Seguence 445, App | Sequence 26, Appl | Sequence 18, Appl | Sequence 18, Appl | Sequence 445, App | 18, 7            | Sequence 18, Appl | Sequence 18, Appl | 11,              | 31,              | Sequence 34, Appl |
|----------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|
| ID                         | US-10-074-956-24  | US-10-074-956-27  | US-10-074-956-28  | US-09-929-552-2   | US-09-932-613-445 | US-09-984-010-26  | US-09-833-041-18  | US-09-833-117-18  | US-09-932-322-445 | US-09-832-501-18 | US-09-833-118-18  | US-09-833-245-18  | US-10-424-999-11 | US-10-425-000-31 | US-10-433-108-34  |
| DB<br>DB                   | 13                | 13                | 13                | σ                 | 10                | 10                | 10                | 10                | 10                | 10               | 11                | 11                | 12               | 12               | 12                |
| *<br>Query<br>Match Length | 195               | 241               | 268               | 585               | 585               | 585               | 585               | 585               | 585               | 585              | 585               | 585               | 585              | 585              | 585               |
| &<br>Query<br>Match        | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0            | 100.0             | 100.0             | 100.0            | 100.0            | 100.0             |
| Score                      | 7.0               | 70                | 70                | 70                | 70                | 70                | 70                | 70                | 70                | 70               | 70                | 70                | 70               | 70               | 70                |
| Result<br>No.              | н                 | 7                 | m                 | 4                 | ស                 | 9                 | 7                 | ۵                 | σı                | 10               | 11                | 12                | 13               | 14               | 15                |

| Sequence 5, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 1, Appli<br>Sequence 15, Appli<br>Sequence 15, Appli | DISORDERS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ; Length 195;<br>5; Indels 0; Gaps 0;                                                                   | DISORDERS                                                                                                                                                                                     |
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| 13 US-10-153-064-5 14 US-10-153-604A-5 14 US-10-319-263-1 14 US-10-319-263-2 14 US-10-319-263-2 14 US-10-414-469-2 15 US-10-413-832-1 15 US-10-413-832-2 15 US-10-413-832-2 15 US-10-413-832-2 15 US-10-413-832-2 15 US-10-413-832-2 15 US-10-413-832-2 16 US-10-413-832-2 17 US-10-313-678-2 18 US-10-153-604A-7 19 US-10-35-604A-7 19 US-10-35-604A-7 19 US-10-35-604A-7 19 US-10-237-866-2 14 US-10-237-866-2 14 US-10-237-866-2 15 US-10-237-866-2 16 US-10-237-866-2 17 US-10-237-866-2 18 US-10-237-866-2 19 US-10-433-108-15 10 US-10-433-108-15 10 US-10-433-108-15                                                                                                                                                                          | HPS6  TREATING BLADDER  10/074,956  3,175  Braion 4.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 0.0%; Score 70; DB 13<br>0.0%; Pred. No. 5.1e-0<br>e 0; Mismatches<br>14                                | 10074956<br>12A1<br>nne<br>s OF TREATING BLADDER<br>11<br>US/10/074,956                                                                                                                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | US-10-074-956-24  US-10-074-956-24  Publication No. US2002019332AL  GENERAL INFORMATION:  TIPLE OF INVENTION:  FILE REFERENCE: 08191-022001  CURRENT FILING DATE: 2002-06-11  CURRENT FILING DATE: 2002-06-12  CURRENT FILING DATE: 2001-02-02  NUMBER OF SEQ ID NOS: 29  SOFTWARE: FASTEROFE  SOFTWARE: FASTEROFE  TYREE: RATESOF FOR WINDOWS VARIABLE  TREE: PRICE TIME OF SEQ ID NOS: 29  SEQ ID NO SEQ ID NOS: 29  SEQ ID NO SEQ ID NOS: 29  TYREE: PRICE TIME OF SEQ ID NOS: 29  SEQ ID NO SEQ ID NOS: 29  TREE: PRICE THE OF SEQ ID NOS: 29  SEQ ID NOS: 24  LENGTH: 195  TYREE: PRICE THE OF SEQ ID NOS: 29  SEQ ID NOS: 24  LENGTH: 195  TYREE: PRICE THE OF SEQ ID NOS: 29  SEQ ID NOS: 24  LENGTH: 195  TYREE: PRICE THE OF SEQ ID NOS: 29  SEQ ID NOS: 20  SEQ ID NOS: 24  LENGTH: 195  TYREE: PRICE THE OF SEQ ID NOS: 29  SEQ ID NOS: 20  SEQ ID NOS: 24  LENGTH: 195  TYREE: PRICE THE OF SEQ ID NOS: 29  SEQ ID NOS: 20  SEQ ID | Query Match Best Local Similarity 100 Matches 14; Conservative Oy 1 TVATLRETYGEMAD Db 76 TVATLRETYGEMAD | RESULT 2 US-10-074-956-27 Sequence 27, Application US, Publication No. US2002019333; GENERAL INFORMATION: APPLICANT: Hedley, Mary LYT TITLE OF INVENTION: METHODS FILE REFERENCE: 08191-02200 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                         |                                                                                                                                                                                               |

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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concataener. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthitis, asthma, sepsis, cirrhosis, dermatitis, psoriacis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple scherosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                               Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 4-5; 89pp; English.
                                                                                                                                                                                                        Aziz N,
                                                    14-JUL-2000, 2000US-0218381P.
18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
                    16-JUL-2001; 2001WO-US022263.
                                                                                                                                                                                                          Hedley ML, Urban R,
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                                                                                                                                                                    (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 241 AA;
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Chen H, Etemad-Moghadam B,

Gaps . 0 Query Match 100.0%; Score 70; DB 5; Length 241; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 14; Conservative 0; Mismatches 0; Indels

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1 TVATLRETYGEMAD 14

100 TVATLRETYGEMAD 113 ઠ g Search completed: April 19, 2004, 11:51:17 Job time : 9.23453 secs

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diabetes; uveitis; coeliac disease
                                                                                                                                                                                                                                                                                                                     or autoimmune disorders.
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Best Local Similarity
                                                                                                                                                                                                              (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 236 AA;
                                                   WO200206316-A2.
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                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                              the internitor retained to movel numban secretical polypoptides. The polypoptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypoptide. The polypoptides are also useful for dentifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypoptide wectors comprising the nucleic acids encoding the polypoptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                        Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel human secreted polypeptides.
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100.0%; Pred. No. 8.8e-05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 205; 765pp; English.
Novel human secreted protein #365.
                                                                                                                                                                                                                                                    rang Yr, Liu C, Drmanac RT,
                                                                                                                                                          16-APR-2001; 2001WO-US008656
                                                                                                                                                                                    18-APR-2000; 2000US-00552929
26-JAN-2001; 2001US-00770160
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                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 214 AA;
                                                                                                      WO200179449-A2.
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                                                                              Homo sapiens
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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concataent. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermaticis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a peptide described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
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100.0%; Pred. No. 9.8e-05;
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                                                                 14-JUL-2000; 2000US-0218381P.
18-MG-2000; 2000US-0226382P.
66-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
16-JUL-2001; 2001WO-US022263
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The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having a badder disorder, and administering; (a) an isolated mucleic acid (NI) comprising an un-methylated CpG sequence to the mammal; (b) an isolated nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal; or (c) a peptide that binds to a melanocortin receptor to the mammal. The method is useful for modulating immune response in a mammal having a bladder disorder, where administration of (NI) results in an amelioration of of one or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (NI) results in a decrease in tumour size or activity).

Or for modulating immune response in a mammal having interstitial or the modulating immune to a Thi response). The method is also useful for modulating immune response to a Thi response). The method is also useful for modulating immune response in a mammal having bladder disorder interstitial cysticis or associated with a disorption of the integrity of incerstitial cysticis or associated with a disorption of the integrity of the bladder lining. This is the amino acid sequence of human serum all munim residues 1-195 that can be used in the creation of melanocyte stimulating hormone (alpha-MSH) concatamers resulting in secretion of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating immune responses in a mammal with a bladder disorder e.g. bladder cancer, by administering nucleic acids comprising un-methylated CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to the mammal.
Gaps
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Mismatches
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                                        1 TVATLRETYGEMAD 14
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    14; Conservative
                                                                          76 TVATLRETYGEMAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HEDL/) HEDLEY M L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002193332-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                     ABU10022;
    Matches
                                                                                                                                          RESULT 11
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The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA, to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Bach HSA fragment was synthesised from overlapping oligonuclectide fragments that were extended. This sequence represents the sequence of the HSA fragment HSA-I encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression vector, yeast host cells carrying the recombinant expression vector and the process for producing human serum albumin in the yeast host cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                 Recombinant; human serum albumin; HSA; yeast codon bias; host cell; overlapping oligonucleotide; expression vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 70; DB 3; Length 204; 100.0%; Pred. No. 8.3e-05;
                                                                                                                                                       Yeast codon-biased recombinant HSA protein fragment HSA-I.
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                                                                                                                                                                                                                                                                                                                                                                                   BIOENGINEERING CO LTD.
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                                                                     AAY83947 standard; protein; 204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU29874 standard; protein; 214
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                                                                                                                                                                                                                                                                                                                               98CN-00102506.
                                                                                                                                                                                                                                                                                                                                                         98CN-00102506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     especially in secretory mode
TVATLRETYGEMAD 89
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA10092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                    (HAIJ-) HAIJI
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                                                                                                                                                                                                                             Homo sapiens.
Synthetic.
                                                                                                                             28-JUL-2000
                                                                                                                                                                                                                                                                                                                              17-JUN-1998;
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                                                                                                AAY83947;
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Matches
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                                          RESULT 12
AAY83947
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Gaps

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Length 195;

100.0%; Score 70; DB 7; Length 19 ilarity 100.0%; Pred. No. 7.9e-05; Conservative 0; Mismatches 0; Indels

Local Similarity nes 14; Conserv

Query Match Best\_Loca Matches

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent or physiological interactions of the polypeptide. Vectors comprising the for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to compress them are also useful for producing the proteins. The proteins are useful in genetic vaccination, teeting and therapy, and can be used as nutritional supplements. They may be used to increase stem cell candon to requise the mematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
                                                                                                                                                                                                                                                                                                                  ö
        nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. RAUZSGIO-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
physiological interactions of the polypeptide. Vectors comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation, haematopoiesis, nerve tissue regeneration;
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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                                                                                                                                                                                                                                                                       100.0%; Score 70; DB 4; Length 156; 100.0%; Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU33271 standard; protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted protein #3762.
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                            1 TVATLRETYGEMAD 14
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                                                                                                                                                                                                                                                                                              Local Similarity 100.
Les 14; Conservative
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                                                                                                                                                                                                                                 Sequence 156 AA;
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                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-melanocyte stimulating hormone; rhemn's distriction asthma; cirrhosis, dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; disabetes; uveitis; coeliac disease.
AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation; autoimmune disease; gene therapy; sepsis;
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Pred. No. 7.9e-05;
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                                                                                                                                         Score 70; DB 4; Lr
Pred. No. 6.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA017048 standard; protein; 195 AA
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18-AUG-2000, 2000US-0226382P.
06-OCT-2000, 2000US-023880P.
29-DEC-2000, 2000US-0258764P.
14-UNN-2001, 2001US-0298317P.
                                                                                                                                                         100.08;
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                                                                                                                                                                                                                       14; Conservative
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Best Local Similarity
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Best Local Similarity
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                                                                                              Sequence 156 AA;
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                                                                                                                                                                                                                       Matches
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AA017048
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Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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Les 14, Conservative
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                         2001-514838/56
                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                 Liu C,
    (HYSE-) HYSEQ INC
                              N-PSDB; AAI82561.
                                                                                                                                           Sequence 124 AA;
                                                                                                                                                                                                                                                                                        WO200179449-A2.
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Best Local S
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                                                                                                                                                                 Matches
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberran expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used an untritional supplements. They may be used to increase stem cell proliferation; to requiate haematopolesis, and in bone, cartilage, tenden and/or nerve tissue growth or regeneration; immune suppression and/or attitude as antitional engineers. Autusential inflammantory agents; and in treatment of leukaemias. Autusells proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 70; DB 4; Length 134; Best Local Similarity 100.0%; Pred. No. 5.2e-05; Matches 14; Conservative 0; Mismatches 0; Indels
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 134 AA;
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                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to pytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 16522; 1399pp + Sequence Listing; English.
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                                                                     Tang YT, Liu C, Drmanac RT;
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26-JAN-2001; 2001US-00770160.
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The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the antibodies to the polypeptides are useful for with altered levels of polypeptide. The polypeptides are also useful for with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agoniers and antagoniers) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or

Drmanac RT;

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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18-MAY-2000; 2000US-00577409
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18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
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  Homo sapiens.
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                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptidac therapy; stem cell growth factor; hacmatopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                            Human polypeptide SEQ ID NO 18316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-00577409.
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N-PSDB; AAI84355.
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                                                                                                                                                                                                                                                           Homo sapiens.
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                        AA001996 standard; protein; 119 AA
                                                                                                                                                                                                Human polypeptide SEQ ID NO 15888.
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18-MAY-2000; 2000US-00577409.
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 1 TVATLRETYGEMAD 14
                                                                                                                                                                  (first entry)
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N-PSDB; AAI81927.
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                                                                                                                                                                                                                                                                                                       Homo sapiens.
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inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                        100.0%; Score 70; DB 4; Length 114; 100.0%; Pred. No. 4.3e-05; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.5e-05;
tive 0; Mismatches 0;
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18-MAY-2000; 2000US-00577409.
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Matches 14; Conservat
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N-PSDB; AAI84377.
                                                                                                          Local Similarity
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                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, itssue growth factor activity, immunomodilatory activity and activity, insue growth factor activity, immunomodilatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence date for this patent did not form part directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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Claim 20; SEQ ID NO 15888; 1399pp + Sequence Listing; English.
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Best Local Similarity 100.'
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of cher cytokines in other cell populations. The polynucleotides and polynpeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                      Aap90387
Aap900389
Aap900390
Aau290391
Aau290391
Aap32019
Aap32019
Aap93344
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Aar96562
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                                                      AAP90389
AAP90390
AAP90390
AAU29976
AAU29976
ABB32019
ABG7281
ABG7281
AAP90383
AAP90388
AAR96389
AAR26607
AAR26607
AAR26607
AAR26007
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AAO20111
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18-MAY-2000; 2000US-00577409
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  WPI; 2001-514838/56.
N-PSDB; AA189519.
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WO200164835-A2
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                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                       protein search, using sw model
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AAOO4446
AAOO1996
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AAO16984
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AAU29942
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AAU29708
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2001s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
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Maximum Match 100%
Listing first 45 sv
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Search completed: April 19, 2004, 12:00:01 Job time: 7.40351 secs

Best Loca Matches

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIR=ATC 19089 / CB15;

NIETINE=21173699; PubMed=11259647;

Nietnam W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Risen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Botocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBOY R.T., Dodson R.C., Durkin A.S., Gwhin M.L., Haft D.H.,

A DeBOY R.T., Vanter J.C., Shappiro L., Fraser C.M.;

Complete genome sequence of Caulobacter crescentus.";

T. Complete genome sequence of Caulobacter crescentus.";

RISE, AE005809; AAK23323.1; -.

RISE, AE005809; AAK23323.1; -.

RISE, GO: 00005824; F:APP binding; IEA.

GO; GO:0005824; F:APP binding; IEA.

GO; GO:0006820; F:Slycine-tRNA ligase activity; IEA.

GO; GO:0006820; F:Slycine-tRNA ligase activity; IEA.

GO; GO:0006820; F:Slycine-tRNA aminoacylation; IEA.

INTERPO; IRRO0211; tRNA synt Zf; 1.

RICEPO; IRRO0211; tRNA synt Zf; 1.

RICEPO; IRRO0211; tRNA synt Zf; 1.

RICEPO; IRRO0211; Sylvine-tRNA ligase activity; EA.

RICEPO; IRRO0211; LRNA synt Zf; 1.

RENEY SPOROS1; RNA Synt Zf; 1.

RENEY SPOROS1; RNA Synt Zf; 1.

RENEY SPOROS1; RNA SYNTHGB: II GLYAB; 1.

RENEY SPOROS1; AATRNA_IIGASE II GLYAB; 1.

RW Aminoacyl-tENA synthetese; Complete proteome.

SEQUENCE 692 AA; 76060 WW; 3CDB48730D097846 CRC64;
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MEDLINE=22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
                   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobactera. VCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; PubMed=11572948;
Omura S. 1kreda H., 1shikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M., Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 16; Length 692;
Pred. No. 1.3e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Best Local Similarity 50.00,
Best Local 7; Conservative
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
BRBL; APRO13885; AABS4246-1; -.
PTR; H89009; H89009.
WormPep; R08F11.4; CE12586.
GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
InterPro; IPR000051; SAM bind.
SEQUENCE 354 AA; 3936§ MW; CB422510DFA3ECOA CRC64;
"Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003),
EMBL; BX640432; CE38219.1; -.
Complete protecom.
SEQUENCE 281 AA; 30591 MW; C97P4A51E40E3315 CRC64;
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                   Score 42; DB 16; Length 281; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%; Score 41; DB 5; Length 354; 75.0%; Pred. No. 63;
                                                                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of C. elegans cosmid RO8F11.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
R08Fil.4 protein.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
synthetase, beta subunit.
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                                                                                                                                                                                                                                                                             1; Mismatches
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
                                                                                                                                                                                                                Similarity 66.7%;
Similarity 66.7%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                266 ATLRRLYGELID 277
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Minx P.;
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Best Local Similarity
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01-JUN-2001 (
01-JUN-2001 (
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Glycyl-tRNA s
CC1342.
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None:

RESULT 13
1001889
1001888
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Q9A8L1

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RESULT 14 Q9A8L1

Best Loc Matches

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Gaps

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STRAIN-TOHANG TO ATCC BAA-589 / NCTC 13251;

WENDINE-2237954, PubMed-1291071;

WENDINE-2237954, PubMed-1291071;

A Harris D.E., Holden M., Prescon A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M., Churcher C.M., Bentley S.D., Mungall K.L.,

A Gardeno-Tarraga A.M., Temple L., James K., Harris B., Quall M.A.,

A Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Harris D.E., Holden M., Cronin A., Davis P., Doggett J.,

A Harris D.E., Monle S., Norberzak H., Ol'Neil S., Ormond D., Price C.,

A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

A Barris S., Simmond M., Skelton J., Squares R., Squares S., Stevens K.,

Annin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

R Bordetella parapertussis and Bordetella bronchiseptica.";

BENEL, BX640414; CAE41588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkilla 1282/ ArCC BAA-587;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MATCH D.E., Holden M., Temple L., James K., Harris B., Quail M.A.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Aktin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella parapertussis.
Bacteria; Potteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBL_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 16; Length 271;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative exported protein.
                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                  271 AA
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                                                                                                                     PRT;
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256 ATLRRLYGELID 267
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Matches 8; Conservative
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                                                                                                                     PRELIMINARY;
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                                                                         RESULT 11
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=22827954; PubMed=12910271;

RA PATKINII U., Sebainia M., Preston A., Murphy L.D., Thomson N.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Eather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Rabinowitsch E., Rutter S., Sanders M., Squares D., Seeger K.,

RA Juwin L., Whitehead S., Barrell B.G., Maskell D.J.;

R. "Comparative analyte's of the genome sequences of Bordetella pertussis,

RT "Comparative analyte's of the genome sequences of Bordetella pertussis,

RT Bordetella parapertussis and Bordetella bronchiseptica.";

NRE Genet 35:32-40(2003).

DE EMBL; Exception and Bordetella bronchiseptica.";
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                                                                                                                                                                                                                                     MEDLINE=21595285; PubMed=11759840; Kaneko T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligenaceae, Bordetella.
NCBI_TaxID=518,
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Pred. No. 29;
1; Mismatches 4; Indel8
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Pred. No. 31;
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                                                                                                                       p. (strain PCC 7120).
Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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PIR; AH2433; AH2433.
Hypothetical protein; Complete proteome.
Hypothory 252 AA; 29440 MW; 3ABDCE406345B50F CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative exported protein.
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein All5024.
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Best Local Similarity 66.7.
Best Local 8; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                  NCBI_TaxID=103690;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Bacteria; Cya
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Q7WIF5 Q7WIF5;

RESULT 10 Q7WIFS

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RESULT 6

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-FVB/N; TISSUE-Salivary gland;

Attausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Attausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Attachul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhar N.K.,

Attachul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soates M.B., Bonaldo M.F., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RABAR S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards S.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Tones S.J., Marra M.A.;

RA Generation and Initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 23;
3; Mismatches 2; Indels
                                                                                                                         60.0%; Score 42; DB 11; Length 116; 61.5%; Pred. No. 13; ative 3; Mismatches 2; Indels
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STRANIE-YOR/N; TISSUE-Salivary gland;
Stransberg N.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058868; AAH55858.1; -.
Hypothetical protein 27722 MW; 09421AC54204F79B CRC64;
SEQUENCE 201 AA; 22722 MW;
Nature 420:563-573(2002).
EMBL; AKO41748; BAC31052.1; -.
MGD; MGI.1350360; Phem.
GO; GO:005522; C:intracellular; IDA.
SEQUENCE 116 AA; 12587 MW; 7638C7C4CFD2CDDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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61.5%; Pred
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Best Local Similarity 61.59
                                                                                                                                                                                                                                       and mouse cDNA sequences.
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                                                                                                                         Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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QBYMBO;
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ID Q8YMI
AC Q8YMI
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MEDLINE-CSTEL/61; TISSUE-Liver;

MEDLINE-CSTEL/61; TISSUE-Liver;

The FAUTON Consortium,

The FAUTON Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

B the RIKEN Genome Exploration Research Group Phase I & II Team;

B MCD, 700 tull-length CONNS.";

B MCD, MCI: 87991; Alb.

A GO, GO: 0006810; P: transport IEA.

B CO, GO: 0006810; P: transport JRA.

B PRODON; PRO0273; transport JRCt; 3.

R PRODON; PRO0273; ALBUMIN; 3.

R SMART; SMO0103; Albumin; 1.
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SERALIE-CS/BL/60; TISSUE=Thymus;
MEDIINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
                           Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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                           Indels
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SEQUENCE 608 AA; 68722 NW; 292F600EED3A61B4 CRC64;
                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pan hematopoletic expression.
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    Pred, No. 13;
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                        2,
61.5%;
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 61...
8; Conservative
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69 IPNLRENYGELAD 81
                                                                 2 VATLRETYGEMAD 14
                        Conservative
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    Best Local Similarity
Matches 8; Conserv
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QBC9N0;
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Q8C7H3,
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RESULT 7

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SEQUENCE FROM N.A.

STRAIN=CSTBEL/6J, TISSUE=Thymus;

A The FARNICATOR Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration of Team;

A the RIKEN Genome Team;

A the
                             01-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Albumin (Fragment).
Mam musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 11 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                            D SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=129/SVEYTACIBE;
Van Reeth T., Dreze P.L., Gabant P., Szpirer J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ277794; CACG1903.1;
CACKITACACHIAN SPACE; IEA.

R GO; GO:0005386; F:carrier activity; IEA.

R GO; GO:0005810; P:tansport; IEA.

R InterPro; IPR000264; Serum albumin.

R Pfam; PF00273; transport prot;
R Pfam; PF0013; Aransport prot;
R PRINTS; PR00103; ALBUMIN.

R SMART; SM0103; ALBUMIN.

T NON_TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.7%; Score 46; DB 11; Length 205; 61.5%; Pred. No. 4.5; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 AA; 23624 MW; 0A982E85C7474BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 61.5%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 IPNLRENYGELAD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VATLRETYGEMAD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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QBC7C7
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Component in murine infection with Schistosoma mansoni.";

Albumin precursor homolog is a novel T helper cell immunogenic egg component in murine infection with Schistosoma mansoni.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBU databases.

Bub., AF418550, AAL08579.1; ---

R GO, GO:0005615; C:extracellular space; IEA.

R GO; GO:0005615; C:extracellular space; IEA.

R GO; GO:0005610; P:transport, IEA.

R GO; GO:000610; P:transport, IEA.

R HOLLY PRO0273; transport prot; 3.

R PROME PRO0273; ALBUMIN; 1.

R PRODOM; PRO02486; Serum albumin; 1.

R PRODOM; ALBUMIN; 3.

R RRAET; SR00121; ALBUMIN; 3.

R REQUENCE GOS AA, G8225 MW; RSEABB28EICGGES4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma mansoni (Blood fluke).
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                       Felis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                           Reininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P., Rumpold H., Valenta R., Spitzauer S.; Ruscherichia coli expression and purification of recombinant calbumin: 1gs recognition, induction of basophil activation and Jumphoproliferative responses in atopic parients "; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 81.4%; Score 57; DB 6; Length 584; Local Similarity 78.6%; Pred. No. 0.15; les 11; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 49; DB 5; Length 608; 61.5%; Pred. No. 4.2; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 584 AA; 65908 MW; B51002F12902C9CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q55VB7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                            Last sequence update)
Last annotation update)
  584 AA
                                                     Created)
  PRT;
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8; Conservative
                                               01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TVATLEBTYGEMAD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 TVASLRDKYGEMAD 89
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101 IPTLRDSYGELAD 113
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PRELIMINARY;
                                                                                                                                        Albumin (Fragment).
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                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                    NCBI TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6183;
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Length 576;
                                                                                                                                           65002 MW; F85733E99AE37F04 CRC64;
                                                                                                                                                                                          DB 11;
                                                                                                                                                                                          65.7%; Score 46;
Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERUMALBEMIN.
PRODOD; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
                                                                                                                                                                                          Query Match
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Q835p5 enterococcu Q835p5 enterococcu Q866d5 streptococcu Q86017 streptococcu Q8613 plasmodium Q9113 deinococcus Q9123 thodothermu Q92gf5 heliobacill Q20143 caenorhabdi Q918p5 enterococcus Q9cel0 lactococcus Q9cel0 lactococcus Q9cel0 lactococcus Q9cel0 lactococcus Q913b5 thodobacter Q9719 thodobacter Q9719 thodobacter Q9719 thodobacter Q9719 thodobacter Q9719 calcobacter Q9719 thodobacter Q9719 for coccus Q918b5 streptococcus Q918b5 mucosal dis Q9265 bovine vira Q9265 bovine vira Q9265 bovine vira Q8x5p0 ralstonia s Q8x5p0 ralstonia s Q8x71 pyrobaculum g8x77 ralstonia s Q7x23 nonomuraea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 1.1. Carlotter of the month                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 70; DB 4; Length 396; 100.0%; Pred. No. 0.00047; ive 0; Mismatches 0; Indels
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to serum albumin precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI; 396 AA
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    Q913FP
Q97RZ1
Q87BZ1
Q87BZ1
Q96413
Q97Z1G3
Q97Z1G3
Q97Z87
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Best Local Similarity 100.0
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Q8IUK7
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Q7YSG3
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Q7yag3 felis silve
Q95yb7 schistosoma
Q8cg74 mus musculu
Q8c77 mus musculu
Q8c77 mus musculu
Q8c707 mus musculu
Q8c707 mus musculu
Q8cmb0 anabaena sp
Q7wf5 bordetella
Q7wf5 bordetella
Q7wf13 bordetella
Q7w613 bordetella
Q7w613 bordetella
Q7w613 bordetella
Q78311 caulobacter
Q8298 streptomyce
Q855f7 leptospira
                                                                                                                                                                                                                                                           April 19, 2004, 11:37:09; Search time 5.40351 Seconds (without alignments) 817.479 Million cell updates/sec
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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70
1 TVATLRETYGEMAD 14
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           - protein search, using sw model
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1: Sp. archea:*

2: Sp. bacteria:*

3: Sp. fungi:*

5: Sp. invan:*

5: Sp. invan:*

6: p. invan:*

7: Sp. organelle:*

8p. organelle:*

8p. phage:*

8p. phage:*

8p. phage:*

8p. virus:*

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Q97XSG3
Q97XSG3
Q95XBG3
Q8C7H3
Q8C7H3
Q8C7H3
Q8C7H3
Q77XMB
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                        Run on:
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Gaps

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Query Match
57.1%; Score 40; DB 1; Length 409;
Best Local Similarity 70.0%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps
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<sup>2</sup> VATLRETYGE 11 : |||:|||| 217 IMTLRKTYGE 226

Search completed: April 19, 2004, 11:52:48 Job time : 3.02124 secs

of 2-oxoglutarate

Ź 409

STANDARD;

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SCIENCE 269:496-512(1995).

-!- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF 3 ENZYMATIC COMPONENTS: 2-OXOGLUTARATE DEHYDROGENASE (E1), DIHYDROCLOPAMIDE SUCCINYLITRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: SUCCINY1-COA + dihydrolipoamide = COA + S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINERA, TW20 / ATCC 51907;
STRAINERA, TW20 / WALC
STRAINERA, TW20 / WALC
BLEISCHMANN R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
MCKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterlack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                               Haemophilus influenzae.
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellacee, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           succinyldihydrolipoamide.
-!- COFACTOR: Contains 1 covalently bound lipoyl cofactor (By
                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dihydrolipoamide succinyltransferase component
SUCB OR HI1661.
                                                                                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, SS0917; S50317.

GermOnline; 142863; -
GermOnline; 142863; -
GGO, S0004801; GCV2.
GO, GO:0004375; F:glycine dehydrogenase (decarboxylating) act. . .; IEB.
GO; GO:0006730; P:one-carbon compound metabolism; IGI.
InterPro, IRPRO3437; GDC-P.
TIGREAMS; TIGR00461; GCP-P: 1.
TIGREAMS; TIGR00461; GCPP; 1.
Oxidoxal phosphate; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: The glycine cleavage system catalyzes the degradation of glycine. The P protein binds the alpha-amino group of glycine through its pyridoxal phosphate cofactor; COC2 is released and through its pyridoxal phosphate sofactor; COC2 is released and the remaining methylamine moiety is then transferred to the lippanide ocfactor of the H protein.

-!- CATALYTIC ACTIVITY: Glycine + lippylprotein = S-
aminomethyldihydrolippylprotein + CO(2).
-!- CATALYTIC ACTIVITY: Glycine + lippylprotein = S-
-!- SUBCELLULAR LOCATION: Milcochondrial (By similarity).
                                                                                                                                                                                                             MEDLINE=90120340; PubMed=7498764; Sinclair D.A., Dawes I.W.; Sinclair D.A., Dawes I.W.; "Genetics of the synthesis of serine from glycine and the utilization of glycine as sole nitrogen source by Saccharomyces cerevisiae."; Genetics 140:1213-1222(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITÓCHONDRION (PÔTENTIAL).

GLYCINE DEHYPROGENARE [DECARBOXYLATING]

PYRIDOXAL PHOSPEATE (BY SIMILARITY).

114451 MW; F4D526422808DA041 CRC64;
                                                                                                                                                                                                                                                                                                           SECURIOR FROM N.A.
SECURIOR FROM N.A.
SETRAIN-S286C / AB972;
MEDLINE-97313268; PubMed-9169872;
MEDLINE-97313268; PubMed-9169872;
Bowman S., Churcher C.M., Baddock K., Brown D., Chillingworth T., Bowman S., Dedman K., Dew J., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
With nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
Nature 387:90-93 (1997).
                                        precursor
system P-
                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1; Length 1034;
Pred. No. 14;
Mismatches 2; Indels
   Last sequence update)
Last annotation update (decarboxylating), mitochondrial (decarboxylase) (Glycine cleavage
01-FEB-1996 (Rel. 33, Last sequence up 10-007-2003 (Rel. 42, Last annotation Glycine dehydrogenase (decarboxylation (EC 1.4.4.2) (Glycine decarboxylation)
                                                                           protein)
GCV2 OR GSD2 OR YMR189W OR YM9646.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U20641; AAB18933.1; -. EMBL; Z47815; CAA87810.1; -.
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=4932;
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similarity).
-!- PATHRAY: Tricarboxylic acid cycle.
-!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral symmetry (By similarity).
-!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
-!- SIMILARITY: Contains 1 lipoyl-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Acyltransferase; Lipoyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPOYL (POTENTIAL).
POTENTIAL.
POTENTIAL.
3FBF62BC17433839 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR001078; 20xoacid dh.
InterPro; IPR001089; Biotin lTpoyl.
InterPro; IPR004167; E2_binding.
InterPro; IPR003016; Lipoyl_BS.
InterPro; IPR003016; Lipoyl_BS.
InterPro; IPR00555; SucB.
Ffam; PF00189; 2-oxoacid dh; 1.
Ffam; PF02817; e3_binding; 1.
ProDom; PF001115; 20xoacid dh; 1.
INTERPAMS; IIGR01347; sucB.
PROSITE; PS00189; LIPOYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U32839; AAC23307.1; -. PIR; D64135; D64135. HSSP; P07016; 1C4T. TIGR; HI1661; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ricarboxylic acid cycle;
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380
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384
409 AA;
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TVARLDDTYGDM 1017

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RESULT

8; Conservative 1 TVATLRETYGEM 12

Matches

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Local Similarity

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  -i- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-i- SUBCELDULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Plasma.
-i- ALLERGEN: Causes an allergic reaction in human. Binds IgE. Partially heat-labile allergic with the bind-egg syndrome.
-i- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-i- SIMILARITY: Contains 3 albumin domains.
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EMBL; V00381; CAA23680.1; --
EMBL; V00381; CAA23680.1; --
EMBL; V00381; CAA23680.1; --
EMBL; V00381; CAA23680.1; --
ENGLS; ERGH, ERGH
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Pred. No. 7.9;
2; Mismatches 3; Indels
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ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
BY SIMILA
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GCSP YEAST
CCSP YEAST
AC P49095;
DT 01-PEB-1996 (Rel. 33, Created)
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tes 8; Conservative
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615 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21381307; PubMed=11488669;
Quirce S., Maranon F., Umpierrez A., de las Heras M.,
Fernandez-Caldas E., Sastre J.;
"Chicken serum albumin (Gal d 5*) is a partially heat-labile inhalant and food allergen implicated in the bird-egg syndrome.";
Allergy 56:754-762(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Alpha-livetin) (Allergen Gal d 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 608;
Pred. No. 5.1;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUELiver;
Cassady A.I., Salklid C.K., Baverstock P., Wallace J.C.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5BB497A282411AB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 78:1060-1066(1977)
COPPER.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF.
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MEDLINE=78019943, PubMed=911327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68718 MW;
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53.8%;
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Best Local Similarity
Matches 7; Conserv
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MEDLINE=7901617; PubMed=80265;

Apyagi Y., Ikenaka T., Ichida F.,
Apyagi Y., Ikenaka T., Ichida F.,
Apyagi Y., Ikenaka T., Ichida F.,
Topper (II)-binding ability of human alpha-fetoprotein.";

Cancer Res. 38:3483-3486(1978).

Cancer Res. 38:348417.

Cancer Res. 38:3484FVVDB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   SEQUENCE OF 1-18, AND PROCESSING.
MEDLINE=77249657; PubMed=893447;
Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
"Rat liver pre-proalbumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
messenger RNA.";
                                                                                                                                                                                                                                     SEQUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.;
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                                                                                                                                    SEQUENCE OF 25-222.

MEDLINE=78109429; PubMed=564345;
Isemura S., Ikanaka T.;
"Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage of rat serum albumin.";
J. Biochem. 83:35-48(1978).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 166-174.
TISSUE-Plasma,
MEDILINE-819805; PubMed-2437111;
Carraway R.B., Mitra S.P., Cochrane D.E.;
Carraway R. B., Mitra S.P., Cochrane O.E.;
Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(8).";
J. Biol. Chem. 262:5968-5973(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROTENSIN-RELATED PEPTIDE.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
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HSSP; P02768; IE7B.
InterPro; IFR000264; Serum_albumin.
Pfam; PF00427; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom, P000248; Serum_albumin; 1.
SWART; SM01038 ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
SIGNAL
PROPED
PROPED
CHAIN
25 608 SERUM ALBUMIN.
 Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
                                                                                                            Biol. Chem. 252:6846-6855(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V01222; CAA24532.1; -.
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166
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212
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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P02770; P11382;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratius norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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BEDLINES 1223722, PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
"Nucleotide sequence of cloned rat serum albumin messenger RNA.";
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3E556B0DD1A1F4FF CRC64;
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SERUM ALBUMIN.
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ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 5;
4; Mismatches
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99 IPSLREHYGDLAD 111
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Best Local Similarity
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SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND DEVELOPMENTAL
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Musinge; MusicBl_TaxID=10090;
                                                                                                  Nicholson R.H., Pantano S., Bliason J.F., Galy A., Weiler S., Kaplan J., Hughes M.R., Ko M.S.; "Phemx, a novel mouse gene expressed in hematopoietic cells maps the imprinted cluster on distal chromosome 7."; Genomics 68:13-21(2000).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 6).
MEDILIBE21575689; PubMed=11718897;
Robb L., Tarrant J., Groom J., Ibrahim M., Li R., Borobakas B.,
Wright M.D.;
                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
STRAIN=129/Sv. and C57BL/6;
MEDLINE=20377495; PubMed=10915772;
Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O. Davies K., Reinhardt R., Reik W., Walter J.;
"Sequence conservation and variability of imprinting in the Beckwith-Wiedemann Syndrome gene cluster in human and mouse.";
Hum. Mol. Genet, 9:1829-1841(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=1;
IsoId=Q9JHH2-2; Sequence=VSP_003939;
                                                                                        MEDLINE=20408882; PubMed=10950922;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adulthood.
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CONFLICT
                 VARSPLIC
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=09JHH2-6; Sequence=VSP_003939, VSP_003940, VSP_003942; TISSUB SPECIFICITY: Expressed exclusively in hematopoietic tissues. Expression detected in spleen, thymus, bone marrow and peripheral blood leukocytes but not in heart, brain, lung, liver, kidney or testis.

DEVELOPMENTAL STAGE: Expressed from early embryogenesis through to
"Molecular characterisation of mouse and human TSSC6: evidence that SSSC6 is a genuine member of the terraspanin superfamily and is expressed specifically in haematopoietic organs."; Biochim. Biophys. Acta 1522:31-41(2001).
                                                                                                                                                                                                                                                STRAIN=C57BL/6; TISSUE=Spleen;
MEDLINE=21290667; PubMed=11396961;
MEDLINE=21290667; PubMed=11396961;
Marada Y., Harada H., Downing J.R., Kimura A.;
"A hematopoietic-specific transmembrane protein, Art-1, is possibly regulated by amll.";
Blochem. Blophys. Res. Commun. 284:714-722(2001).
-i. SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
-i. ALTERNATUE PRODUCTS:
Event=Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9JHH2-4; Sequence=VSP_003939, VSP_003942, VSP_003943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9JHH2-5; Sequence=VSP_003939, VSP_003940, VSP_003941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9JHH2-3; Sequence=VSP_003939, VSP_003941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comment=Additional isoforms seem to exist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=09JHH2-1; Sequence=Displayed;
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EMBL; AF175771; AAG27268.1; -. EMBL; AJ251788; CAB94716.1; -.

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                                                                                                                                                                                                                                                Missing (in isoform 1, isoform 2, isoform 3, isoform 4 and isoform 5).

/FITIGE-VSP 003939.
Missing (in isoform 4 and isoform 5).
/FITIGE-VSP 003940.
Missing (in isoform 2 and isoform 4).
/FITIGE-VSP 003941.
DCIQSIRNYTWINTHYSIASILICTSL -> IPWFPDPGTQPL
QWDLGWAGASMPC (in isoform 3 and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haldwin G.S., Weinstock J.;

Baldwin G.S., Weinstock J.;

Nuclectide sequence of porcine liver albumin.";

Nuclectide sequence of porcine liver albumin.";

Nucleic Acids Res. 16:9045-9045(1988).

Include the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmocile pressure of blood.

In SINCELNILAR LOCATION: Secreted.

In ISSUE SPECIFICITY: Plasma.

SINLIARITY: Belongs to the ALB/AFP/VDB family.

SIMLIARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 1; Length 256;
Pred, No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28905 MW; A20EF0F6248FF67A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            /Frid=vSP 003942.
Missing (In isoform 3).
/Frid=vSP 003943.
Q -> L (IN REF. 1).
Y -> F (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P08835; Q29018;
01-NOV-1968 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                               GO; GO:0016021; C:integral to membrane; NAS. GO; GO:0005622; C:intracellular; IDA. InterPro; IPR008952; Tetraspanin.
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                                                                                                                                                                      Alternative splicing.
                                                                                                                                                                                                                       POTENTIAL
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MEDLINE-89016582; PubMed-3174440;
EMBL, AJ251835, CAB94777.1; EMBL, AJ279791, CAB94719.1; EMBL, AJ279792, CAB94719.1; EMBL, AJ279793, CAB94721.1; EMBL, AJ279794, CAB94722.1; EMBL, AJ279794, CAB94722.1; EMBL, AJ279795, CAB94723.1; EMBL, AY291455, AAK8130.1; EMBL, AY291455, AAK83110.1; CABP, MGD, MGI:1350360, Phemx.
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80 TIATVREAHGLMA 92
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                                                                                                                                                             InterPro; IPR008
Transmembrane; A
TRANSMEM 15
TRANSMEM 61
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Sus scrofa (Pig)
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TRANSMEM
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STRAIN=New Zealand white; TISSUE=Liver;
Sheffield W.P., Syed S., Schuyler P.D.;
Submitted (DEC-1994) to the BMEL/Genbank/DDBJ databases.
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- Subming capacity for water, Ca(2+), Na(+), K(+), fatty acids,
--- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
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G9JHH2; Q92G9; Q9ESH0; Q9HQ9; Q9JHR0; Q9JHR1; Q9JHR2; Q9JHS8; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phemx protein (AML1-regulated transmembrane protein 1).
PHEMX OR TSSC6 OR ARTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.4%; Score 43; DB 1; Length 608;
63.6%; Pred. No. 3.3;
.ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Repeat, Signal, Copper.
By SIMILARITY.
BY SIMILARITY.
SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 3.
COPPER.
BY SIMILARITY.
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HSSP; PO2768; 1BTB.

InterPro; IPR00264; Serum albumin.
Pfam; PF00272; ranapport prot; 3.
PRINTS; PR00302; SERUMALEUMIN.
ProDom; PD002486; Serum albumin; 1.
SWART; SM00103; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; SIGNAL
I B SS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; SIGNAL
I B SSO0212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; SIGNAL
I B ST SIMILA
DOMAIN 22 608 SERUM ALB
DOMAIN 212 397 ALBUMIN 2
DOMAIN 404 595 ALBUMIN 3
METAL
DISULFID 77 86 BY SIMILA
DISULFID 194 195 BY SIMILA
DISULFID 269 277 BY SIMILA
DISULFID 269 277 BY SIMILA
DISULFID 302 313 BY SIMILA
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Best Local Similarity 63.6%;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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-> D (IN REF. 6).
-> I (IN REF. 6).
292F7C7EED3A61B4 CRC64;
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ID ALBU RABIT

AC P4906;

PT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum albumin precursor.

GN ALB.

OS Oryctolagus cuniculus (Rabbit).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebra:

OC Mammalia; Butheria; Lagomorpha; Leporidae; Oryctox

NCBI_TAXID=9986;

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RP SEQUENCE FROM N.A.
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or send an email to license@isb-sib.ch)
                                                                                        EMBL, AJ011413; CAA06617.1.

EMBL, AX010025; BAB26650.1; --

EMBL, MAC111, AAA37190.1; --

EMBL, MI6111, AAA37190.1; --

EMBL, MIG187991, ABL, Interpret Drot; January, SMO0246; Serum albumin, I.

FRONET, SMO0103; ALEUMIN, 3.

FROSTIF, PROOC25; SERUM ALBUMIN; J.

EMBRAT, SMO103; ALEUMIN, 3.

EMBRAT, SMO103; ALEUMIN, 3.

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DOMAIN 25 205 ALEUMIN 1

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Best Local Similarity
Matches 8; Conserv
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STRAIN-C7STBL/6J; TISSUE=Tongue;
STRAIN-C7STBL/6J; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alizawa K., Izawa M., Nishi K., Kiyoswa H., Konno J., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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    Repeat; Signal; Copper; Allergen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.1%; Score 54; DB 1; Length 608; ilarity 71.4%; Pred. No. 0.028; Conservative 3; Mismatches 1; Indels
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ID ALBU MOUSE

OP7724, Q61802,

DT 01-APR-1988 (Rel. 07, Created)

DT 15-UUL-1999 (Rel. 38, Last sequence update)

DT 15-WAR-2004 (Rel. 43, Last annotation update)

Serum albumin precursor.

GN ALB OR ALBI OR ALB-1.

OS Mus musculus (Mouse).
                                                              SERUM ALBUMIN
                      POTENTIAL.
Metal-binding, Lipid-binding;
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608 AA;
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RA Schrigh L. W., Scaubil F., Burnki R., Tomita M., Nagner L., Washio T.,

R. Barkes J., Deciden I., Durgon W. Namon, "Endance Ben, Book B.

R. Barkes J., Deciden I., Durgon W. Namon, "Endance Ben, Book B.

R. Burcherschi M.J. Balt C., Flätcher C., Philas M., Garlboddi M.,

R. Burcherschi M.J., Balt D., Mashina M., Mazzarzlii J., Nochbests P.,

R. Mandel M., Salo K., Schonbach C., Seys T., Shibata W., Scrocch K. P.,

R. Mandel M., Salo K., Schonbach C., Seys T., Shibata W., Scrocch K. P.,

R. Mandel M., Salo K., Schonbach C., Seys T., Shibata W., Scrocch K. P.,

R. Manner R. D. Condan M., Mashina M. M., Seasol M., Schasolo M.,

R. Manner R. D. Collins P. M. Mandel M., Robert C. M., Schuler G. D.,

R. Manner R. D. Collins P. M. Mandel M., Robert M. M., Garling M., Manner R. D.,

R. Manner R. D. Collins P. M., Sanger M. M., Scherger M., Schemer C. P., Shah N. K.,

R. Manner R. D. Collins P. M., Sanger M. M., Scherger M., Schemer P. P.,

R. Manner R. D. Collins P. M., Scherger M. M., Garlin G. M., Manner M. M.,
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TISSUB-SAlivary gland;

TISSUB-Salivary gland;

MEDLINE=94201492; PubMed=7512102;

MEDLINE=94201492; PubMed=7512102;

MEDLINE=94201492; PubMed=7512102;

Machl S., Edwelger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Edwelger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Edwelger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Edwelger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Edwelger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Edwelger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Edwelger C., Sperr W.R., Pandpain as a cross-reactive

J. Allergy Clin. Immunol. 93:614-627(1994)

Muchl S., Edwelger C., Sperr W.R., Pandpain and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

J. Sumitar Location. Secreted.

J. TISSUE SPECIFICITY: Plasma.

J. AllERGEN: Gauses an allergic reaction in human.

J. AllERGEN: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseesisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   Dixon J.W., Sarkar B.;
"Isolation, amino are sequence and copper(II)-binding properties of
"pepride (1-24) of dog serum albumin.";
J. Biol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Heart;
MEDLINE=99163340; PubMed=9504812;
MEDLINE=99163340; PubMedler C.H.;
MEDLINE=99163340; PubMedler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
                                    Caris familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                              Pandjaitan B., Swobda I., Brandejeky-Pichler F., Rumpold H., Valenta R., Spitzauer S., Escherichia Goli expression and purification of recombinant dog albumin, a cross-reactive animal allergen.";

J. Allergy Clin. Immunol. 105:279-285 (2000).
                                                                                                                                                            Hilger C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
     Serum albumin precursor (Allergen Can f 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL, Y1737; CAA76841.1; -
EMEL, S72946 AAB30434.1; -
ESSP, P02768; 1578.
HSC-2DPAGE; P49822; DOG.
INTERPRO; PRO00264; Serum albumin.
PEAM; PRO0273; transport Drot; 3.
PRINTS; PRO0802; SERUMALBUMIN.
SWART; SMO0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 25-48.
MEDLINE=75011422; PubMed=4414013;
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                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Beagle, TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 25-38.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=9615;
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstated not the between the Swiss Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Gaps
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BY SIMILARITY.
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SERUM ALEUMIN.
ALEUMIN 1.
ALEUMIN 2.
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COPPER.
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InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALEBUMIN.
ProDom; PD002486; Serum_albumin; 1.
ProDom; PD002486; Serum_albumin; 1.
PROSTITS; S800212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; 8.
SIGNAL
19 RS SIMILAL
PROPEP 19 608 SERUM ALBUMIN; 1000AIN 25 205 ALBUMIN; 1000AIN 404 595 ALBUMIN; 27 27 COPPER.
DISULPID 99 115 BY SIMILAN
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ID ALBU CANFA

AC P49822: 077705; Q9TS24;

AC D-0CT-1996 (Rel. 34, Cre.)

DT 16-0CT-2001 (Rel. 40, Las

DT 10-0CT-2003 (Rel. 42, Las
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RESULT

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send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown J.R.;

"Structure of serum albumin: disulfide bridges.";

"Structure of serum albumin; disulfide bridges.";

Fed. Proc. 33:1389-1389(1974).

-! FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-! SUBCELLUIAR LOCATION: Secreted.

-! TRSUB SPECTIFICITY: Plasma.

-! ALLERGEN: Causes an allergic reaction in human.

-! SIMILARITY: Belongs to the ALB/AFP/VDB family.

-! SIMILARITY: Contains 3 albumin domains.
                                                                SEQUENCE OF 1-32.
MEDLINE=80024278; PubMed=488109;
McGillivray R.T.A., Chung D.W., Davie E.W.;
"Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin.";
Eur. J. Biochem. 98:477-485(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND REVISIONS TO 118-119 AND 180.
MEDLINE-91083649; PubMed=2260975;
"Itayama K., Akashi S., Furnya M., Fukuhara K.-I.;
"Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";
Biochem. Biophys. Res. Commun. 173:639-646(1990).
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MEDIATRE=88267456; PubMed=3389500;
HEIGH J.C., Lin F.P., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical isoclectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";
Anal. Biochem. 170:1-8 (1988).
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MEDLINE=77134075; PubMed=843354;
Patterson J.E., Geller D.M.;
"Bovine microsomal albumin: amino terminal sequence of bovine
                                                                                                                                                                                                                                                                                              MEDLINE-82023364; PubMed=7283978;
Reed R.G., Putnam F.W., Peters T. Ur.;
"Sequence of residues 400-403 of bovine serum albumin.";
Bjochem. J. 191:867-868(1980).
            Wu H.T., Huang M.C.; "The complete cDNA sequence of bovine serum albumin."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214. Brown J.R.;
"Structure of bovine serum albumin.";
Fed. Proc. 34:591-591(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
                                                                                                                                                                                                                                             Brown J.R.;
Submitted (APR-1975) to the PIR data bank.
SEQUENCE FROM N.A., AND VARIANT THR-214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vilbois F.;
Submitted (AUG-1998) to Swiss-Prot
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REVISIONS TO 190-195.
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EMBL; X8989; CAA41735.1; -.
REMIL; X8989; CAA41735.1; -.
REMIL; X8989; CAA41735.1; -.
REMIL; AFF42068; AAN17824.1; -.
REMIL; AFF42068; AAN17824.1; -.
REMIL; AFF42068; AAN17824.1; -.
REMIL; AFF642068; AAN17824.1; -.
REMIL; AFF642068; AAN17824.1; -.
REMIL; AFF00273; Cransport prot; Remil Proton; PRO02466; Serum albumin.
REMINTS; PRO02465; AERUMALBUMIN.
REMINTS; PRO0212; ALBUMIN; 3.
RECSITE; PS00212; ALBUMIN; 3.
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Felis slivestris catus (Cat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.
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C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

ST -> TS (IN REF. 6).

ST -> TS (IN REF. 6).

K -> R (IN REF. 6).

K -> R (IN REF. 6).

K -> R (IN REF. 6).
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ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
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01-FEB-1996 (Rel. 33, Last sequence update)
10-FCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Fel d 2).
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Pred. No. 0.005
2; Mismatches
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SEQUENCE FROM N.A.
MEDLINE=96194824; PubMed=8647469;
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PIR, 534053; ABHOS.
HSSP; P02768; IRTB.
Interpro; IPRO00264; Serum albumin.
Fam; PRO0273; transport prot; 3.
PRINTS; PR00802; SERUMALEUMIN.
PRODOM; PS002486; Serum albumin; 1.
SMART; SMO0103; ALBUMIN; 3.
Metal-binding; Lipid-binding; Reper; SIGNAL
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MEDLINE-9345495, PubMed-8344282,

MEDLINE-9345495, PubMed-834482,

MEDLINE-9346495,

MEDLINE-9346495, PubMed-834649,

MEDLINE-9346495,

MEDLINE-93464
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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                ALBUMIN 1.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTY HORSE STANDARD; PRT; 607 AA. P35747; 601-JW-194 (Rel. 29, Created) 10-JW-1994 (Rel. 29, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Serum albumin precursor (Allergen Equ. c 3).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Boe.
Repeat; Signal; Copper; Allergen. By SiMILARITY.
BY SIMILARITY.
SERUM ALBUMIN.
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85.7%; Pred. No. 0.0014;
rative 1; Mismatches 1; Indels
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                        ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY)
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Best Local Similarity 85.79
Watches 12; Conservative
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VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106. MEDLINE=91062352; Pubmed=2247440; Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J., Watkins S., Putnam F.W.; "Mutations in genetic variants of human serum albumin found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90115852; PubMed=2104980;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
"Albumin Redhill (-1 Arg, 320 Ala--Thr): a glycoprotein variant of
"muman serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOWAGOME-3 HIS-23; KOMAGOME-2 ARG-152 AND KOWAGOME-1 GLU-396.

KOMAGOME-2 ARG-152 BubMed-1946412;

Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsind Y.-1., Amaki I., Putnam F.W.;

"Genetic variants of sour albumin in Americans and Japanese.";

Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
                                                                                                                                                                                                                                                                             VARIANT CANTERBURY ASN-337.
MEDLINE-87157744; PubMed=3828358;
MEDLINE-87157744; PubMed=3828358;
MEDLINE-87157744; PubMed=3828358;
"Albumin Canterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin.";
Biochim. Biophys. Acta 912:191-197(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
MEDLINE=90115905; PubMed=2404284;
Arai K., Madison J., Shhamuzu A., Putnam F.W.;
"Point substitutions in albumin genetic variants from Asia.";
Prog. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=91296740; PubMed=2068071;
Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
Minchiotti L., Putnam F.W.;
Adonor splice mutation and a single-base deletion produce two
carboxyl-terminal variants of human serum albumin.";
Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
                                                                                                                                                                              Jacobsen C.;
"Lysine residue 240 of human serum albumin is involved in high-affinity binding of bilirubin.";
Biochem. J. 171:453-459(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
MEDLINE=89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M., Neel J.V., Sakurabayashi I., Putnam F.W.;
"Point substitutions in Japanese alloalbunins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88068523; PubMed=3479777;
Takshashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M., Satoh C., Neel J.V.; Takahashi I., Isobe T., Putnam F.W., Fujita M., Amino acid substitutions in inherited albumin variants from Amerindian and Japanese populations.";
Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
                                                        Saber M.A., Stockbauer P., Moravek L., Meloun B., "Disulfide bonds in human serum albumin."; Collect. Czech. Chem. Commun. 42:564-579(1977).
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Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990)
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Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
Electrophoresis 15:1459-1465(1994)
                                                                                                                                     BILIRUBIN-BINDING SITE.
MEDLINE=78186630; PubMed=656055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION OF VARIANT REDHILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT VENEZIA.
                                      DISULFIDE BONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE=90098888; PubMed=2602160;
Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
"Nucleotide and deduced amino acid sequence of sheep serum albumin.";
Nucleic Acids Res. 17:10495-10495 (1989).

-I. FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmocic pressure of blood.
-I. SUBCELLULAR LOCATION: Secreted.
-I. TISSUE SPECIFICITY: Plasma.
-I. SIMILARITY: Belongs to the ALB/AFP/VDB family.
                                                                                                                                                                 MEDLINE=92190239; PubMed=1347703; Minchiotti L., Crespeau H., Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H., Rochu D., Porta F.; "Two alloabumins with identical electrophoretic mobility are produced "Two alloabumins with identical electrophoretic mobility are produced
                                                   Peach R.J., Brennan S.O.;
"Structural characterization of a glycoprotein variant of human serum
albumin: albumin Casebrook (494 Asp-->Asn).";
Blochim. Blochys. Acta 1097:49-54(1991).
                                                                                                                                                                                                                                                                                                        Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
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0
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PIR; S06936; ABSHS.
HSSP; P02768; LBCB.
InterPro; IPR00264; Serum albumin.
PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDon; PD02466; Serum albumin; 1.
ProDon; P002466; Serum albumin; 1.
PROSITE; P600212; ALBUMIN; 3.
PROSITE; P600212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
SIGNAL
PROPEP
19 BY SIMILARITY.
                                                                                                                              [25]
VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
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(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607 AA
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                VARIANT CASEBROOK ASN-518.
MEDLINE=91316157; PubMed=1859851;
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01-APR-1990 (Rel. 14, Last seq
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                  Local Similarity
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P14639;
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ALBU_SHEEP
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TISSUELIVET FROM N.A.

TISSUELIVET, and Skeletal muscle;

TISSUELIVET, bubMed=12477921;

MEDLINE=238257;

PubMed=12477921;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Holeh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Torahiyuk S., Caraninci P., Prange C.,

Brownstein M.J., Usdin T.B., Torahiyuk S., Caraninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzaten P.H.,

Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunzaten P.H.,

Richards S., Worley K.C., McKetteman M., Madan A., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko, V., Bouffard G.G.,

Rhichards A., Grimwood J., Schmutz J., Myers R.M.,

Butkefield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The chemistry and physiology of the human plasma proteins, pp.23-40, Pergamon Press, New York (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE OF 1-26 FROM N.A.
MEDLINE=86140099; PubMed=2419329;
Urano Y., Watanabe K., Sakai M., Tamaoki T.;
urano Indumin gene. Characterization of the 5' and 3' flanking regions and the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
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Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
    IISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.,
Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lysine residue 199 of human serum albumin is modified by
                                                                                                                                                             Huang M.C., Wu H.T.; "The cDNA sequences of human serum albumin."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 25-609.
MEDLINE=7618790; PubMed=1225573;
Meloun B., Moravek L., Kostka V.;
"Complete amino acid sequence of human serum albumin.";
FEBS Lett. 58:134-137(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Menaya J., Parrilla R., Ayuso M.S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                        [6]
SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown J.R., Shockley P., Behrens P.Q.; (In) Bing D.H. (eds.);
The chemistry and physiology of the hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=76257808; PubMed=955075; Walker J.E.;
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FEBS Lett. 66:173-175(1976).
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TISSUE-Liver;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-82105994; PubMed-6275391;
Dugaiczyk A., Law S.W., Dennison O.E.;
"Nucleotide sequence and the encoded amino acids of human serum
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SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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P02768; 095574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0; 21-UUL-1986 (Rel. 01, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
E45C871A670E740B CRC64;
COPPER (BY SIMILARITY).
BILIRURIN (POTENTIAL).
BY SIMILARITY.
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MEDLINE=86196112; PubMed=3009475;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Query
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rattus norv bovine vira herpes simp lactobacill porcine rot

| 35 50.0 238 1 YAKA_SCHPO Q09921 schizosacch 35 50.0 251 1 VACJ_ECOLI P76506 eschorichia 35 50.0 251 1 YACJ_ECOLI P74506 eschorichia 35 50.0 251 1 YACJ_ERIFL P43262 shigella £1 35 50.0 305 1 PLSX_CHLPN Q92606 chlamydia ₱ P35 50.0 331 1 DMPL_PSESP P719730 pseudomonas 50.0 394 1 SRAJ_YEAST P55359 saccharomyc 35 50.0 429 1 SDAC_ERIFL Q83659 eschorichia 35 50.0 429 1 SDAC_ERIFL Q836400 shigella £1 35 50.0 429 1 TIG_ETRO Q95314 streptomyce 35 50.0 555 1 DNLT_ARCFU Q95314 streptomyce 35 50.0 555 1 DNLT_ARCFU Q29632 archaeoglob | MANUACKU STANDARD; PRT; 600 AA.  MANUACKU STANDARD; PRT; 600 AA.  MANUACKU STANDARD; PRT; 600 AA.  MANUACKU STANDARD; SCREATED  10.1007/1997 (Rel. 35, Created)  10.1007/1997 (Rel. 35, Created)  10.1007/1997 (Rel. 35, Last sequence update)  Macaca mulata (Rhesus macaque)  Macaca mulata (Rhesus macaque)  Macaca mulata (Rhesus macaque)  Maryicas Macaca:  MANUACKU STANDARDA (Macaca)  MARCALINE STAIL971 (Macaca)  MANUAL MACACACACACACACACACACACACACACACACACACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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A; Molecule type: DNA
A; Residues: 1-1034 «SIN»
A; Cross-references: EMBL:U20641; NID:g676869; PIDN:AAB18933.1; PID:g676871
A; Sinclair, D.A.; Hong, S.P.; Dawes, I.W.
R; Sinclair, D.A.; Hong, S.P.; Dawes, I.W.
A). Microbiol. 19, 611.623, 1996
A; Title: Specific induction by glycine of the gene for the P-subunit of glycine decarbox A; Reference number: S70896; MuID:96228709; PMID:8830251
A; Accession: S70896
                            A;Cross-references: EMBL:Z47815; NID:g642280; PIDN:CAA87810.1; PID:g642281; MIPS:YMR189q
Absorbated to the EMBL Date Library, Rebruary 1995
A; Reference number: 859809
A; Reference number: 859810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, ;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. ;Reference number: A95000; MUID:21357209; PMID:11463916
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A;Cross-references: GB:AE005672; PIDN:AAK74786.1; PID:914972111; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown
A;Molcoule type: DD
A;Residues: 1-77;V',79-121,'VS',124-247,'L',249-381,'T',383-517,'H',519-1034 <SIW>
A;Cross-references: EMBL:UZ0641
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Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
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A;Cross-references: SGD:S0004801
A;Map position: 13R
C;Keywords: phosphoprotein; pyridoxal phosphate; transferase
F;773/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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Pred. No. 36;
2; Mismatches 2; Indels
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Search completed: April 19, 2004, 12:02:23 Job time : 2.70637 secs

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Query Match
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Jubec-1993
C;Accession: S1571; A05078; Ā13451
R;Cassady, A.I.; Salkild, C.K.; Baverstock, P.; Wallace, J.C.
submitted to the EWBL Data Library, July 1991
A;Reference number: S15571
A;Rolecule type: mRNA
A;Residues: 1-615 < CAS>
A;Cross-references: EMBL:X60688; NID:g63747; FIDN:CAA43098.1; FID:g63748
A;Residues: 1-615 < CAS>
A;Cross-references: EMBL:X60688; NID:g63747; FIDN:CAA43098.1; PID:g63748
A;Residues: 1-615 < CAS>
A;Cross-references: EMBL:X60688; NID:g63747; PIDN:CAA43098.1; PID:g63748
A;Reference number: A05078; MulD:83161037; PMID:6187737
A;Reference number: A05078; MulD:83161037; PMID:6187737
A;Recession: A05078
A;Residues: 1-28 < CAS>
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Ryanonymous, The C. elegans Sequencing Consortium.

Ryanonymous, The C. elegans Sequencing Consortium.

Ryanonymous, The C. elegans Sequencing Consortium.

A; Title: Genome sequence of the nematcde C. elegans: a platform for investigating biolog A; Reference number: A75000; MUID: 9969613; PMID: 9851916

A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; Anotes: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; Astatus: preliminary

A; Note: weak similarity to methyltransferases

C; Genetics:

A; Note: weak similarity to methyltransferases

A; Map position: 5
Accessing the control of the control
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C,Species: Caenorhabditis elegans
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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Pred. No. 13;
3; Mismatches 3; Indels
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Pred. No. 11;
1; Mismatches
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Matches 7; Conservative 3
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Matches 9; Conserv
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G8741: 19.

G8741: 19.

G8741: 19.

G8741: 20. Part autobacter crescentus

G19cy1-tRNA synthetase, beta subunit [imported] - Caulobacter crescentus

G19cy1-tRNA synthetase, beta subunit [imported] - Caulobacter crescentus

G19cy1-tRNA synthetase, beta subunit [imported] - Caulobacter crescentus

G19cy1-tRNA synthetase contains and contains a
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A; Molecule type: protein
A; Residues: 19-23, // / .25-30 cROS>
Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
mones (weak bonds with these hormones promote their transfer across the membranes), thy
C; Superfamily: serum albumin, serum albumin repeat homology
C; Superfamily: serum albumin, serum albumin repeat homology
C; Superfamily: serum albumin serum predicted cARO>
F; 1-18 / Domain: signal sequence #status predicted cARO>
F; 2-206 / Domain: serum albumin repeat homology cSA1>
F; 22-38 / Domain: serum albumin repeat homology cSA2>
F; 30-26 / Domain: serum albumin repeat homology cSA3>
F; 30-80 / Domain: serum albumin repeat homology cSA3>
F; 30-80 / Domain: serum albumin serum shount shoulogy cSA3>
F; 30-89 / Domain serum shount serum shount serum shount serum shount serum shount serum shount shoulogy cSA3>
F; 30-89 / Domain serum shount shoulogy cSA3>
F; 30-89 / Domain serum shount serum shoulogy cSA3>
F; 30-80 / Domain serum shount serum shount serum shoulogy cSA3>
F; 30-80 / SA3 /
A;Cross-references: GB:V00381; NID:g63038; PIDN:CAA23680.1; PID:g63039
R;Rosen, A.M.; Geller, D.M.
Biochem. Biochys. Res. Commun. 78, 1060-1066, 1977
A;Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin. A;Reference number: A13451; MUID:78019943; PMID:911327
A;Reference number: A13451
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Pred. No. 20;
2; Mismatches 3; Indels
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A,Gene: CC1342
C,Superfamily: glycine-tRNA ligase beta chain
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673 TLATVRDAMGQVAD 686
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Matches 8, Conservative
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Serum albumin precursor - rat

Nalitarate names preproalbumin
C:Species: Ratus norvegicus (Norway rat)
C:Accession: Asyaria Asyaria Asyaria (Norway rat)
Proc. Mail. Acad. Soil U. S. N. 78, 243-246, 1981
A;Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUD:81223722; PMID:7017712
A;Nolecule type: mRNA
A;Reference number: A93872
A;Nolecule type: Renate, C. D: Donohue, A.M.; Rodkey, U.A.; Alberts, A.W.
U. Biol. Chem. 222, 6846-6855, 1977
A;Nolecule type: Procein
A;No
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A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: 23-288;572-608 <1S2>
A.Mote: 262-Leu was also clound
B.Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A.Title: Copper(II) -binding ability of human alpha-fetoprotein.
A.Reference number: A90758; MUID: 79001617; PMID: 80265
A.Title: Copper(II) - copper binding
B.Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A.Title: Structures of histamine-releasing peptides formed by the action of acid protes
A.Reference number: A45800; MUID: 89341406; PMID: 2474609
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Mol. Cell. Biol. 7, 2425-2434, 1987
Mol. Cell. Biol. 7, 2425-2434, 1987
A;Title: Determinants of rat albumin promoter tissue specificity analyzed by an improve A;Reference number: 157621; MUID:87286876; PMID:3475566
A;Accession: 157621
A;Accession: 157621
    F;27-199/Domain: serum albumin repeat homology <SA1>
F;216-39J/Domain: serum albumin repeat homology <SA2>
F;410-589/Domain: serum albumin repeat homology <SA3>
F;410-589/Domain: serum albumin repeat homology <SA3-5
F;75-84,97-113,112-123,145-190,189-198,221-257,266-274,286-300,299-310,337-382,381-390,
F;261/Binding site: bilirubin (Lys) #status predicted
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Pred. No. 13;
4; Mismatches 2; Indels
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                           60.08;
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                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 53.8
Matches 7; Conservative
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A,Molecule type: protein
A,Residues: 166-173 <CAR>
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A/Status: translation not shown
A/Returs: translation:
A/Crose-references: EMEL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
A/Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mineral
A/Reterence number: A61006, MUID:89269769; PMID:2728927
A/Returs: Serum albumin and its acid hydrolysis peptides dominate preparations of mineral
A/Recession: A61006
A/Molecule type: protein
A/Residues: 23-51, X', 53-54; XXX09', 146, 'E', 148, 'E', 150-151, 'XVN', 155 <LIM>
A/Residues: 23-51, X', 53-54; XXX09', 146, 'E', 148, 'E', 150-151, 'XVN', 155 <LIM>
A/Reprimental source: dental enamel proteins are also found in bone
C/Comment: Serum albumin synthesized in the liver as preproalbumin. It binds copper, tercid hormones (weak bonds with these hormones promote their transfer across the membra C/Superfamily: serum albumin, serum albumin repeat homology
C/Reywords: carrier protein; duplication; metal binding; plasma
F/11-16/Domain: signal sequence (fragment) #status predicted <SIG>
F/12-2/Domain: propeptide #status predicted <MAT>
F/23-605/Product: serum albumin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Argotherical protein all5024 [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
C.Species: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C.Accession: AH2433
Makazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
NA Res. 8, 205-213, 2001
NA, Reference number: AB1807; MUID:2159285; PMID:11759840
A.Reference number: AB1807; MUID:2159285; PMID:11759840
A.Residues: 1-252 <KUR>
A.Residues: 1-252 <KUR
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Dace: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S01382; Aslono
R;Weinstock, J; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Fitle: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:3174440
                                                                                                                                                                                                                                  Gaps
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0
F;123-296/Domain: serum albumin repeat homology <SA2>
F;315-453/Domain: serum albumin repeat homology (fragment) <SA3>
                                                                                                                                 Score 46; DB 2; Length 453;
Pred. No. 1.7;
2; Mismatches 3; Indels
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Pred. No. 4.9;
1; Mismatches
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                                                                                                                            Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 5
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Best Local Similarity 64.3
Matches 9, Conservative
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Accession: Accession albumin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A05139; 148638
R;Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
Mol. Biol. Evol. 2, 347-358, 1985
A;Title: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudx A;Reference number: A93055; MUID:88216123; PMID:2452956
A;Accession: A05134
A;Accession: A05134
A;Residues: 1-418 cMIN>
A;Residues: 1-418 cMIN>
A;Residues: Lefterances: GB:Mi611; NID:g191764; PIDN:AA37190.1; PID:g191765
B;Boccaccio, C.; Deschatrette, J.; Meunier-Rotival, M.
A;Reference number: 148638; MUID:90269606; PMID:1971802
A;Accession: 148638
A;Accession: 148638
A;Accession: 148638
A;Accession: Lagasa F;27/Binding site: copper (His) #status predicted F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392, RESULT 6
S57632
serum albumin precursor - cat
C;Species Felis allvestris catus (domestic cat)
C;Date: 19-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 20-Aug-1999
C;Accession: 074660, S57632
R;Hilger, C; Grigioni, F: Hentges, F.
Gene 169, 295-296, 1996
A;Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A;Reference number: 074660; MUID:96194824; PMID:8647469
A;Accession: 074660
A;Molecule type: mRNA
A;Residues: 1-608 AHIZ.
A;Accession: 074660
A;Molecule type: mRNA
A;Residues: 1-608 AHIZ.
A;Cross-references: EMBL:X84842; NID:9886484; PIDN:CAA59279.1; PID:9886485
A;Experimental source: liver
C;Comment: This protein is the major protein component in plasma. It functions as a cin has 35 conserved cystesine residues.
C;Superfamily: serum albumin; serum albumin repeat homology
C;Kywords: liver; plasma
F;1-18/Domain: signal sequence #status predicted <BRP>
F;20-202/Domain: serum albumin repeat homology <SA3>
F;20-202/Domain: serum albumin repeat homology <SA3>
F;21-394/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3> ö A,Molecule type: DNA A;Residues: 379-453 <BDC>
A;Residues: 379-453 <BDC>
A;Residues: 379-453 <BDC>
A;Cross-references: EMBL:X13060, NID:g52939, PIDN:CAA31458.1; PID:g899334
C;Superfamily: serum albumin, serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-104/Domain: serum albumin repeat homology (fragment) <SA1> . 0 ; 0 Length 607; Query Match 81.4%; Score 57; DB 2; Length 608; Best Local Similarity 78.6%; Pred. No. 0.023; Matches 11; Conservative 2; Mismatches 1; Indels 0; Indels Score 58; DB 1; Pred. No. 0.015; 2; Mismatches Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative 100 TVASLRDKYGEMAD 113 101 VASLRETYGDMAD 113 2 VATLRETYGEMAD 14 ઠે d ઠે g A Macessain STORE

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A Macessain S A,Molecule type: protein
M,Residues: 25-41 <4815.
R,Streawich, E.; Glimcher, M.J.
Bur. J. Biochem. 191, 47-56, 1990
A,Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A,Reference number: \$10780; MUID:90336641; PMID:2379503
A,Accession: \$10780 A,Title: Biosynthesis of bovine plasma proteins in a cell-free system.
A,Reference number: A91258, MUID:80024278; PMID:488109
A,Accession: A91258
A,Molecule type: protein
A,Residues: 1-32 <AMG>
R;HSieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Blochem. 170, 1-8, 1988
A,Title: Blectroblotting onto glass-fiber filter from an analytical isoelectrofocusing symplement a60808; MUID:88267456; PMID:3389500
A,Reference number: A60808; MUID:88267456; PMID:3389500

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A/Rocessiani 3319-33
A/Rocessiani 3210-33
C/Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the memb)
C/Superfamily: serum albumin, serum albumin repeat homology
C/Reywords: carrier protein; duplication; metal binding; plasma
F/19-24/Domain: signal sequence #status predicted <PRO>
F/25-60/Product: serum albumin repeat homology <ARD>
F/20-393/Domain: serum albumin repeat 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: 834053
R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
A;Hille: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nn
A;Reference number: 834053; MUID:93345495; PMID:8344282
                F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392.
F;263/Binding site: bilirubin (Lys) #status predicted
                                                                                                                                                                      Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 607;
                                                                                                                                                                      Score 62; DB 1; Length 607
Pred. No. 0.0027;
1; Mismatches 0; Indels
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85.7%; Pred. No. 0.0041;
ative 1; Mismatches 1; Indels
                                                                                                                                                                            Query Match

Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S06936
R;Brown, W.M.: Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10493; 1989
A;Title: Nuclectide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: $06936; MUD: 90098888; PMID: 2602160
A;Reference number: $06936; MUD: 90098888; PMID: 2602160
A;Recession: S06936
A;Molecule type: mRNA
A;Residues: 1-607 -8BNO-
A;Cross-references: EMBL:X17055; NID:g1386; PIDN:CAA34903.1; PID:g1387
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membra C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
C;Superfamily: serum albumin #status predicted <AIC-
F;19-24/Domain: serum albumin repeat homology <SA1>
F;20-393/Domain: serum albumin repeat homology <SA2>
F;21-391/Domain: serum albumin repeat homology <SA2>
F;27/Binding site: copper (His) #status predicted
A;Contents: annotation; binding sites
R;Harper, M.E.; Dugaiczyk, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A;Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
A;Reference number: A90028; MUDD:83279982; PMID:6192711
A;Contents: annotation; gene position
R;Walker, J.E.
FEBS Lett. 66, 173-175, 1976
A;Title: Lyahine residue 199 of human serum albumin is modified by acetylsalicyclic acid.
A;Reference number: A46755; MUD:76257808; PMID:955075
A;Contents: annotation
A;Reference number: A66-268, 1992
A;Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phospha
A;Reference number: A56294; MUD:92183881; PMID:1544460
A;Contents: annotation
A;Reference number: A56294; MUD:92183881; PMID:1544460
A;Contents: annotation
A;Reference number: A56294; MUD:92183881; PMID:1544460
A;Contents: annotation
A;Note the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; in p
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A/Gene: GDB:BALB
A/Genes: GDB:BB.Denses: GDB:BB.Denses: GDB:BB.Denses: GDB:BB.Denses: GDB:BB.Denses: GDB:BD.Denses: GDB:BD.De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak C:Comment: A large number of variants of human serum albumin have been described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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A, Molecule type: protein
A, Residues: 25-54;354-357,431-447 < KAU>
A, Residues: 25-54;354-357,431-447 < KAU>
A, Rotadues: 25-54;354-357,431-447 < KAU>
A, Rotadues: 25-54;354-357,431-447 < KAU>
B, Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A, Title: Structures of histamine-releasing peptides formed by the action of acid protes
A, Reference number: A45800; MUID:89341406; PMID:2474609
A, Accession: A45800
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A,Residues: 166-173 <CAR>
F,Rogard, M.H.; Kobayaehi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; F
F,Mogard, M.H.; Kobayaehi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; F
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A,Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tx
A,Reference number: A03239; MUID:86242180; PMID:3087352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Reference number: A9442
A, Contents: annotation; three-dimensional structure and disulfide bonds
R, Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect, Cacch. Chem. Commun. 42, 564-579, 1977
A, Title: Disulfide bonds in human serum albumin.
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                                                A; Reference number: $17599; MUID: 92126241; PMID: 1772598
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Biochem. J. 171, 453-459, 1978
A.Title: Lysine residue 240 of human serum albumin is A.Reference number: A90299; MUID:78186630; PMID:656055
A.;Contente: annotation; bilirubin-binding site
R.;Peters, T.; Reed, R.G.
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A; Accession: 801/4'
A; Cross-references: EMBL: 102961; NID: 9763428; PIDN: AAA64922.1; PID: 9763431
B; Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
B; Cross-references: EMBL: 102956; P.M.; Peach, R.J.; Brennan, S.O.
B; A; Title: Endoproceolytic processing of recombinant proalbumin variants by the yeast Kex2
A; Title: Endoproceolytic processing of recombinant proalbumin variants by the yeast Kex2
A; Reference number: 855314; MUID: 95275251; PMID: 775581
A; Reference number: 855314; MUID: 95275251; PMID: 775581
A; Reference number: 1975
A; Reference number: A91420; MUID: 76187907; PMID: 1225573
A; Accession: A91420; MUID: 76187907; PMID: 1225573
A; Accession: A91420; MUID: 76187907; PMID: 1225573
A; Recernce number: A91420; MUID: 76187907; PMID: 1225573
A; Residues: 25-117; EQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-333, 'A', 395-345111 is labelation and structure elucidation of middle-molecular weight peptides from ur
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A;Accession: 13944/
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A;Accession: 13946: DNA
A;Accession: 13946: DNA
A;Accession: 136928
A;Accession: 159286
A;Accession: 159286
A;Cross-references: GS:U.S.A: 91, 2275-2279; 1994
A;Title: A nucleotide insertion and frameshit cause analbuminemia in an Italian family.
B;Accession: 159286
A;Accession: 15938
A;Accession: 159313
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A,Rofecesion: 806422
A,Molecule type: protein
A,Molecule type: protein
A,Rofeseluces: 25-48 - ROB>
R/Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
A,Residuces: 25-48 - ROB>
A,Frinch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
A,Reference number: 836882; MUID:93384321; PMID:8373198
A,Frite: Mass spectrometric identification of modifications to human serum albumin treat
A,Reference number: 836882; MUID:93384321; PMID:8373198
A,Rofession: 836882
A,Rofession: 83
                                                                                                                                                                                                                                                                                                                               and 3' flanking regions and
                                                                                                                                                                                        PIDN:CAA23753.1; PID:g28590
                                                                                                                                                                                                                                                                                                                               'n
A.Molecule type: mRNA
A;Residues: 1-120, G',122-609 <DUG>
A;Cross-references: RMBL:V00494; NID:928589; PIDN:CAA237;
R;Urano, Y: Matanabe, K: Sakai, M: Tamaoki, T.
J. Biol. Chem. 264, 3244-3251, 1986
A;Title: The human albumin gene. Characterization of the A;Reference number: 139427; MUID:86140099; PMID:2419329
A;Status: translation ---
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 19, 2004, 11:37:59; Search time 1.70637 Seconds (without alignments) 789.208 Million cell updates/sec Run on:

US-09-832-929-18\_COPY\_76\_89 70 1 TVATLRETYGEMAD 14

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

| Description         | serum albumin prec | albumin pre | albumin | albumin pre |       | albumin pre | c      | hypothetical prote | - 54  | albumin | protein R08F11.4 [ | serum albumin prec | glycyl-tRNA synthe | aminomethyltransfe | ABC transporter, A | hypothetical prote | dihydrolipoamide S | 66K merozoite surf | acid   | probable 4-vinyl r | cal    | hetical | VacJ lipoprotein p | phosphoenolpyruvat | aminopeptidase N N | hypothetical prote | shikimate kināse ( | 굶      |      |
|---------------------|--------------------|-------------|---------|-------------|-------|-------------|--------|--------------------|-------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|------|
| SOMMAKIES           | A47391             | ABHUS       | ABSHS   | ABHOS       | ABBOS | S57632      | A05139 | AH2433             | ABPGS | ABRTS   | нвэооэ             | ABCHS              | G87415             | S50917             | A95074             | E97941             | D64135             | A39238             | B75265 | T31452             | T22606 | C86853  | AF0805             | D75361             | F81086             | T42697             | AE3257             | D96945 | 4637 |
| DB                  | 8                  | Н           | н       | Н           | Н     | ~           | ~      | 7                  | -1    | -       | 0                  | н                  | 7                  | ~                  | ~                  | N                  | ~                  | ~                  | ~      | ~                  | ~      | N       | 7                  | ۲3                 | 7                  | ~                  | 7                  | N      | 7    |
| Length              | 009                | 609         | 607     | 607         | 607   | 609         | 453    | 252                | 605   | 609     | 354                | 615                | 692                | 1034               | 330                | 330                | 409                | 563                | 585    | 202                | 157    | 179     | 251                | 780                | 867                | 1350               | 169                | 228    | 251  |
| %<br>Query<br>Match | 100.0              | 00          |         | 87.1        | ٠     | 81.4        |        |                    |       | 0.09    | 58.6               | 58.6               | 58.6               | 58.6               |                    |                    | 57.1               | 57.1               | 57.1   | 56.4               |        |         |                    |                    |                    |                    | 52.9               |        |      |
| Score               | 70                 | 70          | 62      | 61          | 58    | 57          | 4.6    | 42                 | 4.2   | 4,      | 41                 | 41                 | 41                 | 41                 | 40                 | 40                 | 40                 | 40                 | 4      | 39.5               |        |         | 38                 | 38                 | (L)                | 37.5               | 37                 | 37     | 37   |
| Result<br>No.       | -1                 | 7           | ٣       | 4           | Ŋ     | 9           | 7      | 00                 | σ     | 10      | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19     | 20                 | 21     | 22      | 23                 | 24                 | 25                 | 56                 | 27                 | 28     | 29   |

| 8-oxoguanine DNA g | tryptophanyl-tRNA | IMP dehydrogenase | DNA topoisomerase | hypothetical prote | probable dimethyl | hypothetical prote | anaerobic dimethyl | hypothetical prote | amino acid ABC tra | probable amino aci | MG439 homolog E09_ | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| E69045             | H83924            | DEBSMP            | T43031            | AD2310             | T27925             | T39790             | D95250             | A69513             | C85896            | B83496             | AH0403             | G91051             | D64637             | E71877             | 873529             |
| ~                  | 7                 | -                 | (1                | N                  | N                  | N                  | N                  | N                  | N                 | 7                  | N                  | N                  | ď                  | N                  | 01                 |
| 312                | 332               | 488               | 759               | 1172               | 1278               | 378                | 69                 | 83                 | 145               | 157                | 205                | 209                | 256                | 257                | 287                |
| 52.9               | 52.9              | 52.9              | 52.9              | 52.9               | 52.9               | 52.1               | 51.4               | 51.4               | 51.4              | 51.4               | 51.4               | 51.4               | 51.4               | 51.4               | 51.4               |
| 3.7                | 37                | 37                | 37                | 37                 | 37                 | 36.5               | 36                 | 36                 | 36                | 36                 | 36                 | 9.                 | 36                 | 36                 | 9.                 |
| 30                 | 31                | 32                | 33                | 34                 | 35                 | 36                 | 37                 | 38                 | 33                | 40                 | 41                 | 42                 | 43                 | 44                 | 4.<br>Ω            |

## ALIGNMENTS

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A47394
Series: Macaca malatta (rhesus macaque)
C;Species: Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A47391
R;Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwilet, J.; Putnam, F.
Proc. Natl. Acad Sci. US.A. 90, 2409-2413, 1993
A;Title: CDNA and protein sequence of polymorphic macaque albumins that differ in biliz
A;Reference number: A47391; MUID:93211971; PMID:8460152
A;Contents: B/B Homozygote
A;Accession: A47391
A;Residues: Dreliminary
A;Molecule type: mRNA; protein
A;Residues: 1-600 < WAT>
A;Residues: 1-600 < WAT>
A;Conserreferences: GB:M90463; NID:9342294; FIDN:AAA36906.1; PID:9342295
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:128280; NCBIP:128281)
C;Superfemental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:128280; NCBIP:128281)
C;Superfemily: serum albumin; serum albumin repeat homology < SA1>
F;21-386/Domain: serum albumin repeat homology < SA3>
F;21-386/Domain: serum albumin repeat homology < SA3>
F;405-584/Domain: serum albumin repeat homology < SA3>
F;40
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100.0%; Pred. No. 8.9e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 14, Conservative
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## 92 TVATLRETYGEMAD 105 1 TVATLRETYGEMAD 14 ઠે d

serum albumin precursor (validated) - human

N'Alternate names preproalbumin N'Alternate names preproalbumin C'Ontains: kinetensin C'Species: Homo sapiens (man) C'Date: 29-Jul-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000 C'Date: 29-Jul-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000 C'Accession: A9143; A93945; J39427; J39427; J59286; I59313; G01747; S55314; A91420; S06422; S3 R'Lawn, R.W.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Scebu Nucleic Acids Res. 9, 6103-6114, 1981 A'Title: The sequence of human serum albumin cDNA and its expression in Escherichia col A'Reference number: A93743; MUID:82081882; PMID:6171778

A; Molecule type: mRNA A; Residues: 1-419, K', 421-609 <LAW> A; Residues: 1-419, K', 421-609 <LAW> A; Residues: 1-419, K', 421-609 <LAW> B; Cross-references: EMBL: W00495; GB: U0078; GB: L00132; GB: L00133; NID: G28591; PIDN: CAA2 B; Dugaiczyk, A:, Law, S.W.; Dennison, O.E. Proc. Natl: Acad. Sci. U.S.A. 79, 71-75, 1982 A; Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA. A; Reference number: A93936; MUID: 82105994; PMID: 6275391

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100.0%; Score 38; DB 4; Length 610;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-153-064-133

(Sequence 133, Application US/10153064

(Patent No. 6663485

(GERRAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

WHORE REPLOR DATE: 2002-05-24

WUMBER OF SEQ ID NOS: 137

WUMBER OF SEQ ID NOS: 137

SEQ ID NO 133

LENGTH: 651

TYPE: REPLOR TITLE OF SEQ ID NOS: 137

SEQ ID NO 133

LENGTH: 651

TYPE: REPLOR CHEMOKINE PROTEIN: CREANISM: Homo sapiens

US-10-153-064-133
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: April 19, 2004, 12:05:19 Job time : 2.22622 secs
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                                                                                                                                                                                                                                                                                                                                                       78 VADESAEN 85
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Gaps

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PHARMACEUTICAL COMPOSITION
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 38; DB 2; Length 610; 100.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-0ct-2001
CLASSIFICATION & UNKNOWN:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-UJU-1994
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INPORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 9-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
         APPLICATION NOTE: 28-JAN-1993
ATTORNA DATE: 28-JAN-1993
ATTORNA INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
       PCT/FR93/00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09984186
Patent No. 6886179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                          REFERENCE DOCKET WINEBER: STORY TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (610) 454-
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 VADESAEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VADESAEN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-984-186-2
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APPLICANT: Fleer, Reinhard

APPLICANT: Fournier, Alain

APPLICANT: Guitton, Jean-Dominique

APPLICANT: Jung, Gerard

APPLICANT: Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

TITLE OF INVENTION: ONTAINING SAID POLYPEPTIDES,

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

COUNTRY: USA

COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
  Afamin: A Human Serum Albumin-Like Protein
                                                                         ADDRESSEE: Adden Center, Patent Operations/RRC STREET: 1840 DeHavilland Drive Caltr: Thousand Oaks CTATE: 1840 DeHavilland Drive CTATE: California COUNTRY: U.S.
ZTATE: 91320-11789
COUNTRY: U.S.
ZER: 91320-11789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: ISM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USSS/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macincosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION WUMBER: US/08/797,689
FILING DATE: 31.4N-1997
CLASSIFICATION: 435
PRIOR APPLICATION WUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION WUMBER: ER 92/01064
FILING DATE: 31.4N-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08797689
Patent No. 5876969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acid
STRANDENNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-04075-3
TITLE OF INVENTION: A:
TITLE OF INVENTION: P:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 VADESAEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VADESAEN 8
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Sequence 977, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Burchinder, Jenny
TITLE OF INVENTION: GENEE EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12

PRIOR FILING DATE: 2000-10-12

SOFTWARE: PERL PROGRAM
SEQUENCE: 1143

SOFTWARE: PERL PROGRAM
SEQUENCE: 100 977
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                          Sequence 7, Application US/10153064
GREERL NO. 6663485
GREERL INFORMATION:
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
TITLE OF INVENTION CHEMBER: US/10/153,064
CURRENT APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; OTHER INPORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS9504075
GENERAL INFORMATION:
APPLICANT: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens US-10-153-064-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 VADESAEN 85
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                               1 VADESAEN 8
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US-09-976-594-977
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                                                                                                             RESULT 10
US-10-153-064-7
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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DB 1; Length 609;
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100.0%; Score 38; DB 4
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08897956A
Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Mary Ellen Digan
APPLICANT: Hermann Gram
ITILE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244(DR)
CURRENT FILING DATE: 1997-07-21
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 2
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 38;
Best Local Similarity 100.0%; Pred. No. '
Matches 8; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-433-037-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo Sapiens
US-08-897-956A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VADESAEN 8
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100.0%; Score 38; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
APPLICANT: Lichenstein, Henri
APPLICANT: Wurfel, Mark
APPLICANT: Wurfel, Mark
APPLICANT: Wiffit, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
UNDBER OF SEQUENCES: 33
CORRESPONDENCES. ANGEN Center, Patent Operations/RRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CTTY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PATENTIN VETRION 3.1
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sreekrishna, Kotikanyadan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08222619
Patent No. 5652352
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US-08-433-037-4
'SGR433-037-4
'SGRAENT NO. 5707828
'SGENERAL INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
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; MOLECULE TYPE: protein
US-08-222-619-3
                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-064.5
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US-08-222-619-3
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US-08-746-2

| Sequence 2, Application US/08769746
| Patent No. 6274305
| Patent Solo, Ana M. Pablich No. 1 Pablich No
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100.0%; Score 38; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels
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US-10-153-064-5
Sequence 5, Application US/10153064
Patent No. 666485
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVERTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PFS56
                               LENGTH: 585 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-572-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 585 amino acids
amino acid
   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-769-746-2
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Sequence 1, Application US/08984176

Sequence 1, Application US/08984176

Sequence 1, Application US/08984176

GENERAL INFORMATION:
APPLICANT: ACKTER, DANIEL C

APPLICANT: ACKTER, DANIEL C

APPLICANT: ACKTER, PLORIAN

TITLE OF INVENTION: OXYGEN-TRANSFORTING ALBUMIN-BASED BLOOD REPLACEMENT

TITLE OF INVENTION: OXYGEN-TRANSFORTING ALBUMIN-BASED BLOOD WORLD ALBUMIN-BASED BLOOD WO
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Sequence 2, Application US/08702572

Patent No. 2865386

GENERAL INPORMATION:
APPLICANT: Rarry-Williams, Sean M
APPLICANT: Gilbert, Sarah C
TITLE OF INVENTION: Yeast Strains and Modified Albumins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
COUNTRY: Ring of Prussia
COUNTRY: Pennsylvania
COUNTRY: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFERATION SYSTEM: MS-DOS
SOFTWARE: MACIOSOFT WORD 6.0
CURRENT APPLICATION NUMBER: US/08/702,572
FILING DATE: 11-NOV-1996
CLASSIFICATION NUMBER: WO 95/23857
FILING DATE: IMAR-1995
APPLICATION NUMBER: MB 944270.2
FILING DATE: B-MR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Naoni Biswas
NAME: Naoni Biswas
REGISTRATION NUMBER: 38,384
REGISTRATION NUMBER: CE0114 US
TELECOMMUNICATION INDERER: CE0114 US
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Best Local Similarity 100.0%;
Matches 8; Conservative (
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens
US-08-984-176-1
                                                                    54 VADESAEN 61
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1 VADESAEN
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US-08-984-176-1
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PETER NO. 5780594

GENERAL INFORMATION:
APPLICANT. CARTER, DANIEL C.
TITLE OF INVENTION: ELOCATCALLY ACTIVE PROTEIN FRAGMENTS
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES:
ADDRESSE: NASA
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES:
ADDRESSE: NASA
TITLE OF INVENTION: ELOCATCALLY
STREET: MARSHALL SPACE FLIGHT CENTER
TITLE OF THE TRANSA
TOPOLOGY
TELECHOMICATION INFORMATION:
TELECHOMICATION INFORMATION:
TELECHOMICATION OF SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: SEC anino acids
TYPE: anino acid
TYPE: anino acid
TYPE: ALLO ATTORNEY ACTIVE
TOPOLOGY: Interex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 38; DB 1; Length 585; Best Local Similarity 100.0%; Pred. No. 7.2; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           /note= "Alternative C-termini of HSA(1-n)"
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amino acid sequence of natural HSA"
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
                                                                                                                                            FEATURE:
NAME/KEY: Region
LCCATION: 369..419
OTHER INFORMATION: /
CHERE INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: Region
LOCATION: 1.585
OTHER INFORMATION: 1
US-08-153-799-14
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TELEX: 219484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acids
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TYPE: amino acid
TOPOLOGY: linear
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US-08-153-799-14
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Sequence 1, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 105, Appli
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                                                                                                       April 19, 2004, 11:40:29 , Search time 1.22622 Seconds (without alignments) 336.813 Million cell updates/sec
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Sequence
Sequence
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2: /cgn2 6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2 6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2 6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-484-195A-3
US-08-684-195A-3
US-08-97-2
US-08-702-572-2
US-10-153-064-5
US-08-97-30-74
US-10-153-064-133
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                           US-09-832-929-18_COPY_54_61
38
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                      1 VADESAEN 8
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                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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29 38 100.0 676 4 US-10-153-064-127 Sequence 127, App 29 100.0 676 4 US-10-153-064-135 Sequence 129, App 31 30 38 100.0 676 4 US-10-153-064-135 Sequence 123, App 32 100.0 680 4 US-10-153-064-135 Sequence 123, App 32 100.0 680 4 US-10-153-064-132 Sequence 123, App 33 38 100.0 680 4 US-10-153-064-132 Sequence 123, App 33 38 100.0 680 4 US-10-153-064-132 Sequence 123, App 33 38 100.0 680 4 US-10-153-064-130 Sequence 10.0 App 33 38 100.0 787 2 US-00-997-689-16 Sequence 10.0 App 33 38 100.0 787 2 US-00-997-96-13 Sequence 12, App 13 58 38 100.0 787 2 US-00-997-96-16 Sequence 13, App 14 US-00-997-96-16 Sequence 14, App 14 US-00-997-96-16 Sequence 14, App 14 US-00-997-96-16 Sequence 15, App 14 US-00-997-96-16 Sequence 17, App 14 US-00-997-96-16 Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCOAADKAACLLP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 BETCALFKEHPDDLLSAFIHEEARNHPDLYPPAVLLLTQQYGKLVEHCCEEEDKDKCFAE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 HKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%; Score 726.5; DB 1; Length 36.9%; Pred. No. 1.2e-46; ive 74; Mismatches 155; Indels
                                                                                                                                                                                               EMBL; M18350; AAA49636.1; --
PIR; A41682; ABXL68.
PIRSP; P02768; IB79.
InterPro; IR700264; Serum albumin.
Pfam; PP00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum albumin; 1.
SNART; SM0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper. SIGNAL
PROPER
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COPPER (BY SIMILARITY) .
BY SIMILARITY.
of the colloidal osmotic pressure of blood.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Plasma.
--- SIMILARITY: Belongs to the ALB/AFF/VDB family.
--- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                             kDa SERUM ALBUMIN.
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Best Local Similarity 36.99
Matches 139; Conservative
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606 AA;
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                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 146:489-496(1985).

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. (a(2+), Na(+), K(+), fatty acids, normans, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
Schorpp M., Doebbeling U., Wagner U., Ryffel G.U.;
"5. flanking and 5. proximal exon regions of the two Xenopus albumin
genes. Deletion analysis of constitutive promoter function.";
J. Mol. Biol. 199:83-93 (1988).
                                                                                                                                                                                                 Wolffe A.P., Glover J.F., Martin S.C., Tenniswood M.P.R., Milliams O.L., Tata J.R., Tata J.R., Perinduction of transcription of Xenopus 74-kDa albumin genes and destabilization of mRNA by estrogen in vivo and in hepatocyte
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-> D (IN REF. 3).
592BA4177A36B66B CRC64;
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COPEN (BY SIMILARITY).
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74 kDa SERUM ALBUMIN.
ALBUMIN 1.
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Pred. No. 1.4e-49;
0; Mismatches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M21442; AAA49637.1; --
EMBL; M2276; AAA49642.1; --
PIR; B41682; ABKL72.
HSSP; P02768; LE7B.
InterPro; IPR000264; Serum_albumin.
PF00273; transport_pro; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
ProDom; SM0012; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
PROPEP
CHAIN
25 607 74 KDS SEDOMAIN
21 396 ALBUMIN 3
DOMAIN 21 396 ALBUMIN 3
DOMAIN 21 396 ALBUMIN 3
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MEDLINE=85126974; PubMed=3971963;
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38.4%;
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607 AA;
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157; Indels

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SQPITEFTEDPHYCEXYAENNEVFLGRYLHAVSRKHQELSEQFLLQSAKEYSSLLNKCCK 385
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                                                                                                                                                                                                                                                 183 DELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTKVH 242
                                                                                                                                                                                                                                                                                                                                    302
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                                                                                                                        EKPVGTLFFDKLCADPAVGVNYEWSKECCAKODPERAQCFKAHRDHEHT---SIKPEPEE 145
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Eur. J. Blochem. 146:489-496(1985).
Eur. J. Blochem. 146:489-496(1985).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hormones, bilirubin and drugs. Its main function is the regulation
                        HKSEVAHRFKDLGBBNFKALVLIAFAQYLQOCPFEDHVKLVNEVTEFAKTCVADESAENC
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                                                                                DKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDV
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SEQUENCE OF 1-48 FROM N.A.
MEDINE=8812470; PubMed=2451026;
Schorpp M., Deabheling U., Wagner U., Ryffel G.U.;
Schorpp M., Deabheling U., Wagner U., Ryffel G.U.;
"S'-flanking and S'-proximal exon regions of the two Xenopus albumin genes. Deletion analysis of constitutive promoter function.";
U. Mol. Biol. 199:83-93(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Xenopus lasvis serum albumin: sequence of the complementary deoxyribonucleic acids encoding the 68- and 74-kilodalton peptides and the regulation of albumin gene expression by thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-ARN-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 141, Last senotation update)
68 kDa serum albumin precursor.
Kanopus lasvis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphabia; Batrachia; Anura; Mesobatrachia; Pipoidea; Zenopus.
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MEDLINE=8126974; PubMed=3971963;
MEDLINE=8126974; PubMed=3971963;
Williams J.L., Tata J.R.;
Williams J.L., Tata J.R.;
"Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilization of mRNA by estrogen in vivo and in hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE ## SATGENT F.D., Smith L.H. Jr., Pastori R.L.,
Schoenberg D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during development.";
Mol. Endocrinol, 3:464-473(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 TDNPPECYKDGADRF 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 AADPHECYAKVFDEF 377
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      NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLERGENIC PROPERTIES.

MEDLINE=21381307, PubMed=11488669;

Quirce S., Maranon F., Umplerrez A., de las Heras M.,

Quirce S., Maranon F., Umplerrez A., de las Heras M.,

Quirce S., Maranon F., Umplerrez A., de las Heras M.,

Ternandez-Caldas E., Sastre J.,

Ternandez-Caldas E., Sastre J.,

Tallergy 156,754-762(2001).

-!- FUNCTION! Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

-!- SUBCELLULAR LOCATION: Secreted.

-!- ALLERGEN! Causes an allergen that may cause both respiratory and food-allergy symptoms in patients with the bird-egg syndrome.

-!- SIMILARITY: Belongs to the ALB/ARP/VDB family.

-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                         SECUENCE OF 1-28 FROM N.A. MEDLINES1161037; Wheleds18737; MEDLINES1161037; PubMeds6187737; Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.; "The 5' noncoding and flanking regions of the avian very low density abolisportetin II and serum albumin genes. Homologies with the egg white protein genes."; J. Biol. Chem. 258:4556-4564(1983).
                                                                                                                                                                                                                                                                                                                                             Rosen A.M., Geller D.M.; "Chicken microsomal albumin: amino terminal sequence of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR, S15571, ABCHS.
HSSP, P02768; 1ETB.
HSSP, P02768; 1ETB.
HINTERPRO; IRPRO0264; Serum albumin.
Pfam; PF00073; transport prot; 3.
PRINTS; PR00802; SERUMALEUMIN.
PRODOM; P0002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
MCtal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
                                                           Cassady A.I., Salkild C.K., Baverstock P., Wallace J.C., Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
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ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                    SEQUENCE OF 19-30.
MEDLINE=78019943; PubMed=911327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X60688; CAA43098.1; -. EMBL; V00381; CAA23680.1; -.
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SEQUENCE FROM N.A.
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"Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acids encoding the 68- and 74-kilodalcon peptides and the regulation of albumin gene expression by thyroid hormone during development.";
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01-APR 1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
74 kDa serum albumin precursor.
Xenopus laevis (African clawed frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Amora; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL)
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MEDLINE-89313788; PubMed-2747653;
Moskaitis J.E., Sargent T.D., Smith L.H. Jr., Pastori R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.2%; Score 1038.5; DB 1; Length 47.9%; Pred. No. 8.7e-70; tive 75; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> M (IN REF. 3).
E59E4BBCAEC066C6 CRC64;
BY SIMILARITY.
CHORACO.
CHO
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SEQUENCE OF 1-48 FROM N.A.
MEDLINE=88172470; PubMed=2451026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 F
69918 MW;
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ID ALB2 XI

DT 01-APR

DT 01-APR

DT 01-NOV

DT 28-FEB

DE 74-KDB

OC BUKATY

OC AMPHID

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TISSUE-Liver;

XX MEDLINE-93162044; PubMed=1286668;

RA Giometic C. S., Taylor U, Tollaksen S.L.;

RA diometic C.S., Taylor U, Tollaksen S.L.;

RT dimensional gel electrophoresis a catalog of proteins detected by two-dimensional gel electrophoresis.";

Electrophoresis 13:970-931(1932).

CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, commonses, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC -!- SUBCEDLULAR LOCATION: Secreted.

CC -!- SUBCEDLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.

CC -!- SIMILARITY: Contains 3 albumin domains.

CC -!- SIMILARITY: Contains 3 albumin domains.
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Rodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Railus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 99-516 FROM N.A.
MEDLINE=88215133; PubMed=245256;
MAIDTHE=88215133; PubMed=245256;
Minghetti P.P., Law S.W., Dugaiczyk A.;
"The rate of molecular evolution of alpha-fetoprotein approaches that of pseudogenes.";
MAIDTHE SEQUENCE OF 477-358(1985).
[5]
SEQUENCE OF 477-551 FROM N.A.
MEDLINE=90269606; PubMed=1971802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boccaccio C., Deschatrette J., Meunier-Rotival M.; Empty and occupied insertion site of the truncated LINE-1 repeat located in the mouse serum albumin-encoding gene."; Gene 88:181-186(1999)
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EMBL; AKC10029
EMBL; BC049971; AA44971.1; -
EMBL; BC049971; AA437190.1; -
EMBL; M1611; AA437190.1; -
EMBL; M1611; AA437190.1; -
EMBL; M1611; AA437190.1; -
EMBL; M1611; AA437190.1; -
EMBL; M1619; AA631458.1; -
EMBL; M1619; AA631458.1; -
EMBL; M1619; AA631458.1; -
EMBSP; P02768; LE7B.
EMBSP; P02768; LE7B.
EMBSP; P027724; MOUSE.
EMBSP; M175; PR000264; Serum_albumin.
Efam; PP00279; Transport. prot; 3.
ERINTS; PR00802; SERUMALEUMIN.
EMBSP; SM0021; ALBUMIN; 3.
EMBSP; PR00212; ALBUMIN; 3.
EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMBSP; EMB
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SEQUENCE OF 25-44.
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PROPEP
CHAIN
                   RANGE BERNEL HER RESTREET FOR STANKE SER SEE STEEL FOR SERVICE ```

SERUM ALBUMIN

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61 NCDKSLHTLFGDXLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 NCDKSLHTLFGDKLCAIPNLRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPELLFFAKRYKAAFTECCQAADXAACLLP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 VNKECCHGDILECADDRAELAKYMCENQATISSKLQTCCDKPLLKKAHCLSEVEHDTMPA 324
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
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ALBU CHICK

ALC

O1-NOV-1990 (Rel. 16, Created)

DT

O1-NOT-1990 (Rel. 23, Last sequence update)

DT

O1-NOT-2003 (Rel. 23, Last sequence update)

DT

O1-NOT-2003 (Rel. 23, Last sequence update)

DE

Serum albumin precursor (Alpha-livetin) (Allergen Gal G S).

GN

ALB.

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom

OC

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasia

OX

NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                   76.6%; Score 1584; DB 1; Length 608; 71.8%; Pred. No. 2.8e-110; ive 56; Mismatches 53; Indels
                                                                                                                                                                                                                                                                              H -> D (IN REF. 6).
H -> D (IN REF. 6).
Q -> I (IN REF. 6).
MW; 292F7C7EED3A61B4 CRC64;
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 2.
COPPER.
BY SIMILARITY.
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DISULPID
DISULPID
DISULPID
DISULPID
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DISULPID
DISULPID
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DISULFID
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
DOMAIN
DOMAIN
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METAL
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STRAIN=C57BJ/6J; TISSUB=Tongue;

RAMAN=C57BJ/6J; TISSUB-T; TI, Bono H., Rabukawa T., Saito R.,

RAMOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RAMOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RAMOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RAMOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RAMOTA K., Matsud Y., Rikaido I., Pesole G., Quackenbush J.,

RAMOTA K., Okido T., Furuno M., Aon H., Baldarelli R., Barsh G.,

RAMOTA M., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,

RICHARD R., Hill D., McGann M., Hume D.A., Kamiya M., Lee N.H.,

RAMOTA M., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RAMOTA M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RAMOTA M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RAMOTA M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RAMOTA M., Sato K., Wang K.H., Weitz C., Whittaker C., Willming L.,

RAMOTA M., Weitz C., Whittaker C., Willming L.,

RAMOTA M., Weitz K., Rawaji H., Kohtsuki S.,

RAMOTA M., Weitz M., Rawaji H., Kohtsuki S.,

RAMOTA M., Weitz M., Rawaji H., Kohtsuki S.,

RAMOTA M., Weitz M., Rawaji H., Rohtsuki S.,

RAMOTA M., Weitz M., Rawaji H., Rohtsuki S.,

RAMOTA M., RAMOTA M., RAMOTA M., RAWAN M., RA
                                      147 AMCTAFQENAEAFMGHYLHEVARRHPYFYGPELLYLADKYTAVLTECCAADDKGACLTFK 206
                                                                                                                                                                                                                                                                                   267 TQECCHGDLLECADDRAELAKYMCENQASISSKLQACCDKEMLQKSQCLAEVEHDDMPAD 326
                                                                                                                                                                                                                                               242 HTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPAD 301
                                                                                                                                                                                                                                                                                                                                                                                                          122 VMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPK
                                                                                                                                                              LPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCC
                                                                                                                              LDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKV
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STRAIN=FVB/N; TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALBU_MOUSE STANDARD, PRT; 608 AA.
ALBU_MOUSE STANDARD,
01-ARE-1988 (Rel. 07, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 34, Last annotation update)
Serum albumin precursor.
ALB OR ALB1 OR ALB-1.
EWAR-2014 (Mouse).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUTENCE FROM N.A. TISSUBE-Liver; van Recht T., Gabant P., Dreze P., Szpirer J., Szpirer C.; submitteed (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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ALBU MOUSE
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                                                                                                          CDKSLHTLFGDKLCSLPNFGEKYAEMADCCAKQEPERNECFLQHKDDNPQLPPFKRAEPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Copper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.6%; Score 1585; DB 1; Best Local Similarity 73.6%; Pred. No. 2.4e-110; Matches 284; Conservative 40; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIGHER POSSES | DESCRIPTION |

InterPro; IPRO0264; Serum_albumin.

Prom; PRO0202; Transport proc; 3.

PRINTS, PRO0802; SERUMALBUMIN.

ProDom; PRO0202; ALBUMIN; 3.

ROSITE; PRO0212; ALBUMIN; 3.

ROSITE; PRO0212; ALBUMIN; 3.

ROSITE; PRO0212; ALBUMIN; 3.

ROSITE; PRO0212; ALBUMIN; 3.

ROSITE; PRO0812; ALBUMIN; 3.

ROMAIN 213 3.8 RIMILARITY.

DOMAIN 213 3.8 RIMILARITY.

DOMAIN 405 596 ALBUMIN 1.

DOMAIN 405 596 ALBUMIN 3.

METAL.

DISULPID 115 126 BY SIMILARITY.

DISULPID 193 202 BY SIMILARITY.

DISULPID 270 278 BY SIMILARITY.

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DISULPID 270 278 BY SIMILARITY.

DISULPID 341 386 BY SIMILARITY.

DISULPID 341 385 BY SIMILARITY.

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DISULPID 341 BY SIMILARITY.

DISULPID 581 BY SIMILARITY.

DISULPID 588 BY SIMILARITY.

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EROJENCE FROM N.A.
STRAIN-MGS IDR, TISSUB=Liver;
MEDLINE-98116663, PubMed=9455485;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
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                                                                                                                                                                                                                                                                                    Length 608;
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                                                                                                                                                                                                                                                                CF5E92647AAFE9A2 CRC64;
                                                                                                                                                                                                                                                                                    ; Score 1585; DB 1;
; Pred. No. 2.4e-110;
57; Mismatches 55;
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BY SIMILARITY.
SERUM ALBUMIN 1.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                 68914 MW;
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  608 AA;
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                                                                                                                                                 DVWCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCOAADKAACLLF
                                                                                                       KLDELRDEGKASSAKQRLKCASLQKPGBRAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
                                                                                                                                                                               VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA
     DAHKSEVAHRPKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000264; Serum_albumin.
Pfam, PR00273; transport prof; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom, PD002486; Serum_albumin; 1.
SWART; SM00103; ALBUMIN; 3.
PROSTE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
                                                                                                                                                                                                                                                                                                                                                                    (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
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HSSP; P02768; 1E7B.
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01-FEB-1996 (Rel. 33, La
28-FEB-2003 (Rel. 41, La
Serum albumin precursor.
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P49065;
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Conservative
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Matches 279; Conserv
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P02770, P11382,
P1-701-1986 (Rel. 01, Created)
21-701-1986 (Rel. 01, Last sequence update)
22-1011-1986 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
-1...min precursor [Contains: Neurotensin-related peptide (NRP)].
                                                                                                                                                                                                                                                                                                                                                    61 NODKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNBCFLGHKDDNPNLPRLVRPEV
                                                                                    GCDKSLHTLFGDELCKVATLRETYGDMADCCEKQEPERNECFLNHKDDSPDLPKL-KPEP
                                                                                                                                                           144 DILCAEFKADEKKFWGKYLYEVARRHPYFYAPELLYYANKYNGVFQECCQAEDKGACLLP
                                                                                                                                                                                                                               VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA
                                                                                                                                                                                                                                                                                                   DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                  KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
                                                                                                                                       DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.;
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-38, AND PROCESSING.
MEDLINE=77249657; PubMed=893447;
Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.
strauss A.W., Espaibumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
messenger NNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
MEDULINE-81223722; PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
Nucleotide sequence of cloned rat serum albumin messenger RNA.";
Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
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Isemura S., Ikenaka T.;
"Amino acid sequences of fragments I and
bromide cleavage of rat serum albumin.";
J. Biochem. 83:35-48(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                                                                                                                                                                              CAKEDPHACYATVFDKLKHLVDEPQNL 410
                                                                                                                                                                                                                                                                                                                                                                                                                           CAAADPHECYAKVFDEFKPLVEEPONL
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SEQUENCE OF 166-174.
TISSUE=Plasma;
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F
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Comper (II) binding ability of human alpha-fetoprotein.";

A Aoyagi Y., Ikenaka T., Ichida F.,

A Aoyagi Y., Ikenaka T., Ichida F.,

"Copper (II)-binding ability of human alpha-fetoprotein.";

Cancer Res. 38:3483-3486(1978).

Cancer Res. 38:3483-3486(1978).

Cancer Res. 38:3483-3486(1978).

Cancer Res. 38:3483-3486(1978).

Informanes, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CIPUNCTION: NRP regulates fat digestion, lipid absorption, and blood flow (Potential).

CIPUSTION: NRP regulates fat digestion, lipid absorption, and blood flow (Potential).

CIPUSTION: PRESECTION: Secreted.

CIPUSTION: PRESECTION: Secreted.

CIPUSTION: Secreted.

CIPUSTION: ALB ARBARPAND family.
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MEDLINE=87194805; PubMed=2437111;
Carraway R.B., Mitra S.P., Cochrane D.E.;
"Structure of a biologically active neurotensin-related peptide
obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262:5968-5973(1987).
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NEUROTENSIN-RELATED PEPTIDE.
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5BB497A282411AB7 CRC64;
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HSSP; P02768; LETB.
HSSP; P02768; LETB.
PEAM; PF00273; transport prot; 3.
PRONOSO2; SERVIMALBUMIN.
PRODOM; PD002486; Serum albumin; 1.
SWART; SW00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
BROSITE; Lipid-binding; Repeat; Signal; Copper.
SIGNAL
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Pred. No. 3.4e-112;
9; Mismatches 49;
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COPPER.
BY SIMILARITY
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                                                                                                                                                            Problem W.M., Distagle was a K.M., Foreman R.C., Saunders N.R.,

Brown W.M., Distagle was a K.M., Foreman R.C., Saunders N.R.,

"Nucleotide and deduced amino acid sequence of sheep serum albumin.";

Nucleotide and deduced amino acid sequence of sheep serum albumin.";

Indian Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmetic pressure of blood.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: 3 albumin domains.
                                   Eukaryos, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalya; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
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BY SIMILARITY.
BY SIMILARITY.
SERUM ALBUMIN.
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; XI7055, CAA34903.1; -...
PIR; S06936; ABSHS.
INTELPRO; PO2768; LETB.
INTELPRO; IERO00264; Serum albumin.
Pfam; PF00273; transport prot; 3.
PRODOM: PD002486; SERUMALBUMIN.
PRODOM: PRODOM: ALBUMIN.
PROSITE; PS00212; ALBUMIN.
SMART; SM00103; ALBUMIN.
SMART; SM0103; Lipid-binding; Repeat; Mrtal-binding; Lipid-binding; Repeat; STONAL
PROPEP 19 24 BY SIMILAR
CHAIN 25 607 SERUM ALB
DOWAIN 21 396 ALBUMIN.
                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Liver,
MEDLINE=90098888; PubMed=2602160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 GCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKL-KPDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.5%; Score 1622.5; DB 1; Length 607; 75.2%; Pred. No. 4e-113; Live 46; Mismatches 49; Indels 1;
  Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
                                                                                                                                                                                                                                                                                                                                    A -> T.

C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

N -> D (IN REF. 6).

ST -> TS (IN REF. 6).

K -> R (IN REF. 6).

K -> R (IN REF. 12).

SB -> RS (IN REF. 6).

W, 39167DFF768585D4 CRC64;
                                                                                                     SIMILARITY)
                                                 SERUM ALBUMIN.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIM:
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ID ALBU SHEEP STANDARD;
OF 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Created)
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493
607 AA;
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ALBUMIN 1.
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ALBUMIN 3.
COPPER (BY SIMILARITY).
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Brown J.R.;
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                                                                                                        VALCADFQEDEQKFWGKYLYEIARRHPYFYAPELLYYAIIYKOVFSECCQAADKAACLLP
                                                                                                                                 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEGIIINE=80024278; PubMed=488109; McGillivray R.T.A., Chung D.W., Davie E.W.; Richilivray R.T.A., Chung D.W., Davie E.W.; Blosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin."; Eur. J. Biochem. 98:477-485(1979).
                   DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae; Bos.
NCBI_TaxID=9913;
 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F., Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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Indels
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databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete cDNA sequence of bovine serum albumin."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
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SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214
 46;
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                                                                                                                                                                                                                                                                                                                ALBU BOVIN STANDARD; PRT; 607 AA. P02769; 002787; 21-JUL-1986 (Rel. 01, Created) 10-FBB-1996 (Rel. 33, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Serum albumin precursor (Allergen Bos d 6).
 Mismatches
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  49
  Conservative
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Submitted (JUL-1994)
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Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
"Rapid confirmation and revision of the primary structure of bovine
serum albiumin by ESIMS and Prit-FAB LC/MS.";
Biochem. Biophys. Res. Commun. 173:639-646(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 25-41.
MEDLINE=88267456; PubMed=3389500;
Hsieh J.C., Lin F.P., Tam M.F.;
Halet blotting onto glass-fiber filter from an analytical
isoelectrofocusing gel: a preparative method for isolating proteins
for N-terminal microsequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  bovine
                                                                                                                                                                                             SEQUENCE OF 402-433.
MEDLINE-82023364; PubMed=7283978;
Reed R.G., Putnam F.W., Peters T. Jr.;
"Sequence of residues 400-403 of bovine serum albumin.";
Biochem. J. 191:867-868(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=77134075; PubMed=843354;
Patterson J.E., Geller D.M.;
"Bovine microsomal albumin: amino terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
                                                                                                                                             the PIR data bank
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EMBL; K58989; CAA41735.1; -.
EMBL; Y17769; CAA76847.1; -.
EMBL; AF542068; AAN17824.1; -.
HSSP; P02768; IE7B.
INTERPRO; IPRO0264; Serum_albumin.
Pfam; PP00273; transport_proct; 3.
PRINTS; PR00802; SERUMALBUMIN.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
"Structure of bovine serum albumin."; Fed. Proc. 34:591-591(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vilbois F.;
Submitted (AUG-1998) to Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anal. Biochem. 170:1-8 (1988).
                                                                                                                                             Submitted (APR-1975) to
                                                                                     REVISIONS TO 190-195
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Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                            01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor (Fragment).
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DR PIR; S34053; ABHOS.

DR HSPSP; P027648; DE278.

DR PETPOROS 1: PROMOSC4; Serum_albumin.

DR PFO0273; transport_prot; 3.

DR PROSSTE; SRUMALBUMIN.

DR SMART; SM00103; ALBUMIN; 1.

DR RNOSTE; SM0012; ALBUMIN; 3.

DR RNOSTE; PS00212; ALBUMIN; 3.

DR RNOSTE; PS00212; ALBUMIN; 3.

DR RNOSTE; PS00212; ALBUMIN; 3.

TROPE 19 24 BY SIMILARITY.

TROPE 25 607 SERUM ALBUMIN.

25 204 ALBUMIN 1.

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Best Local Similarity 77.3%; Pred. No. 6e-116;
Matches 299; Conservative 40; Mismatches 47; Indels 1;
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AC 08835; Q29018;
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RECUING—89016582; PubMed=3174440;

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REDINE=89016582; PubMed=3174440;

REDINE=89016582; PubMed=3174440;

REDINE=10016168 Res. 16:9045-9045(1988)

OF TISSUES REQUINE Serving albumin, ";

Nucleic Acids Res. 16:9045-9045(1988)

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OF THIS SWISS-PROT ENTY IS CONTENTY IS COPYIGHT. IT is produced through a collaboration of the Swiss Institute of Bloinformatice and the EMBL outstation.

CHE Buropean Bioinformatics Institute. There are no restrictions on its concern below the Swiss Institute. There are no restrictions on its concern below the Swiss Institute. There are no restrictions on its concern below the statement is no way concerned an equires a license agreement (See http://www.isb-sib.ch/announce/corrected and email to license@isb-sib.ch).
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-> D (IN REF. 1; AAA30988)
3E556BODDIALF4FF CRC64;
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R EMBL; M36782; ABPGS.
R EMBL; M36782; ABPGS.
R EMBL; M36782; ABPGS.
R EMBL; M36782; ABPGS.
R InterPro; IPRO00264; Serum albumin.
R Promp. PRO0264; Serum albumin.
R Promon; PRO0212; ALBUMIN; 3.
R PROSTIE; PS00212; ALBUMIN; 3.
T SIGNAL -1 16 BY SIMILARITY.
T CHAIN 23 605 ALBUMIN; 2.
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Best Local Similarity
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605 AA

Length 608;

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SEQUENCE OF 215-478 FROM N.A.

SEQUENCE OF 215-478 FROM N.A.

TISSUE-Salivary gland;

TISSUE-SAlivary Gland C., Scheiner O., Kraft D., Rumpold H.;

TISSUE SPECIFIC TISSUE AND ALIDAMIN, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), K(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), K(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), K(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), K(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), K(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), fatty acids, brinding capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for all and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for all and capacity for all and capacity for water, Ca(2+), Na(+), fatty acids, call and capacity for all and capacity for all and capacity for the AlbAPPY/VDB family.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Euteria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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                  Indels
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81.7%; Score 1690; DB 1;
Best Local Similarity 78.3%; Pred. No. 3.9e-118;
Matches 303; Conservative 39; Mismatches 45;
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85 NCEKSLHELLGDKLCTVASLRDKYGEMADCCEKKEPERNECFLQHKDDNPGFGQLVTPEA 144
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                          1 DAHKSEVAHREKDIGEENFKALVIJAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
                                           25 EAHQSEIAHRFNDLGEEHFRGLVLVAFSQYLQOCPFEDHVKLVNEVTEFAKGCVADQSAA 84
                                                                                                                                         121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=75011422; PubMed=4414013;
Dixon J.W., Sarkar B.;
Isolation, amino acid sequence and copper(II)-binding properties of
peptide (1-24) of dog serum albumin.";
J. Biol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn M.J., Corbett J.M., Wheeler C.H., "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins."; Electrophoresis 18:2795-2802(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant dog
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MEDLINE=20148667; PubMed=10669848;
Pandjatran B., Swoboda I., Brandejsky-Pichler F., Rumpold Valenta R., Spitzauer S.;
"Escherichia coli expression and purification of recombina albumin, a cross-reactive animal allergen.";
J. Allergy Clin. Immunol. 105:279-285 (2000).
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 41;
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01-OCT-1596 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Can f 3).
 34; Mismatches
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STRAIN=Beagle; TISSUE=Liver;
 Matches 312, Conservative
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                                                                                                                                                                           Euteleostomi;
Felis.
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SERUM ALBOMIN.
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                                                                                              Feliø silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Bammalia, Eutheria, Carnivora, Fissipedia, Felidae,
NCBI_TaxID=9685,
                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Fel d 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X84842; CAA59279.1;
PIR, JC4660; S57632.
HSSP; PO2768; LETB.
InterPro; IPR000264; Serum albumin.
Pfam; PF00273; transport proc; SRINTS; PR008062; SERUMALBUMIN.
ProDom; PD002486; SERUM albumin; 1.
SMART; SM00103; ALBUMIN; 1.
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Metal-binding; Lipid-binding;
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Score 1727; DB 1; Length 608; Pred. No. 7e-121;

83.5%; 80.6%;

Query Match Best Local Similarity

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RESULT 3
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**SEQUENCE FROM N.A.

**SEQUENCE FROM N.A.

**MEDLINE-93211971; PubMed=8460152;

**WATKINS S.A.; Sakemoto Y., Madison J.M., Davis E.M., Smith D.G.,

**WATKINS S.A.; Sakemoto Y., Madison J.M., Davis E.M., Smith D.G.,

**WATKINS S.A.; Sakemoto Y., Madison J.M., Davis E.M., Smith D.G.,

**WATKINS TO V.** Bequence of polymorphic macaque albumins that differ

**The billing sakemoto Y.** Polymorphic macaque albumins that differ

**The billing capacity for water, Ca(2+), Ma(+), K(+), fatty acids,

**Driving capacity for water, Ca(2+), Ma(+), K(+), fatty acids,

**Driving capacity for water, Ca(2+), Ma(+), K(+), fatty acids,

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**Driving capacity for water, Ca(2+), Ma(+), K(+), fatty acids,

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**Driving capacity for water, Ca(2+), Ma(+), K(+), fatty acids,

**Driving capacity for water, Ca(2+), Ma(+), K(+), fatty acids,

**Driving capacity for water, Ca(2+), Ma(+), Ma(+), K(+), fatty acids,

**Driving capacity for water, Ca(2+), Ma(+), Ma(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
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                                                                                                                                                  DAHKSEVAHRPKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                           DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                   NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
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                                                                                        Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                        ;
                       Length 609;
                                                         3.5e-146;
                           DB 1;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                         Pred. No. 3.5
Mismatches
                       100.0%; Score 2068; 100.0%; Pred. No. 3.5
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                                                                                    Conservative
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                                                      Best Local Similarity
Matches 387; Conser
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                           Query Match
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SERUM ALBUMIN 1.
ALBUMIN 1.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
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SIMILARITY.
E45C871A670E740B CRC64;
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3; Mismatches 8:
                                                                                                                                                           Signal;
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                                                                                                                                                   Metal-binding, Lipid-binding, Repeat,
NON TER 1 1 10 BY SIMILA
PROPEP 11 16 BY SIMILA
PIR; A4731, A4731.
HSSP, P02768, 1E78.
Interpro, IPRO0264; Serum albumin.
Pfam; PRO0273; transport prot; PRINTS; PRO0802; SERUMALBUMIN.
Probom; PDO02486; Serum albumin, 1.
SWART; SMO0103; ALBUMIN; 3.
PROSITE; PG00212; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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[16]
VARIANT
RARKER REARKER               MEDILINE-2238627; Pubmed=1247932;

A TISSUE=12786277; Pubmed=1247932;

A Klausner R.D., Colling F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Lachul S.F., Zeeberg B., Buttow K.H., Schemen C.F., Bhat N.K.,

A Distchenck L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Distchenck L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Distchenck L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Raha S.A., McDwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.Etteman M., Sodergren S.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Scherman K.J., Maran M.C.,

B Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The chemistry and physiology of the human plasma proteins, pp.23-40,
Pergamon Press, New York (1979).
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Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Lygine residue 240 of human serum albumin is involved in high-affinity binding of bilirubin.";
Biochem. J. 171:453-459(1978).
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MEDLINE=86140099; PubMed=2419329;
Urano Y., Watanabe K., Sakai M., Tamaoki T.;
Urano T., Watanabe C., Sakai M., Tamaoki T.;
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regions and the polymorphic gene transcripts.";
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human serum albumin.";
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       and Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-609.
MEDLINE=76187907; PubMed=1225573;
MeDloun B., Moravek L., Kostka V.;
"Complete amino acid sequence of F
FEBS Lett. 58:134-137(1975).
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MEDLINE=78186630; PubMed=656055;
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MEDLINE=76257808; PubMed=955075;
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VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
MEDLINE=22190239; PubMed=1347703;
MINCHIOTELI L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.,
"Two alloalbumins with identical electrophoretic mobility are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
MEDLINE-91062352; PubMed-2247440;
Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
Matkins S., Putnam F.W.;
"Mutations in genetic variants of human serum albumin found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human serum
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MEDLINE=9011585; PubMed=2104980;
Breman S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
Bremin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KONAGOME-3 HIS-23; KONAGOME-2 ARG-152 AND KOWAGOME-1 GLU-396.
MEDIJUNE-92052189; PubMed-1946412;
Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Madison J., Amaki I., Putnam F.W.;
"Genetic variants of serum albumin in Americans and Japanese.";
Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
VARIANT CANTERBURY ASN-337,
MEDLINE=87157744; PubMed=3828358;
Bremnan S.O., Harbert P.;
Blemnan Canterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA
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Arai K., Madison J., Shimuzu A., Putnam F.W.;
"Point substitutions in albumin genetic variants from Asia.";
Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
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MEDLINE-88068523; PubMed=3479777;
Takshashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
Satoh C., Neel J.V.,
"Amino acid substitutions in inherited albumin variants from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      produce
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WEDILINE-1296740; Pubbmed=2068071;
Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M., Minchiotti I., Putnam F.W.;
Minchiotti I., Putnam F.W.;
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Peach R.J., Brennan S.O.;
"Structural characterization of a glycoprotein variant of albumin: albumin Casebrook (494 Asp-->Asn).";
Biochim. Biophys. Acta 1097:49-54(1991).
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Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987)
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MEDLINE=89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satch (
Neel J.V., Sakurabayashi I., Putnam F.W.;
"Point substitutions in Japanese alloalbumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989)
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Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
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macaca mula
felis silve
canis famil
equus cabal
sus scrofa
bos taurus
hos taurus
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rattus norv
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## ALIGNMENTS

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2 Z	serum arbumin precursor. ALB.
S	sapiens (Human).
ပ္ပ	Metazoa; Chordata; Craniata; Vertebrata; E
Ö	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X Z	NCBI_TaxID=9606;
RP	SECUENCE FROM N.A.
ž	PubMed=3009475;
<b>&amp;</b> ;	Minghetti P.P., Ruttner D.E., Kuang W.J., Dennison O.E., hawkins U.W.
\$ £	i albumin gene i
1 E	2 of chromosome 4.";
IJ	nem. 261:6747-6757(1986).
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æ	Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;
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2 0	CEDITENCE FROM N.A. (PRO0903/PRO1708/PRO2644/PRO2619/PRO2675).
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R	hang S., Wei H., Bi J., Zhou G.,
RA	He F., Zhang Y., Ouyang S., Luo L.;
R T	prediction of the coding sequences
R.	y analysis of cDNA Clones from numan
7 Z	o cile ambu/ delibalin/ bbbo dacab
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RA	M.C., Wu H.T.;
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Z Z	Submitted (AUG-2002) to the EMBD/Genbank/DDBO watabases. [7]
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Search completed: April 19, 2004, 12:02:20 Job time : 48.169 secs

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Cyaccesion: JC4258 P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczyk, A. R.Nishlo, H.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczyk, A. Gene 162, 213-220, 1995
A.Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to A.Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to A.Reference number: JC4258; MuID:96032345; PMID:7557431
A.Recension: JC4258
A.Molecule type: DNA
A.Residues: 1-609 ANIS>
A.Cross-references: GB:U21916; NID:9841311; PIDN:AAA91641.1; PID:9841312
C.Comment: This protein is a plasma protein produced in the fetal and neonatal liver of cimilar properties and structure.
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A; Gene: afp
A; Map position: 3p
A; Interfamily: 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3;
A; Interfamily: serum albumin; serum albumin repeat homology
C; Keywords: glycoprotein
F; 21-50 Domain: signal sequence #status predicted <SIG>
F; 21-609/Product: alpha-fetoprotein #status predicted <MAT>
F; 22-202/Domain: serum albumin repeat homology <SA1>
F; 21-394/Domain: serum albumin repeat homology <SA2>
F; 413-592/Domain: serum albumin repeat homology <SA3>
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 27-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999
                                                                                     82 QSAGCLENQLPAFLEELCREKEILEKYGH-SDCCSQSEEGRHNCFLAHKKPTFASIPFFQ
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C; Superfamily: serum albumin; serum albumin repeat homology
C; Superfamily: serum albumin; serum albumin repeat homology
C; Superfamily: serum albumin; duplication; metal binding; plasma
F; 1-18/Domain: signal sequence #status predicted <PRO>
F; 1-2-60/Domain: propeptide #status predicted <PRO>
F; 2-202/Domain: serum albumin repeat homology <SA1>
F; 221-394/Domain: serum albumin repeat homology <SA2>
F; 413-592/Domain: serum albumin repeat homology <SA3>
F; 413-592/Domain: serum albumin repeat homology <SA3>
F; 413-612 Compain: serum albumin repeat homology <SA3>
F; 10 Copper (His) #status predicted
F; 10 Copper (His) #status predicted
F; 10 Copper (His) #status predicted
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C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
mones (weak bonds with these hormones promote their transfer across the membranes), thy
                                                                                                                                                                                                                                                                                                                                                                      68K serum albumin precursor - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Date: 31-Dec-1993 #text_change 28-Apr-1995 C; Datession: A41682; 802692 R; Moskaitis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R. Mol. Endocthiol. 3, 464-473, 1989 A; Tille: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic eduring development.
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PSLAADFVESKDVCKNYAEAKDVFLCMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCA 362
                                                                                                            SOPITEFTEDPHVCEKYAENNEVFLGRYLHAVSRKHQELSEQFLLQSAKEYESLLNKCCK
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A,Accession: A41682
A;Molecule type: mENA
A;Molecule type: mENA
A;Cross_references: GB:M18350
A;Cross_references: GB:M18350
B;Schorpp, M.; Doebbeling, U.; Wagner, U.; Ryffel, G.U.
J. Mol. Biol. 199, 83-93, 1988
A;Title: 5'-flanking and 5'-proximal exon regions of the that the tender unuber: S02692; MUID:88172470; PMID:2451026
A;Accession: S02692
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74K albumin precursor - African clawed frog
C,Species; Xenpous lacvis (African clawed frog
C,Species; Xenpous lacvis (African clawed frog)
C,Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 22-Jun-1999
C,Accession: B41682; 802693; A05288
R,Accession: B41682; 802693; A05288
A,Title: Xenopus lacvis serum albumin: sequence of the complementary deoxyribonucleic & during development.
A,Reference number: A41682; MUD:89313788; PMID:2747653
A,Accession: B41682
A,Accession: B41682
A,Accession: B41682
A,Accession: B41682
A,Accession: B41682
A,Residues: 3-607 cMOS>
A,Cross-references: GB:M21442; NID:g213930; PIDN:AA449637.1; PID:g213931
R,Schorppy, M.: Doebbeling, U.; Wagner, U.; Ryffel, G.U.
J, Mol. Biol. 199, 83-93, 1988
A,Title: S'-flanking and S'-proximal exon regions of the two Xenopus albumin genes. Del A,Accession: 802692; MUID:88172470; PMID:2451026
A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,Accession: A,ACCESION A,ACCESI
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C;Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
C;Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
F;19-24/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: 74K serum albumin #status predicted <MAT>
F;22-01/Domain: serum albumin repeat homology <SA2>
F;22-01/Domain: serum albumin repeat homology <SA3>
F;30/Binding site: copper (His) #status predicted
F;80/Binding site: copper (His) #status predicted
F;26/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 455-502, L',504-557 <WOL>
A;Residues: 455-502, L',504-557 <WOL>
A;Cross-references: GB:NZ8276
A;Note: the authors translated the codon TAT for residue 63 as Thr
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
mones (weak bonds with these hormones promote their transfer across the membranes), th)
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A; Readdues: 148 < 4SCH3.
A; Readdues: 148 < 4SCH3.
A; Cross-references: EMBir, 226826
R; Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.;
Eur. J. Biochem: 146, 489-496, 1985
A; Title: Deinduction of transcription of Xenopus 74-kDa albumin
A; Reference number: A05288; MUID:85126974; PMID:3971963
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C; Species: Canis lupus familiaris (dog)
C; Date: O4-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
C; Accession: 146986
R; Spitzauer, S.; Schweiger, C.; Sperr, W.R.; Pandjaitan, B.; Valent, P.; Muhl, S.; Ebner
R; Spitzauer, S.; Schweiger, C.; Sperr, W.R.; Pandjaitan, B.; Valent, P.; Muhl, S.; Ebner
A; Title: Molecular characterization of dog albumin as a cross-reactive allergen.
A; Reference number: 146986; MUID:94201492; PMID:7512102
A; Accession: 146986
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mANA
A; Molecule type: mANA
A; Residues: 1-65 cSpr>
A; Residues: 1-265 cSpr>
A; C; Superfamily: serum albumin; serum albumin repeat homology cSA2>
F;417-596/Domain: serum albumin repeat homology <8A3>
F;30/Binding site: copper (His) #status predicted
F;80-89,102-118,117-128,152-197,196-205,228-274,273-281,293-307,306-317,344-389,388-397,
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                                                                                                                                                                                       Query Match 50.2%; Score 1038.5; DB 1; Length 615; Best Local Similarity 47.9%; Pred. No. 9.4e-70; Matches 185; Conservative 75; Mismatches 125; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAADPHECYAKVFDEFKPLVEEPQNL 387
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A/FRESIDES: 1-615. CADA.

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A/CLOSS-TEFERENCES: EMBL:X60688; NID:963747; PIDN:CAD43098.1; PID:963748

R/Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.

J. Biol. Chem. 258, 4556-4564, 1983

A/Title: The 5' noncoding and flanking regions of the avian very low density apolipopror A/FRESIDES: ADGORDA

A/Accession: A05078

A/Accession: A05079

A/Accession: A.M.; Geller, D.M.

Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977

A/Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.

A/Accession: A13451

A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/Accession: A/ACCESSION A/AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVF 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serum albumin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S15571; A65078; A1851
R;Cassady, A.I.; Salklid, C.K.; Baverstock, P.; Wallace, J.C.
submitted to the EMBL Data Library, July 1991
A;Reference number: S15571
                                                                                                                                                                                                                                                                                                                                                          75 CTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETF
                                                                                                                                                                                                                                                                                                                                                                                                                    CAIPNLRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTKVHTECCHGDLLECA
                                                                                                                                                                                                                                                                                                 Gaps
A;Cross-references: EMBL:X13060; NID:g52939; PIDN:CAA31458.1; PID:g899334 C;Superfamily: serum albumin; serum albumin repeat homology C;Keywords: carrier protein; duplication; metal binding; plasma F;1-104/Domain: serum albumin repeat homology (fragment) <SA1>F;123-296/Domain: serum albumin repeat homology sAA2>F;313-453/Domain: serum albumin repeat homology (fragment) <SA3>F;315-453/Domain: serum albumin repeat homology (fragment) <SA3>F;315-453/Domain: serum albumin repeat homology (fragment)
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                                                                                                                                                                                                                                                                                             47; Indels
                                                                                                                                                                                                                             61.1%; Score 1264; DB 2;
ilarity 70.6%; Pred. No. 1.1e-86;
Conservative 45; Mismatches 47;
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                                                                                                                                                                                                                                                               Similarity
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A; Residues: 1-615 < CAS>
                                                                                                                                                                                                                             Query Match
Best Local Simil
Matches 221; C
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                                                      albumin - Mongolian jird

C;Species: Meriones unguiculatus (Mongolian jird)

C;Species: Meriones unguiculatus (Mongolian jird)

C;Accession: JC5838

R;Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.

My Res. 4, 351-354, 1997

A;Title: Sequencing of CDNA encoding serum albumin and its extrahepatic synthesis in the A;Reference number: JC5838, MUID:98116663; PMID:9455485

A;Accession: JC5838

A;Accession: JC5838

A;Residues: 1-609 < xyos>

A;Cross-references: DDBJ;AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278
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A;Residues: 1-418 <MIN.
A;Residues: 1-418 <MIN.
A;Cocascio, C.; DesGBALGII; NID:g191764; PIDN:AAA37190.1; PID:g191765
R;Boccascio, C.; DesGBALTECTE, J.; Meunier-Rotival, M.
Gene 88, 181-186, 1990
A;Title: Empty and occupied insertion site of the truncated LINE-1 repeat located in the
A;Reference number: 148638; MUID:90269606; PMID:1971802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of pseudod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AMCTAFQENAEAFWGHYLHBVARRHPYPYGPELLYLADKYTAVITECCAADDKGACLTPK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVD 121
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1987 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A05139; 186838
R;Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
Mol. Biol. Bvol. 2, 347-358, 1985
A;Title: The rate of molecular evolution of alpha-fetoprotein approaches that A;Reference number: A93055; MUID:88216123; PMID:2452956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 HTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: liver
C, Superfamily: serum albumin, serum albumin repeat homology
F, 222-395/Domain: serum albumin repeat homology <SA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 76.6%; Score 1585; DB 2; Similarity 73.6%; Pred. No. 1.8e-110; H4; Conservative 40; Mismatches 62;
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A;Molecule type: DNA
A;Residues: 379-453 <BOC>
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Best Local Simi
Matches 284;
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J. Biochem. 79, 1183-1196, 1976

A; Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino A; Reference number: A91940; MUID:76260153; PMID:956149

A; Rocession: A91940; MUID:76260153; PMID:956149

A; Residues: 223-288;572-60und

A; Note: 262-Leu was also found

A; Note: 223-Leu was also found

A; Residues: 223-288;572-60und

A; Title: Copper(II) binding ability of human alpha-fetoprotein.

A; Recerence number: A90758; MUID:9901617; PMID:80265

A; Contents: annotation; copper binding

A; Title: Copper(II) binding ability of human alpha-fetoprotein.

A; Reference number: A90758; MUID:9901617; PMID:2474609

A; Reference number: A45800; MUID:89341406; PMID:2474609

A; Reference number: A45800; MUID:89341406; PMID:2474609

A; Reference number: A5501; MUID:87286876; PMID:347556

A; Reference number: I57621; MUID:8728876; PMID:347556

A; Reference number: I57621; MUID:87286876; PMID:347556

A; Reference number: I57621; PMID:8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: GB: MI6825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C; Superfamily: serum albumin; serum albumin repeat homology
C; Superfamily: serum albumin; serum albumin metal binding; plasma
F; H-18/Domain: signal sequence #status experimental csic.
F; 19-24/Domain: propeptide #status experimental csic.
F; 19-24/Domain: propeptide #status experimental cpro.
F; 29-202/Domain: serum albumin repeat homology csh.
F; 21-394/Domain: serum albumin repeat homology csh.
F; 21-394/Domain: serum albumin repeat homology csh.
F; 27/Binding site: copper (His) #status experimental
F; 77-86, 99-115, 114-125, 148-193, 192-201, 224-270, 269-277, 289-303, 302-313, 340-385, 384-393,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
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NyAlternate names: preproalbumin
C'Special Rattus norvegicus (Norway rat)
C'Special Rattus norvegicus (Norway rat)
C'Special Rattus norvegicus (Norway rat)
C'Date: 31-Nay-1979 #sequence revision 31-Nay-1979 #text_change 22-Jun-1999
C'Accession: A93872; A92211; A91946; A91940; C$5800; I57621; A03233
R'Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Accession: A93872; M.; A.; 78, 243-246, 1981
A;Title: Nuclectide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUD:8123722; PMID:7017712
A;Accession: A93872
A;Accession: A93872
A;Accession: A93872
A;Kesidues: 1-608 cSAR>
A;Cross-references: GB:V01222; GB:J00698; NID:g55627; PIDN:CAA24532.1; PID:g55628
R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 22, 6846-6855, 1977
A;Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analys
A;Residues: 1-38 csar.
A;Accession: A92211
A;Note: cleavages during protein maturation
A;Residues: 1-38 csar.
B;Isemura, S.; Ikenaka, T.
J. B; Sechem. 83, 35-48, 1978
A;Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A;Reference number: A91946; MUD:78109429; PMID:564345
          F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: serum albumin #status predicted <MAT>
F;25-201/Domain: serum albumin repeat homology <SA1>
F;220-393/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;412-591/Domain: serum albumin repeat homology SA3>
F;27/Binding site: copper (His) #status predicted
F;27/Binding site: copper (His) #status predicted
F;263/Binding site: bilirubin (Lys) #status predicted
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A,Molecule type: protein
A,Residues: 25-222 <IS1>
R,Isemura, S., Ikenaka, T.
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A,Reference number: A91457
A,Contents: annotation; disulfide bonds
R;Werlen, R.C.; Offord, R.E.; Rose, K.
Blochem. J. 302, 907-911, 1994
A;Tile: Preparation and characterization of novel substrates of insulin proteinase (EC A,Reference number: S55232; MUID:95031935; PMID:7945219
                                                                                                                                                                                                                                                                                                                    A, Status: preliminary
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
C, Molecule type: protein
C, Superfamily: serum albumin; serum albumin repeat homology
C, Keywords: carrier protein; copper binding; duplication; plasma
C, Keywords: carrier protein; copper algumin sequence #status experimental < PRO>
F, 24 Domain: serum albumin repeat homology < SA1>
F, 25 - 201/Domain: serum albumin repeat homology < SA2>
F, 25 - 201/Domain: serum albumin repeat homology < SA2>
F, 25 - 201/Domain: serum albumin repeat homology < SA3>
F, 114 - 125 / 147 - 192 / 191 - 200, 223 - 269 / 268 - 302 / 301 - 312 / 339 - 384 / 383 - 392 /
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Best Local Similarity 74.9%
Matches 290; Conservative
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C;Accession: A38885; A36401; A91258; B60808; S10780; D45800; A26693; A90309; A91458; A94 R;Holowachuk, E.W.; Stoltenborg, J.K.; Reed, R.G.; Peters Jr., T. submitted to the EMBL Data Library, August 1991
A;Referciption: Bovine serum albumin: cDNA sequence and expression.
A;Reference number: A38885
A;Accession: A38885
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A,Molecule type: protein.
A,Residues: 25-41,'H', 43-57,59-64 <STR>
A,Residues: 25-41,'H', 43-57,59-64 <STR>
Carraway, R.E.; Cochrane. D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A,Title: Structures of histamine-releasing peptides formed by the action of acid proteas A,Reference number: A45800; MUID:89341406; PMID:2474609
A,Accession: D45800
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**Residues: 1-607 < HOLD.**

**A; Residues: 1-607 < HOLD.**

**A; Residues: 1-607 < HOLD.**

**A; Residues: 1-607 < HOLD.**

**B; Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.

**R; Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.

**A; Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.

**A; Hirayama, M.; Residues: Residues: Residues: Residues: Residues: Residues: Residues: Residues: A;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Molecule type: protein
R;Residues: 25-41 - 4812.
R;Strawich, E.; Glimcher, M.J.
Eur. J. Blochem. 191, 47-56, 1990
Eur. J. Blochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A;Reference number: $10780; MUID:90336641; PMID:2379503
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A;Residues: 1-32 <MAG>
R;Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A;Title: Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing
A;Reference number: A60808; MUID:88267456; PMID:3389500
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A;Residues: 163-172 (CAR-)
A;Residues: 163-172 (CAR-)
Y; Biol. Chem. 262, 5968-5973, 1987
J. Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from
A;Reference number: A26693; MUID:87194805; PMID:2437111
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A;Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,
R;Brown, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Molecule type: 25-41, 41-43-189, 'E', 191-213, 'T', 215-323, 'D', 325-393, 'TS', 396-607 < HIR>
A; Readidue: 25-41, 'H', 43-189, 'E', 'D' 'Bavie, E'W.
Eur. J. Biochem. 98, 477-485, 1979
A; Title: Bosynthesis of bovine plasma proteins in a cell-free system.
A; Reference number: A91258; MUID: 80024278; PMID: 488109
A; Accession: A91258
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Fed. Proc. 34, 591, 1975
A,Title: Structure of bovine serum albumin.
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A, Reference number: A94551
A, Accession: A94551
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A;Accession: A91458
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A;Residues: 402-433 <REE>
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A;Residues: 190-195 <BR2>
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Fed. Proc. 33, 1389, 1974
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A;Accession: S06936
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosestations: 1-607 -5BRO-
A;Crosestreferences: EMBL:X17055; NID:g1386; PIDN:CAA34903.1; PID:g1387
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper C;Comment: Serum albumin the period promones (weak bonds with those hormones promote their transfer across the memb) C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                              61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 NTLCDEFKADEKKFWGKYLYEIARRHPYFYAPELLYYANKYNGVFQDCCQAEDKGACLLP 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 NLPPLTADFAEDKDVCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLKLAKEYEATLEEC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 VHKECCHGDLLECADDRADLAKYICDNQDTISSKLKECCDKPLLEKSHCIAEVEKDAIPE 323
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S06936
R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10455, 1989
A;File: Nucleocide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:90098888; PMID:2602160
                                                                                                                                                                                                                            25 DTHKSEIAHRFKDLGEEQFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAKTCVADESHA
                                                                                                                                                                                                                                                                                                                                                                                           121 DVMCTAFHDNBETFLKKYLYBIARRHPYFYAPBILFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                                                                                                DAHKSEVAHRFKDLGEENFKALVL1AFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
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; Score 1618.5; DB 1; Length 607;
; Pred. No. 5.6e-113;
46; Mismatches 50; Indels 1;
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A; Krestauces: 1-vo. vkmi. A; Krestauces: 1-vo. vkmi. A; Krestauces: 1-vo. vkmi. A; Krestauces: 1-vo. vkmi. A; Krestauces: 1-vo. vkmi. A; Chu, M.; Mackinnon, M. Bone Miner. Res. 4, 235-241, 1989
J. Title: Serum albumin and its acid hydrolysis peptides dominate preparations of miners A; Reference number: A61006; MUID:89269769; PMID:2728927
A; Accession: A61006
A; Molecule type: protein
A; Residues: 23-51, X',53-54; XXXGY',146,'E',150-151,'XVN',155 cLIM>A; Residues: 23-51,'X',53-54; XXXGY',146,'E',150-151,'XVN',155 cLIM>A; Experimental source: dental enamel
A; Mote: albumin and other serum proteins are also found in bone C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membi C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; metal binding; plasma P; 1-16/Domain: serum albumin repeat homology cSA1>F; 23-605/Product: serum albumin repeat homology cSA2>F; 21-199/Domain: serum albumin repeat homology cSA3>F; 21-199/Domain: serum albumin repeat homology cSA3>F; 24,97-113,112-123,145-190,189-198,221-267,266-274,286-300,299-310,337-382,381-390, P; 261/Binding site: bilirubin (Lys) #status predicted
F; 21/Binding site: bilirubin (Lys) #status predicted
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CiSpecies: Bos primigenius taurus (cattle)
CiDate: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S01382; A61006
A;Reference Acids Res. 16, 1988
A;Ritle: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DTYKSEIAHRFKDLGEQYFKGLVLIAFSQHLQQCPYEBHVKLVREVTEFAKTCVADESAB
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Best Local Similarity 75.2%
Matches 291, Conservative
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C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, C; Comment: Serum albumin serum albumin repeat homonosy promote their transfer across the membra C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; metal binding; plasma
F; 19-24/Domain: signal sequence #status predicted <PRO>
F; 25-607/Product: serum albumin #status predicted <ARO>
F; 25-607/Product: serum albumin repeat homology <ASA>
F; 29-201/Domain: serum albumin repeat homology <ASA>
F; 212-501/Domain: serum albumin repeat homology <ASA>
F; 27/Binding site: copper (His) #status predicted
F; 77/Binding site: copper (His) #status predicted
F; 263/Binding site: bilirubin (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                             C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S34053
R;HO, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
Eur. J. Biochem. 215, 205-212, 1993
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
A;Reference number: S34053; MUID:93345495; PMID:8344282
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                                                                                                                                                                                                                                                                                                                   serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
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                    DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYBYARRHPDYSVVLLLRLAKTYETTLEKC
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80.3%; Score 1660.5; DB 1;
Best Local Similarity 77.3%; Pred. No. 4.2e-116;
Matches 299; Conservative 40; Mismatches 47;
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A; Residues: 1-607 <HOA>
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F;166-174/Product: kinetensin #status experimental <kip> F;221-394/Domain: serum albumin repeat homology <sa2> F;413-522/Domain: serum albumin repeat homology <sa3> F;413-522/Domain: serum albumin repeat homology <sa3> F;27/Binding site: copper (His) #status predicted F;77-86,99-115,114-125,148-193,192-201,224-270,269-303,302-313,340-385,384-393,4 F;714/Binding site: opyridoxal phosphate (Lys) (covalent) #status experimental Query Match  Query Match  DarkSEVAHPREDICEENFKALVIAFAQYLQQCPEEDHYKLVNEVTEFAKTCVADESAE  Matches 387; Conservative 0, Mismatches 0; Indels 0, Gaps 0;  Matches 387; Conservative 0, Mismatches 0; Indels 0, Gaps 0;  DarkSEVAHPREDICEENFKALVIAFAQYLQQCPFEDHYKLVNEVTEFAKTCVADESAE 84  Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEWADCCAKQEPERNECFLQHKDDNPNLPRLWRPEV 120                                       </sa3></sa3></sa2></kip>	Db 77 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPPLVRPEV 136  Qy 121 DVMCTAPHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180  Db 137 DVMCTAFHDNEATFLKKYLYEIARRHPYFYAPELLFFARRYKAAFTECCQAADKAACLLP 196  181 KLDELRDEGKASSAKCRLKCASLOKFGERAFKAMAVARLSGRFPKAEFAEVGCAADKAACLLF 240  197 KLDELRDEGKASSAKCRLKCASLOKFGERAFKAMAVARLSGRFPKAEFAEVSKLYTDLTK 240  241 VHTECCHGDLLECADDRADLAKYICENQDSISKLKECCEKPLLEKSHCIAEVUDEMPA 300  252 VHTECCHGDLLECADDRADLAKYMCENQDSISSKLKECCEKPLLEKSHCIAEVUNDEMPA 316  Db 257 VHTECCHGDLLECADDRADLAKYMCENQDSISSKLKECCEKPLLEKSHCIAEVUNDEMPA 316  Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTVETTLEKC 376  Qy 361 CAAADPHECYAKVFDEFKPLVEEPQNL 387  CAAADPHECYAKVFDEFKPLVEEPQNL 403  Db 377 CAAADPHECYAKVFDEFKPLVEEPQNL 403
OY 181 KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK 240  Db 205 KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK 244  QY 241 VHTECCHGDLLECADDRADLAKXICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300  Db 265 VHTECCHGDLLECADDRADLAKXICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300  OY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360  Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 384  OY 361 CAAADPHECYAKVPDEFKPLYBEPQNL 387	)-Aug-1999 im albumin.
SULT 2  rum albumin precursor - rhesus macaque  rum albumin precursor - rhesus macaque)  bate: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999  Accession: A47391  Markins, S.; Saxamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F.  oc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993  Title: CDNA and protein sequence of polymorphic macaque albumins that differ in biliru  Reference number: A47391; MUID:93211971; PMID:8460152  Contents: B/B homozygote  Accession: A47391	C; Comment: This protein is the major protein component in plasma. It functions as a mul- ein has 35 conserved cysteine residues. C; Superfamily: serum albumin; serum albumin repeat homology C; Keywords: liver; plasma C; Keywords: liver; plasma C; Keywords: liver; plasma F; 19-24/Domain: signal sequence #status predicted <rig>F; 19-24/Domain: serum albumin #status predicted <rmt> F; 29-202/Domain: serum albumin repeat homology <sa1>F; 221-394/Domain: serum albumin repeat homology <sa2>F; 413-592/Domain: serum albumin repeat homology <sa3> Cuery Match 83:5\$; Score 1727; DB 2; Length 608; Best Local Similarity 80:6\$; Pred. No. 4:6e-121; Matches 312; Conservative 34; Mismatches 41; Indels 0; Gaps 0;</sa3></sa2></sa1></rmt></rig>
A; Status: preliminary A; Molecule type: mRNA; protein A; Molecule type: mRNA; A; Residues: 1-600 < WAT; A; Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295 A; Experimental source: liver A; Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIP:128281) C; Superfamily: serum albumin; serum albumin repeat homology csA1> F; 21-194 (Domain: serum albumin repeat homology csA2> F; 405-584 (Domain: serum albumin repeat homology csA3>	OY  1 DAHKSEVAHRENDLGBENFKALVLIAFAQYLQQCPFEDHVKLVNBVTEFAKTCVADESAE 60  25 BAHQSEIAHRENDLGBEHPRGLVLVAFSQYLQQCPFEDHVKLVNBVTEFAKGCVADQSAA 84  OY  61 NCDKSLHTLFQDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRFBV 120  DS  85 NCEKSLHFLLGDKLCTVASLRETYGEMADCCKKEPPERNECFLQHKDDNPNLPRLVRFBV 120  OY  121 DVMCTAFHDNBETFLKKYLYBIARHPYBYAPELLFFAKRYKAAFTECCQAADKAGLLP 180
Query Match         96.1%;         Score 1988;         DB 2;         Length 600;           Best Local Similarity         94.6%;         Pred. No. 1.6e-140;         Indels         0;         Gaps         0;           Matches 366;         Conservative         13;         Mismatches         8;         Indels         0;         Gaps         0;           QY         1 DAHKSEVAHRFKDLGEENFRALVLARFAQYLQQCPFEBHVKLVNEVTERAKTCVADESAE         60         17 DTHKSEVAHRFKDLGEEHFKGLVLVAFSQYLQQCPFEBHVKLVNEVTERAKTCVADESAE         76           QY         61 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV         120	Db 145 DAMCTATHENEGREIGKYLVEITÄRHPYPYÄPELLYYÄEEYKGVFTECCEÄÄDKÄÄCLTP 204  Qy 181 KLDELRDEGKASSAKQRLKCASLOKFGERAFKANAVARLSORFPKAEFAEVSKLYTDLTK 240  Li

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A Gene: GDB:ALB
A; Gross-references: GDB:118930; OMIM:103600
A; Arcoss-references: GDB:118930; OMIM:103600
A; Map position: 4411-4413
C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyridc
F;1-18/Domain: signal sequence #status predicted <SIG>F;1-28/Domain: propeptide #status experimental <PRO>F;25-609/Product: serum albumin #status experimental <MPT>F;29-202/Domain: serum albumin repeat homology <SA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atase activity
C;Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (wea)
C;Comment: A large number of variants of human serum albumin have been described.
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version 5.1.6
- 2004 Compugen Ltd.
 GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

(without alignments)
789.208 Million cell updates/sec April 19, 2004, 11:37:59 ; Search time 47.169 Seconds Run on:

Title: Perfect score:

US-09-832-929-18\_COPY\_1\_387
2068
1 DAHKSEVAHRFKDLGBENFK......ECYAKVFDEFKPLVEEPQNL 387 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	albumin	serum albumin prec	albumin	albumin			lbumin		serum albumin - mo	umin	albumin - dog (fra	74K albumin precur	68K serum albumin	alpha-fetoprotein	alpha-fetoprotein	alpha-fetoprotein	afamin precursor -	afamin precursor -	alpha-fetoprotein	alpha-fetoprotein	serum albumin prec		1bumin 2	vitamin D-binding	serum albumin - bu	vitamin D-binding	vitamin D-binding	serum albumin - se
ID	ABHUS	A4/391 S57630	ABHOS	ABPGS	ABBOS	ABSHS	ABRTS	JC5838	A05139	ABCHS	146986	ABXL72	ABXL68	JC4258	FPGO	FPHU	A54906	A53195	FPMS	FPRT	859517	ABONS1	ABONS2	VYHUD	A37253	VYRID	A35327	S27941
DB	!	<i>3</i> C	1 +1	н	Н	Н	Н	0	N	Н	7	Н	<b>~</b> I	~	-1	тH	-1	~	rH	Н	(1	Н	н	-	~	-	-	Н
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អ៊	1	1727	· w	62	61	-	1610	1585	-	1038.5	868	766	737.5	724.5	721.5	720.5	691	656	616	603	572.5	468	465	357	353	352	341	311
Result No.		7 K	1 4	ß	9	7	α	o	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27		

cag island protein	cag pathogenicity	mst101-1 protein -	hypothetical prote	serum albumin, mil	major surface glyc	cell surface glyco	phosphoinositide 3	hypothetical prote	glycoprotein antig	embryonic muscle m	hypothetical prote	ENBP1 protein - ba	sperm tail-specifi	hypothetical prote	hypothetical prote	
A71928	G64585	534153	AG2558	B61511	JC2221	JC2300	T42642	S46754	A34498	A59236	E96558	T43213	S51364	T17272	T30010	
~	~	N	7	N	7	7	7	7	7	~	7	N	7	~	7	
1819	1927	344	1348	30	1004	1083	1658	1228	650	1927	765	1701	1390	1780	1974	
7.2	7.2	5.9	5.9	5.4	5.4	ъ.	5.2	5.2	5.1	5.1	5.1	5.0	4.9	4.9	4.8	
149	148.5	122.5	121.5	111	111	109	108.5	107.5	106	106	105	103.5	102	100.5	100	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

Secum albumin precursor [validated] - human
NyAlternate names: preprealbumin
NyAlternate names: preprealbumin
NyAlternate names: preprealbumin
NyAlternate names: preprealbumin
C.Species: Hown sapiens (man)
C.Species: Hown sapiens (man)
C.Species: Hown sapiens (man)
C.Species: And names: pregrence revision 31-Jan-1997 #text change 17-Mar-2000
C.Jaccession: Ap3743; Ap3396; T33427; T59286; I59313; G01747; S55314; A31420; S06422; S2
R.Jawn, R.W.; Adelnan, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seebn
Nucleic, Acids Res. 9, 6103-6114, 1981
A.MClecuse number: A93743; MUD:82081882; PMID:617178
A.MCcession: A93743
A.MCcession: A93743
A.MCcession: A9374
A.MCcession: A9396; MUD:8210894; PMID:617378
A.MCcession: A9396
A.MUD:821046; A.M. Law, S.W.; Dennison, O.E.
R.MCcossion: A9396
A.MUD:821046; A.M. Law, S.W.; Dennison, O.E.
A.MCcession: A9396; MUD:8210594; PMID:6275391
A.Mccession: A9396; MUD:8210594; PMID:6275391
A.Mccession: A9396
A.MCcossion: A9396; MUD:82105994; PMID:2419329
A.Mccession: A9396
A.MCcossion: A9396
A.Mccassion: A9396
A.Mccassion: A9396
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A.Mccassion: A9396
A.Mccassion: A9396
A.Mccassion: A9397
A.Mccassion: A9397
A.Mccassion: A9398
A.Mccassion: AMB
A.Mccassion: A9398
A.Mccassion: AMB
A

A; Accession: I59286

A.Accession: 123-200
A.Accession: 123-200
A.Molecule type: DNA
A.Molecule this frame-shift variant, designated albumin Roma, leads to analbuminemia
A.Molecule this frame-shift variant, designated albumin Roma, leads to analbuminemia
Broc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994
A.Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl
A.Reference number: IS9313; MUID: 94294404; PMID: 8022807

A, Accession: I59313 A, Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA A;Residues: 589-590, ALPRRVKNLLLQVKLP' <MAD> A;Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVREFV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 DVMCTAFHDNEETFLKKXLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 272
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Best Local Similarity 100.0%; Fred. No. 7.3e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0
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RESULT 15
US-10-133-064-125
US-10-133-064-125
Sequence 125, Application US/10153064
Patent No. 6663485
GENERAL INFORMATION:
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFRENCE: FP56
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
CURRENT PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
LENGTH: 677
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Search completed: April 19, 2004, 12:05:17 Job time : 90.6676 secs

CY 481 LVNRRPCFSALEVDETYVPKZFNAETFFHADICTLSEKERQIKKQTALVELVKHKPKAT 540  Db 572 LVNRRPCFSALEVDETYVPKZFNAETFFFHADICTLSEKERQIKKQTALVELVKHKPKAT 531  CY 541 KEOLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585  Db 632 KEOLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 676  RESULT 14  US-10-153-064-129  Sequence 129, Application US/10153064  Patent No. 6663485  GENERAL INPORMATION :  APPLICANT: Bell et at  APPLICANT: Bell et at  THIS OF INTERTION : Chamcking Berg-1 Pusion Droteins	• • • • • • • • • • • • • • • • • • • •	QY         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQBPERNECFLQHKDDNPNLPRLVRPSV 120           Db         152 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQBPERNECFLQHKDDNPNLPRLVRPEV 211           QY         121 DVMCTAFHDNEETFLKKYLYEIARHPYFYAPELLFFAKKYKAAFTECCQAADKAACLLP 180	Db 212 DVMCTAFHDNEEFFLKKKLIVEIARHPYFYAPELLFFAKRYKAAFTECCGAADKAACLLP 271  Qy 181 KLDELRDEGKASSAKQRLKCASLOKFGERAFKWAVARLSQRFPKAEFABVSKLVTDLTK 240  LIE KLDELRDEGKASSAKQRLKCASLQKFGERAFKWAVARLSQRFPKAEFABVSKLVTDLTK 240  272 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFABVSKLVTDLTK 331	OY 241 VHTECCHGDLLECADDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300  332 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 391  ON 301 DIPSTAAPPVESKTOVCKNVARAKDVFIGMFIJVEVARRHPDYSVVLLIRLAKTYETTLEKC 360	392 DIPSIAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLIRLAKTYETTLEKC 361 CAAADPHECYAKVPDEFKPLVEBPONLIKONCELFBOLGEYKFONALLVRYTKKVPOVST 452 CAAADPHECYAKVPDEFKPLVEBPONLIKONCELFBOLGEYKFONALLVRYTKKVPOVST	421 PTLVBVSRNLGKVGSKCCKHPBAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES	Qy 481 IVNRRPCFSALEVDETYVPKEFNAETFFFHADICTLSBKERQIKKQTALVELVKHKPKAT 540	Qy 541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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OY 361 CAAADPHECYAKVFDEFKPLVEEPONLIKONCELFEGLGEYKFONALLYRYTKKVPQVST 420  432 CAAADPHECYAKVFDEFKPLVEEPONLIKONCELFEGLGEYKFONALLYRYTKKVPQVST 491  421 PTLVEVGRULGKVGSKCCKHPEARMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 480  422 PTLVEVGRULGKVGSKCCKHPEARMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 551  433 CAAADPHECYAKVFDEFKPLVEEPONLIKONCELFEGLGEYFFONALLYRYTKKVPQVST 491  424 LIVENSPRINGKVGSKCCKHPEARMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 551  OY 481 LIVERPCFSALEVDETVVPKEFRAETFFFHADICTLSEKERQIKKQTALVELVKHRKAT 540  552 LVNRRPCFSALEVDETVVPKEFRAETFFFHADICTLSEKERQIKKQTALVELVKHRKAT 611  554 KEQLKAVMDDFAAFVEKCKADDKETCFAEBGKKLVAASQAALGL 585  [	VS-10-153-064-127 US-10-153-064-127 US-10-153-064-127 Sequence 127, Application US/10153064 Patent No. 6663485 GENERAL INPORMATION: TITLE OF INVENTION: TITLE OF INVENTION Chemokine Beta-1 Fusion Proteins TITLE OF INVENTION WHER: US/10/153,064 CURRENT APPLICATION NUMBER: US/10/153,064 CURRENT PILING DATE: 2002-05-24 CURRENT FILING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 137 SOFTWARE: Patentin version 3.1 IENGTH: 676 TYPE: PRI TYPE: PRI TYPE: PRI CREAMINGM: Homo sapiens US-10-153-064-127	Query Match  Best Local Similarity 100.0%; Pred. No. 7.3e-287;  Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy I DAHKSBVAHRFKDLGEBNFKALVLJAFAQVLQCPFEDHVKLVNBVTEFAKTCVADESAE 60	Db 92 DAHKSEVARFEKDIGEBNEKALUIAFAQVIQCEFEDHVILVNBITTEFAKTCAALESI 151  Qy 61 NCDKSLHTLFGDKLCTVATLRETYGBMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120  Db 152 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 211	QY         121 DVMCTAFHDNBETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180           DD         212 DVMCTAFHDNBETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 271           DO         181 KIDRIAPBGKAASSAKORIKCASIOKFGRBAPKAMAVARISORPDKAFFBEKKKIVTDITK 240	272 KLDELKUEGKASSAKQRIKCASLQKFGERAFKAMAVRISQKFFKAEFAEVANTILL	301 DLPSLAADFVBSKDVCKNYABAKDVPLGMFLYEYARRHPDYSVVLLLRLAKTYETTLBKC	QY         361 CARADPHECYAKVFDEFKPLVEEFQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420           DD         452 CARADPHECYAKVFDEFKPLVEEFQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 511	Qy 421 PTLVEVSRNLGKYGSKCCKHPEAKRMPCAEDYLGVVLNQLCVLHEKTPVSDRVTKCCTES 480

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Patent No. 6663485
GENERAL INFORMATION:
FILE REPERENCE: PF56
FILE REFERENCE: PF56
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT APLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 130
LENGTH: 656
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; Pred. No. 7e-287;
0; Mismatches 0;
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Best Local Similarity 100.0%;

Matches 585; Conservative 0
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; ORGANISM: Homo sapiens
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                       DUMCTAFHDNEETFLKKYLYBIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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DVMCTAFHDNEETFLKKYLYBIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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Patent No. 6663485
GENERAL INFORMATION:
APPLICANT Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Pro
FILE REPERENCE: PF556
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
SEQ ID NOS: 137
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                              67 DAHKSEVAHRFKDLGBENFKALVLIAFAQYLQQCPFEDHVKLVNEVTBFAKTCVADESAE
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                                                                               61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
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; Patent No. 6663485
; GENERAL INFORMATION:
; TILLE OF INVENTION: Chemokine Beta-1 Fusion Pro
; CURRENT PRILING DATE: 2002-05-24
; PRIOR FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER: Patentin Version 3.1
; SOFTWARE: Patentin Version 3.1
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ORGANISM: Homo sapiens
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US-10-153-064-132
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                                                                                   Length 610;
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; Patent No. 6663485
; GENERAL INPORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
CURRENT APPLICATION UNMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
; PRIOR PRILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SEQ ID NO 133
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 3103; DB 4; Best Local Similarity 100.0%; Pred. No. 6.9e-287; Matches 585; Conservative 0; Mismatches 0;
                                                                               100.0%; Score 3103; DB 4;
100.0%; Pred. No. 6.3e-287;
ive 0; Mismatches 0;
) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-984-186-2
                                                                             Ouery Match
Best Local Similarity 100.
Matches 585; Conservative
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APPLICANT: Fleer, Reinhard

APPLICANT: Fleer, Reinhard

Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard

Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

CONTAINING SAID POLYPEPTIDES

CONTAINING SAID POLYPEPTIDES
                      325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 384
DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYBYARRHPDYSVVLLLRLAKTYETTLEKC 360
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                                                                                                           385 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
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                                                                                                                                                   PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
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CORRESPONDENCE ADDRESS:
ADDRESSES: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegevile
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-200
CLASSIFICATION NUMBER: US/09/984,186
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1993
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 31-JAN-1993
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 31-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMith Ph.D., Julie K.
REFERENCE/DOCKET NUMBER: $792006-US
TELECOMMUNICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09984186
Patent No. 6686179
GENERAL INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                         TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
CORRESPONDENCE: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Callegeville
STATE: PA
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100.0%; Pred. No. 6.3e-287;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                               APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (610) 454-38:
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 585; Conservative
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RESULT 7
US-08-797-689-2
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Sequence 7, Application US/10153064

Patent No. 665485

GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF56
CURRENT APPLICATION NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR PAPLICATION NUMBER: 60/293,212

PRIOR PELING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SEQ ID NO 7

LENGTH: 609
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100.0%; Score 3103; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.2e-287;
Matches 585; Conservative 0; Mismatches 0;
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US-10-153-064-7
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RESULT 6
US-09-076-594-977

Sequence 977, Application US/09976594

Patent No. 6673349

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Purness, Michael
APPLICANT: Purness, Michael
APPLICANT: Purness, Michael
APPLICANT: Purness, Michael
APPLICANT: Buchbinder, Jenny
FULE REFERENCE: PA-0041 US
FULE REFERENCE: PA-0041 US
FURBENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 1143

SEQ ID NO 977

LENGTH: 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FATURE:
MAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
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                                                                                                                                                                 LVNRRPCFSALEVDETYVPKEFNAETPTFHADICTLSEKERQIKKQTALVELVKHKPKAT
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361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
                                                                                PILVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
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Sequence 5, Application US/10153064

Patent No. 6663465

GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT PILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SEQ ID NO 5:

LENGTH: 585
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ilarity 100.0%; Pred. No. 5.9e-287;
Conservative 0; Mismatches 0;
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US-10-153-064-5
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Best Local Simil
Matches 585; C
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Patent No. 6274305

GENERAL INFORMATION:
APPLICANT: Sorto, Ana M
APPLICANT: Sorto, Ana M
ITILE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
STATE: California
COUNTRY: United States of America
STATE: California
COUNTRY: United States of America
STATE: California
COUNTRY: United States of America
STATE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 19-DEC-1996
CURRENT APPLICATION DATE:
FILING DATE: 19-DEC-1996
CLASSITCATION NUMBER: US/08/769,746
FILING DATE: 19-DEC-1996
CLASSITCATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE CHARACTERISTICS:
LENGTH: 585 maino acids
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 maino acids
TTPE: mino acids
TTPE: mino acids
TTPE: Main acids
TTPE: Main acids
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  KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
                      541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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100.0%; Score 3103; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.9e-287;
Matches 585; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein
US-08-769-746-2
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SOFIMARS: MICHOSOLE WOLD BILL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,572
FILING DATE: 11-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/23857
FILING DATE: 1-MAR-1995
APPLICATION NUMBER: GB 9404270.2
FILING DATE: 5-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NAOME BISWARS
                                                                                                                                                                                                                                                                                                                                                               NAME: Naomi Blewae
REGISTRATION NUMBER: 38,384
                  ZIP: 19406-1310
COMPUTER READABLE FORM:
MEDION TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: MS-DGR
SOFTWARE: Mirror
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CE
TELECOMMUNICATION INFORMATION
TELEPHONE: 610/878/4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
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                                                                                                                          /note= "Alternative C-termini
HSA(1-n)"
                                                                                                                                                                                                                                                                                                          100.0%; Score 3103; DB 1;
llarity 100.0%; Pred. No. 5.9e-287;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              /note= "Amino acid sequence natural HSA"
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                         PEATURE:

| NAME/KEY: Region | LOCATION: 369.419 |
| OTHER INFORMATION: H; |
| PEATURE: NEORMATION: H; |
| PEATURE: NAME/KEY: Region | LOCATION: 1.585 |
| OTHER INFORMATION: // OTHER INFORMATION: n |
| US-08-153-799-14
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 585; Conserv
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                                                                                                                                                                                                                         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
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                                                                                                                                                                                                                                                                        DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
                                                                                                                                                                                                                                                                                                            DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPBLLFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                                              DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                               ..
  100.0%; Score 3103; DB 2; Length 585; 100.0%; Pred. No. 5.9e-287;
                                               0; Mismatches
Query Match
Best Local Similarity 100.
Matches 585; Conservative
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RESULT 2
US-08-702-572-2
is Sequence 2, Application US/08702572
is Sequence 2, Application US/08702572
is Patent No. 5965386
is GENERAL INFORMATION:
i APPLICANT: Kerry-Williams, Sean M
is APPLICANT: Gilbert, Sarah C
i TILE OF INVENTION: Yeast Strains and Modified Albumins
i NUMBER OF SEQUENCES:
i NUMBER OF SEQUENCES:
i ADDRESSEE: Centeon L.L.C.
i STREET: 1020 First Avenue

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Sequence 14, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 977, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 120, Appli
Sequence 127, Appli
Sequence 127, Appli
Sequence 125, Appli
Sequence 125, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 16, Appli
                                                                                             April 19, 2004, 11:40:29; Search time 89.6676 Seconds (without alignments) 336.813 Million cell updates/sec
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                                                                                                                                                           US-09-832-929-18
3103
1 DAHKSEVAHRFKDLGEENPK.....TCFABEGKKLVAASQAALGL 585
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1: /cgn2_6/ptodate/2/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodate/2/iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-01-153-064-5

US-01-153-064-7

US-09-97-689-2

US-09-98-186-2

US-10-153-064-1131

US-10-153-064-1131

US-10-153-064-1131

US-10-153-064-1129

US-10-153-064-1129

US-10-153-064-1129

US-10-153-064-1129

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US-10-153-064-1129

US-10-153-064-1129

US-08-56-918-4

US-08-256-918-4

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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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28 3092.5 99.7 652 4 US-10-153-064-96 Sequence 96, Appl 30 3092.5 99.7 652 4 US-10-153-064-105 Sequence 99, Appl 30 3092.5 99.7 652 4 US-10-153-064-105 Sequence 99, Appl 32 3092.5 99.7 660 4 US-10-153-064-95 Sequence 90, Appl 32 3092.5 99.7 660 4 US-10-153-064-95 Sequence 90, Appl 33 3092.5 99.7 676 4 US-10-153-064-95 Sequence 93, Appl 35 3092.5 99.7 676 4 US-10-153-064-95 Sequence 93, Appl 35 3092.5 99.7 676 4 US-10-153-064-99 Sequence 104, Appl 36 3022.5 99.7 676 4 US-10-153-064-92 Sequence 104, Appl 37 3092.5 99.7 676 4 US-10-153-064-104 Sequence 104, Appl 37 3092.5 99.7 184 4 US-10-153-064-102 Sequence 102, Appl 38 3086.5 99.5 692 4 US-10-153-064-101 Sequence 101, Appl 40 2458.5 79.0 583 1 US-08-448-196A-5 Sequence 5, Appli 41 2450.5 79.0 583 1 US-08-448-196A-6 Sequence 6, Appli 44 2389 77.0 582 1 US-08-134-638-1 Sequence 7, Appli 45 1249.5 40.3 609 1 US-08-134-638-1 Sequence 7, Appli 45 1249.5 40.3 609 1 US-08-134-638-1
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# ALIGNMENTS

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RESULT 1

UE-08-153-799-14

Sequence 14, Application US/08153799
Patent No. 576683
Patent No. 576683
Patent No. 576683
Patent No. 576683

APPLICANT: Ballance, David J
APPLICANT: Ballance, David J
APPLICANT: Ballance, David J
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE DARRESS: R
APPLICATION NOUNCAIN AVENUE
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
ZIP: 0797
```

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Sequence 11, Application US/10424999

Fublication No. US20040052810A1

GENERAL INFORMATION:

APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis

TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REFERENCE: STO1027-A

CURRENT APPLICATION NUMBER: 10/233,675

FRIOR APPLICATION NUMBER: 10/233,675

PRIOR PILING DATE: 2002-09-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin version 3.2

SEQ ID NO 1.

LENGTH: 585

TYPE: PRT

ORGANISM: Artificial Sequence
FRATURE:

CHER INFORMATION: Fusion protein human abrogen

US-10-424-999-11
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                                                                                                                                          Query Match 100.0%; Score 38; DB 11; Length 585; Best Local Similarity 100.0%; Pred. No. 20; Matches 8; Conservative 0; Mismatches 0; Indels
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| SEQ ID NO 18
| LENGTH: 585
| TYPE: PRT
| CRGANISM: Homo Sapiens
| US-09-833-245-18
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US-10-424-999-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/09833118
Publication No. US20030219875A1
GENERAL INFORMATION:
APPLICANT: ROSEN, Craig A.
APPLICANT: Baseltine, William A.
ITLLE OF INVENTION: Albumin Fusion Proteins
FILLE REFERENCE: PF944
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/226, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PALCATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 18
LENGTH: 585
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US-09-833-245-18
Sequence 18, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-15
NUMBER OF SEC ID NOS: 2267
SOFTWARE: PATENTING DATE: 2000-04-25
NUMBER OF SEC ID NOS: 2267
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR PRIOR OF SECULO NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 18
LENGTH: 585
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Similarity 100.0%;
8; Conservative 0
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; ORGANISM: Homo Sapiens
US-09-833-118-18
                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-832-501-18
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Best Local Similarity
Matches 8; Conserv
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US-09-833-118-18
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i Sequence 445, Application US/09932322

publication No. US20030194743A1

GENERAL INFORMATION:
APPLICANT: Beltzer, Corp.
APPLICANT: Petter, M. Daniel
APPLICANT: Potter, M. Daniel
APPLICANT: DIV J.
APPLICANT
CURRENT: POTTER
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SEQ ID NO 445
BEQ ID NO 445

LENTH: 585
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100.0%; Score 38; DB 10; Length 585;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 38; DB 10; Length 585; 100.0%; Pred. No. 20;
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Sequence 18, Application US/09832501

Sequence 18, Application US/09832501

Sequence 18, Application US/09832501

Sequence 18, Application US/09832501

SERVAL INFORMATION:
APPLICANT: Ballance, David J.
APPLICANT: Stabep, Darriell J.
APPLICANT: Stabep, Darriell J.
APPLICANT: Stabep, Darriell J.
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF542
CURRENT APPLICATION NUMBER: US/09/832,501
CURRENT APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
CURRENT APPLICATION NUMBER: US/09/833,117;
CURRENT APPLICATION NUMBER: US/09/833,117;
PRIOR APPLICATION NUMBER: 60/229,388
PRIOR FILING DATE: 2000-04-12;
PRIOR FILING DATE: 2000-04-12;
PRIOR FILING DATE: 2000-01-21;
PRIOR PILING DATE: 2000-01-21;
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25;
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver: 2.1

LENGTH: 585
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo Sapiens
US-09-833-117-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HomoSapiene US-09-932-322-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 VADESAEN 61
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RESULT 9
US-09-833-041-18
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CORRESPONDENCE ADDRESS:
ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: OC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/09984010
Publication No. US20030104578A1
GENERAL INFORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-22-613-445

US-09-32-613-445

Sequence 445, Application US/09932613

Fublication No. US2030091565A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Potter, James P.

APPLICANT: Fleming, Tony J.

APPLICANT: Fleming, Tony J.

APPLICANT: Breen BINDING POLYPEPTIDES AND METHODS BASED THEREON TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON FILE REFERENCE: Dyx-025.1 PCT: DYX-025.1 US

CURRENT RAPLICATION UNMBER: US/09/932,613

CURRENT PILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: Patentin version 3.1

SEQ ID NO 445

LENGTH: 585
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 38; DB 9; Length 585; Best Local Similarity 100.0%; Pred. No. 20; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-929-552-2
                 TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: HomoSapiens
US-09-932-613-445
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US-09-984-010-26
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APPLICANT: Sonesachein, Carlos
Soto, Ana M.
Soto, Man M.
Soto, M.
Soto
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                                                                                        Query Match
100.0%; Score 38; DB 13; Length 241;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-074-956-28

Sequence 28, Application US/10074956

Belloation No. US2002019332A1

GENERAL INCRRANTON:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVERNION:
METHODS OF TREATING BLADDER DISORDERS
TITLE PREPRENCE: 08191-02201

CURRENT APPLICATION NUMBER: US/10/074,956

CURRENT PLING DATE: 2002-06-10

PRIOR PILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 29

SOFTWARE PASSEQ FOR Windows Version 4.0

LENGTH: 268
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Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0: Mismarches
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FILING DATE: 19-DEC-1996
ATTORNEY/AGBNT INPORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: MBRI-02584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09929552 Patent No. US20020123080A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens
US-10-074-956-28
; ORGANISM: Homo sapiens
US-10-074-956-27
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TITLE OF INVENTION: CHIMERIC POLYPEPTIDES OF SERUM ALBUMIN AND USES RELATED THERETO
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Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels
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PUBLICATION NO. US20020193332A1

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS

FILE REFRENCE: 08191-022001

CURRENT APPLICATION NUMBER: US/10/074,956

CURRENT FILING DATE: 2002-06-10

PRIOR PILING DATE: 2002-06-10

PRIOR PILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 27

LENGTH: 241

TYPE: PRT
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Sequence 24, Application US/10074956

Publication No. US2020193332A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS

TITLE REFERENCE: 08191-022001

CURRENT APPLICATION NUMBER: US/10/074,956

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 38; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels
                        CURRENT APPLICATION NUMBER: US/09/768,183
CURRENT FILIDE DATE: 2001-01-23
CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/764918
PRIOR PILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 1999-07-19
NUMBER: OF SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mus musculus
US-09-768-183-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-074-956-24
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) ORGANISM: Mus musculus
US-09-764-918-6
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US-09-764-918-6
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Sequence 6, Appli
Sequence 24, Appl
Sequence 27, Appl
Sequence 28, Appl
                                                                                                                                           April 19, 2004, 12:00:25 ; Search time 3.36842 Seconds (without alignments) 654.724 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-074-956-24
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3 US-10-074-956-27
3 US-10-074-956-28
0 US-09-932-513-45
0 US-09-984-010-26
0 US-09-984-010-26
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0 US-09-932-322-445
0 US-09-833-101-18
1 US-09-833-18-18
1 US-09-833-18-18
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Maximum Match 100%
Listing first 45 summaries
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38
1 VADESAEN 8
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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No.
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Sequence 31, Appl Sequence 34, Appl Sequence 5, Appli Sequence 1, Appli Sequence 2, Appli 2, 
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Sequence 13, Appl
Sequence 16, Appl
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Sequence
Sequence
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     US-10-425-000-31

US-10-433-108-34

US-10-133-064-5

US-10-133-064-5

US-10-139-263-1

US-10-319-263-1

US-10-319-263-1

US-10-414-469-1

US-10-413-831-1

US-10-413-832-2

US-10-413-832-2

US-10-413-832-2

US-10-413-832-2

US-10-414-386-2

US-10-414-386-2

US-10-414-386-2

US-10-414-386-2

US-10-414-386-2

US-10-414-386-2

US-10-619-63-26-26

US-09-984-010-7

US-09-984-010-7

US-09-984-010-7

US-09-984-010-7

US-09-984-186-2

US-10-133-667-2

US-10-133-667-2

US-10-237-866-2

US-10-237-866-2

US-10-237-866-2

US-10-237-866-2

US-10-237-866-2

US-10-337-866-2

US-10-337-866-2

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US-10-337-866-2

US-10-337-866-2

US-10-337-866-2

US-10-337-861-3

US-10-337-861-3

US-10-337-861-3

US-10-337-861-3

US-10-337-861-3

US-10-337-861-3
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Sequence 6, Application US/09764918;
Publication No. US20010056075A1
GENERAL INFORMATION:
APPLICANT: Lamphere, J.
APPLICANT: Lamphere, L.
APPLICANT: Lamphere, L.
APPLICANT: Lamphere, US/09/764,918
CURRENT APPLICATION NUMBER: US/09/764,918
CURRENT APPLICATION NUMBER: US/09/764,918
PRIOR PRIOR PRICATION NUMBER: 09/619285
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
SOFTWARE: Patentin version 3.1
SEQ ID NO 6;
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100.0%; Score 38; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels
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Sequence 6, Application US/09768183
Publication No. US20020048571A1
GENERAL INFORMATION:
APPLICANT: Gyuris, J.
APPLICANT: Lamphere, L.
APPLICANT: Morris, A.

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Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
                                                  Aziz N, Chen H, Etemad-Moghadam B, Yin P;
                                                                                                                                 Example 2; Page 48; 89pp; English.
29-DEC-2000; 2000US-0258764P. 14-JUN-2001; 2001US-0298317P.
                                                  Hedley ML, Urban R,
                                                                    WPI; 2002-195801/25.
                             (ZYCO-) ZYCOS INC.
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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact multiple sclerosis, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a peptide described in the exemplification of the invention Sequence 236 AA;

Query Match
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 1 VADESAEN 8

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Gaps

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VADESAEN 85

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Search completed: April 19, 2004, 11:51:16 Job time : 5.70545 secs

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WPI; 2001-611725/70.
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Matches 8; Conserv
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                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 214 AA;
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18-AUG-2000; 2
06-OCT-2000; 2
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THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF THE STANCE OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                            Recombinant, human serum albumin, HSA, yeast codon bias, host cell; overlapping oligonucleotide, expression vector.
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                    Yeast codon-biased recombinant HSA protein fragment HSA-I.
                                                                                                                                                                                                                                                                                                                                                       BIOENGINEERING CO LTD.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 204 AA;
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                                                                                                                                                                                                                                                                                                                                                       (HAIJ-) HAIJI
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                                                                                                                                                                                                                                                                                                               17-JUN-1998;
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                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                    Li S,
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the roughest enemant of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as untitional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or attilage, as anti-inflammatory agents; and in treatment of leukaemias. Autu29510-AAU33304 represent the amino acid sequences of novel human expression and the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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2000US-0226382P.
2000US-0238380P.
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18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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AA017048;

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The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having a badder disorder, and administering: (a) an isolated nucleic acid (NI) comprising an un-methylated CpG sequence to the mammal; (b) an isolated nucleic acid (NZ) comprising sequence encoding alpha-MSH to the mammal; or is a peptide that binds to a melanocortin receptor to the mammal. The method is useful for modulating immune response in a mammal having a bladder disorder, where administration of (NI) results in an amelioration of or now or symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (NI) results in a medial having interstitial correction of the immune response in a mammal having interstitial cystitis from inflammation which is associated with symptoms of that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of interstitial cystitis or associated with a disruption of melanocyte continual promone (alpha-MSH) concatamers resulting in secretion of the stimulating hormone (alpha-MSH) concatamers resulting in secretion of the stimulating hormone (alpha-MSH) concatamers resulting in secretion of the stimulating hormone (alpha-MSH) concatamers resulting in secretion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating immune responses in a mammal with a bladder disorder e.g.
bladder cancer, by administering nucleic acids comprising un-methylated
CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides t
                                                                                         Bladder disorder; cytostatic; antiinflammatory; immune response; un-methylated CpG sequence; alpha-MSH; melanocortin receptor; bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human;
                                                  Human serum albumin residues 1-195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2001; 2001US-0268175P
31-JUL-2003 (first entry)
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                                                                                                                                                                                                serum albumin
                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concataent. The sequences are useful for treating an individual suffering from, or a risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthitis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, luque, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
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100.0%; Pred. No. 5.9;
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                                                                                                                                                                                                                       Human serum albumin (1-195) SEQ ID NO: 56.
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                                                                       AA017048 standard; protein; 195 AA
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18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
25-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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es 8; Conserv
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100.0%; Score 38; DB 7; Length 195; 100.0%; Pred. No. 5.9; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                     (first entry)
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ABU10022;

RESULT 12

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Query Match **datches** 

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The invention relates to movel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acide encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoissis; and in bone, cartilage, tendon and/or and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. All29510-AAU33304 represent the amino acid sequences of novel human expression and the proteins of the invention.
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activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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                                                                                                                                                           Query Match
100.0%; Score 38; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted protein #3564.
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                                                                                                                                                                                                                                                                                                                                                                                         AAU33073 standard; protein; 156 AA.
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                      83 VADESAEN 90
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying a therapeutic agent expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the rucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The polypeptide and charapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or attimulation; as anti-inflammatory agents; and in treatment of leukaemias.

Autusello-Akulajao4 represent the amino acid sequences of novel human expression and/or human are provention.
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                                       Gaps
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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Query Match 100.0%; Score 38; DB 4; Length 156; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #3762.
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26-JAN-2001; 2001US-00770160.
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Best Local Similarity 100.
Matches 8; Conservative
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Claim 20; SEQ ID NO 23481; 1399pp + Sequence Listing; English.

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides and polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, mematopoiseis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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18-MAY-2000; 2000US-00577409.
                                 Liu C, Drmanac RT
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38 VADESAEN 45
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N-PSDB; AAI89520.
                                                                 WPI; 2001-514838/56.
N-PSDB; AAI82560.
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(HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 127 AA;
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                                 Tang YT,
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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to grytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. steem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of canner, leukeamia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
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18-MAY-2000; 2000US-00577409.
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Best Local Similarity 100.
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N-PSDB; AAI92019.
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The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymoleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, namatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity incorp, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                            lated nucleic acids and polypeptides, useful for preventing diagnosing treating e.g. leukemia, inflammation and immune disorders.
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18-MAY-2000; 2000US-00577409.
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18-MAY-2000; 2000US-00577409.
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Best Local Similarity 100.
Matches 8; Conservative
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N-PSDB; AAI84346.
                                                                                                                                                                                                                                     HYSE-) HYSEQ INC
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                                                                   07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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100.0%; Score 38; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA004415 standard; protein; 124 AA.
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                                               Human polypeptide SEQ ID NO 18339
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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N-PSDB; AAI84378.
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                                                                                                                                                                                                                                                                WO200164835-A2.
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RESULT 5

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VADESAEN

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                          Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                        AA004446 standard; protein; 118 AA.
                                                                                                                                                                                  Human polypeptide SEQ ID NO 18338.
                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US004927.
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18-MAY-2000; 2000US-00577409.
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                                                                                                          Gaps
cell death in an organism. The present sequence is a fragment of modified murine serum albumin protein
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                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    AA002642 standard; protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 16534.
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18-MAY-2000; 2000US-00577409
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Best Local Similarity
Matches 8; Conserv
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                                                  Sequence 14 AA;
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                                                       The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymoleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity issue growth factor activity, immunomodulatory activity and activity, inchibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthitis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Claim 20; SEQ ID NO 18338; 1399pp + Sequence Listing; English.
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 118 AA;
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Matches
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AAO04447
ID AAO0
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Mon Apr 19 13:27:25 2004

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RESULT 1
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Aao04446 Human pol
Aao04447 Human pol
Aao04415 Human pol
Aao102629 Human pol
Aao12088 Human ser
Abul10022 Human ser
Abul10022 Human ser
Aay83947 Yeast cod
Aau29874 Novel hum
Aao17051 Human alb
Aao16984 Alpha-MSH
Aao16986 Alpha-MSH
Aao16986 Alpha-MSH
Aao16988 Alpha-MSH
Aao16988 Alpha-MSH
Aao16988 Alpha-MSH
Aao16988 Alpha-MSH
Aao16989 Alpha-MSH
Aao16988 Alpha-MSH
Aao16989 Alpha-MSH
Aau29581 Novel hum
                                                                                                April 19, 2004, 11:24:29 ; Search time 4.70545 Seconds (without alignments) 480.375 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                           1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        1586107 segs, 282547505 residues
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                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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38
1 VADESAEN 8
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*

2: geneseqp200s:*

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5: geneseqp2001s:*

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26	38	100.0	303	7	AAR14178	Aar14178	Human ser
27	38	100.0	373	-1	AAP90387	Aap90387	N-termina
28	38	100.0	388	Н	AAP90389	Aap90389	N-termina
29	38	100.0	389	H	AAP90390	Aap90390	N-termina
30	38	100.0	390	н	AAP90391	2	N-termina
31	38	100.0	401	4	AAU29876	Aau29876	Novel hum
32	38	100.0	407	-	AAP90392	Aap90392	N-termina
33	38	100.0	500	1	ADD32019	Add32019	Heterolog
34	38	100.0	584	v	ABG72381	Abg72381	Mature hu
35	38	100.0	585	Н	AAP93344	Aap93344	Sequence
36	38	100.0	585	Н	AAP90388	Aap90388	Mature hu
37	38	100.0	583	H	AAP91422	Aap91422	Human nor
38	38	100.0	585	N	AAR05318	Aar05318	Human ser
	38	100.0	582	N	AAR08457	Aar08457	Human ser
40	38	100.0	585	~	AAR26207	Aar26207	Human ser
41	38	100.0	582	0	AAR26362	Aar26362	Synthetic
	38	100.0	585	N	AAR20029	Aar20029	Human ser
43	38	100.0	585	0	AAR80301	Aar80301	Human ser
44	38	100.0	585	~	AA020111	Aa020111	HSA prote
45	38	100.0	585	N	AAW59841	Aaw59841	Mature pr

# ALIGNMENTS

SULT 1 719555 AA019555 st AA019555; 28-JAN-2003 Modified mc Serum album	<pre>KW apoptosis; cytostatic. XX XX OS Mus sp. OS Synthetic. XX XX FH Key Location/Qualifiers FT Cross-links 312 FT /note= "cyclise the molecule"</pre>	XX PN WO200270549-A2. XX 12-SEP-2002. XX XX 18-JAN-2002; 2002WO-US001256.	PR 23-JAN-2001; 2001US-00764918. PR 23-JAN-2001; 2001US-00768183. XX PA (GPCB-) GPC BIOTECH INC. XX PY GPUTIS J, LAMPHERE L, MOFFIS A;	XX XX WPI; 2003-018690/01. XX XX New chimeric polypeptide comprising a serum albumin protein having a PT biologically active heterologous peptide sequence inserted into it, PT useful for modulating cell proliferation, cell differentiation, or cell profession an organism.	XX PX XX XX XX XX XX CC The present invention relates to chimeric peptides comprising a serum CC albumin protein having a biologically active heterologus peptide CC albumin protein having a biologically active heterologus peptide cc sequence inserted into it. The protein experiment of biological activity relative to the heterologous peptide sequence itself companies.
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(HUMA-) HUMAN GENOME SCI INC.

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NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
                                                                                                                                                                                                                                                                                                                                                          DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCOAADKAACLLF 180
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                                                                                                                                                                                                                                                                9
three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonucleotide fragments that were extrended. This sequence represents the complete sequence of the HSA encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression vector, yeast host cells carrying the recombinant expression vector, process for producing human serum albumin in the yeast host cell,
                                                                                                                                                                                                                                                                                                                   61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                                                                                                                                                                   1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                        KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
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                                                                                                                                                                     Score 2068; DB 3;
Pred. No. 1.1e-191;
Mismatches 0;
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Best Local Similarity 100.0%; Pi
Matches 387; Conservative 0;
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2000US-0199384P.
2000US-0256931P.
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The present invention relates to albumin fusion proteins, which comprise a therapeutic protein and albumin. The present sequence is the protein sequence for mature human serum albumin (HA), which was used to generate the fusion proteins of the present invention. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukemia), respiratory disorders (e.g. childhood acute myeloid leukemia), arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. phecytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. measles), infictious disorders (e.g. measles), altritable bowel syndrome) and wound healing
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                                                                                                                                 Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders.
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100.0%; Score 2068; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-191;
Matches 387; Conservative 0; Mismatches 0;
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N-PSDB; ABA03057.
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              241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                     DIPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
                                                                          301 DIPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
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                                                                                                                                                                                                                                                                                                                     Human, albumin, ischemic state, serum protein, metal ion salt, perioperative ischemia, ischemia, myocardial infarction, progressive coronary artery disease.
                                                                                                                                                                                                                                                                                             Amino acid sequence of a human albumin protein.
                                                                                                           361 CAAADPHECYAKVFDEFKPLVEEPQNL 387
361 CAAADPHECYAKVPDEFKPLVEEPQNL 387
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98US-00165926.
98US-0102738P.
99US-0115392P.
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Modified-site
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02-0CT-1998;
02-0CT-1998;
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                                                                                                                                                     61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
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                                                                                   DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                                                                                                                                                                                     KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK
                                                                DAHKSEVAHRPKDLGBENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Process for preparing recombined human serum albumin comprising yeast biased sex codons - uses a recombinant DNA technique.
                                 Gaps
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                                Indels
Query Match
100.0%; Score 2068; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.1e-191;
Matches 387; Conservative 0; Mismatches 0;
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The present sequence represents the mature protein of human serum albumin (HSA). The protein is used to exemplify the invention. The specification describes a method for producing mature heterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledon transcription regulator, inducible either during seed maturation or by adding/removing a small molecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein from the cell. Proteins expressed in this manner include mature glycosylated alpha l-antitrypean (AAT) with a glycosylation pattern that significantly increases its serum half-life, mature glycosylated antithrombin III (ATIII), mature human serum albumin (HSA) having the mature active subtilisin BPN'. These proteins are useful therapeutically (e.g. AAT for treating emphysema, AIIII as antithrombotic and HSA as blood replacement) or as industrial enzymes (BPN' is used in detergents)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes.
                                                     Protein expression; monocotyledon plant cell;
glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III;
ATIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema;
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100.0%; Score 2068; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.1e-191;
Matches 387; Conservative 0; Mismatches 0;
               Mature protein of human serum albumin (HSA)
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                                                                                                                    antithrombotic; blood replacement.
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97US-0038168P.
97US-0038169P.
97US-0038170P.
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13-FEB-1997;
13-FEB-1997;
13-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a serum albumin-growth hormone fusion protein - useful to treat growth hormone related diseases such as Down's syndrome. This sequence represents a HSA protein related to the serum albumingrowth hormone protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 585;
hormone fusion protein; growth hormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          useful
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100.0%; Score 2068; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.1e-191;
Matches 387; Conservative 0; Mismatches 0;
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s syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Serum albumin-growth hormone fusion hormone related diseases, e.g. Down'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6; 21pp; Korean.
                                                                                                                                                                                                                                                                                  BIOTECHNOLOGY LTD
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96WO-GB003164.
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Serum albumin-growth
Down's syndrome.
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                                                                                                                                                                                                                                                                                  (DELZ ) DELTA
                                                          Unidentified
                                                                                                KR99076789-A
                                                                                                                                                                                                                    30-DEC-1995;
19-DEC-1996;
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                                                                                                                                                                                                                                                                                                    The cDNA given in AAQ98695, which encodes HSA (AAR80301), was subjected to site-directed mutagenesis to investigate the role of endoproteases in the generation of a 45 kDa albumin fragment obtd. when the CDNA is expressed in S. cerevisiae. Mutations were: R410A; L407A, L408V, V409A; and R410A, K413Q, K414Q. The latter set of mutations, especially, improved stability of HSA to yeast Yap3p proteolytic cleavage, allowing increased prodn. of recombinant HSA. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLPSLAADFVESKDVCKNYAEAKDVFLGMPLYEYARRHPDYSVVLLLRLAKTYETTLEKC
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                                                                                                                                                                                                                          Yeast with reduced levels of aspartyl protease 3 proteolytic activity used to secrete human albumin without prodn. of the 45 kD fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence related to the growth hormone protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2068; DB 2;
    Pred. No. 1.1e-191;
    Mismatches 0;
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                                                                                                                                                                                                                                                                                 Example 1; Page 26-28; 50pp; English
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                                                                                                                                               Gilbert
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Best Local Similarity 100.º
Matches 387; Conservative
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                                                                                                                                               Kerrywilliams SM,
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               38-SEP-1995
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                                                                                                                                                                                                                                                                                                The protein sequence was deduced from the synthetic DNA sequence encoding human serum albumin which was prepd. by ligating eight synthetic HSA gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic gene for prepn. of human serum albumin - comprises synthetic DNA contg. gene coding the albumin using coding in Escherichia coli.
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llarity 100.0%; Pred. No. 1.1e-191;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                    Fig 1; Page 13; 37pp; Japanese
                                                                      91JP-00014600
                                                                                                     90JP-00025682.
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(first entry)
                                                                                                                                      (AJIN ) AJINOMOTO KK
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N-PSDB; AAQ27813.
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Best Local Similarity
Matches 387; Conserv
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17-JAN-1996
       JP04211375-A
                                                                      05-FEB-1991;
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                                       03-AUG-1992.
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Pragments A-C of HSA are expressed as fusion proteins with the signal peptide of E. coli alkaline phosphatase. The fragments are selected for their specific properties. The C-terminal truncated fragment, B. does not bind long-chain fatty acids but does bind to various medicines at the central region. The N-terminal truncated fragment, C, has good stability in protein folding. The central segment, A, has characteristics of both B and C. See also AAQ06096-Q06099. (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
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                                                                                                                                            to medicines and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 1.1e-191;
                                                                                                                                            human serum albumin fragments - used to bond
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Best Local Similarity 100.0%; Pred. No. 1.1
Matches 387; Conservative 0; Mismatches
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                                                                                                                                                                                             Claim 1; Fig 8; 24pp; Japanese
89JP-00217540
                               88JP-00250926
                                                                                                                                                               stable folding of protein(s)
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                                                                                            WPI; 1990-317325/42.
N-PSDB; AAQ06099.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 585 AA;
                               06-OCT-1988;
25-AUG-1989;
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                               host - by culturing transformed removing it.
                                                                                                               Mature HSA-A may be produced using the sequence incorporated into a plasmid vector with suitable controllers, and transfered to a yeast
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100.0%; Pred. No. 1.1e-191;
ive 0; Mismatches 0;
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1, label = B
123. :585
7, label = C
1123. :303
7, label = A
                               Human serum albumin prepn. by yeast plasmid yeast to produce serum, and
                                                                                 Disclosure; Page ?; -pp; Japanese
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expression system
 N-PSDB; AAQ04719
                                                                                                                                                                                 Sequence 585 AA;
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which the codons which are most frequently used by the chosen non-human host were selected. In this case, it is yeast cells (LL20; Leu2-3; 112, His 3-11, 15). The synthetic HSA gene was assembled from 24 cligonucleotide blocks. HSA is used in therapy for the treatment of hypovolaemia, shock and hypoalbuminaemia. It is also used as an additive in perfusion liq. for extracorporeal circulation and as an experimental antigen. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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100.0%; Pred. No. 1.1e-191;
iive 0; Mismatches 0;
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blood
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useful
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    esp.
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Pred. No. 1.1e-191;
Mismatches 0;
  fragments of human serum albumin
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                                                                  Disclosure, Fig 2; 20pp; English
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Best Local Similarity 100.0%;

Matches 387; Conservative 0
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                           plasma expanders.
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plasma expanders.
                                                                 1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTBFAKTCVADESAE
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387; Conservative
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                                                                                                          DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
                                                                                                                                                                                  DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFRKRYKAAFTECCQAADKAACLLP
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                                                        1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                        DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of mature human serum albumin (HSA) as encoded by artificial
                             Gaps
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hypobolaemia; shock; hypoalbuminaemia.
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Length 407;
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Query Match 100.0%; Score 2068; DB 1; Best Local Similarity 100.0%; Pred. No. 6.9e-192; Matches 387; Conservative 0; Mismatches 0;
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(MAGY ) MTA SZEGEDI BIOLOG KOEZPONTI.
(VEPE-) VEPEX CONTRACTOR LTD.
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(first entry)
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 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
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Pred. No. 6.5e-192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP90391 standard; protein; 390
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Best Local Similarity
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25-MAR-2003
01-NOV-1989
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                                                                                                                                                                                   240
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                                                                                         180
                                                                                                               121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
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                                                                                                                                                                             KLDBLRDBGKASSAKQRLKCASLQKFGBRAFKAWAVARLSQRFPKABFABVSKLVTDLTK
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   DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                  NCDKSLHTLPGDKLCTVATLRBTYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                    NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                           DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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(first entry)
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ABR42606
ADC16794
ADC16795
ADD06469
ADD86016
ADD86016
ADD86016
AAR96229
AAR96229
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April 19, 2004, 11:24:29; Search time 227.626 Seconds (without alignments) 480.375 Million cell updates/sec
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2068
1 DAHKSEVAHRFKDLGEENFK......ECYAKVFDEFKPLVEEPQNL 387
                                                                                                                                         1586107
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                            1586107 seqs, 282547505 residues
                                   - protein search, using sw model
                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Abr55695 Human alb Abr42606 Human alb Abr42606 Human ser Adc16767 Human ser Adc16794 Mutant hu Adc16794 Mutant hu Adc16794 Mutant hu Add32014 Heterolog Add8016 Mature fo Aar06794 Fragment Aar9229 Human ser Aar9229 Human ser Aar96913 Human ser Aar96632 Human ser Aar86913 Human ser Aar86914 Human alb Aar86632 Human alb Aar866349 Recombina Aar78147 Pre human Aab76147 Pre human

# ALIGNMENTS

RESULT 1 AAP90389 ID AAP90389 standard; protein; 388 AA. XX AC AAP90389; XX AC AAP90389; XX DT 24-0CT-2003 (revised) DT 25-MAR-2003 (revised) DT 01-NOV-1989 (first entry) XX XX DE N-terminal human serum albumin polypeptide. XX XX XX N-terminal human serum albumin polypeptide; plasma expanders. XX	nainal fragments of human serum albumin spanders.  Page 9; 20pp; English.  Page 9crum albumin used is for HSA or BSA, in tissue culture me correct PA field.) (Updated on 24-OCT-20 orrect PA field.) (Socre 2068; DB 1; similarity 100.0%; Score 2068; DB 1; Similarity 100.0%; Pred. No. 6.4e-1927; Conservative 0; Mismatches 0;
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Description

DB

% Query Match Length I

Score

Result No.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Title: Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Searched:

A Geneseq 29Jan04:\*

1. geneseq11980s:\*
2. geneseq1990s:\*
3. geneseq2000s:\*
4. geneseq2001s:\*
5. geneseq22001s:\*
7. geneseq22003as:\*
7. geneseq22003bs:\*
8. geneseq22003bs:\*

SUMMARIES

9

DAHKSEVAHRFYDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE

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Aap90389 N-termina Aap90391 N-termina Aap90391 N-termina Aap90384 Sequence Aar90388 Human ser Aar03318 Human ser Aar26352 Synthetic Aar26352 Synthetic Aar26361 Human ser Aar26311 Mature pr Aay89346 Yeast cod Aay89346 Yeast cod Aam5256 Mature hu Aae13139 Human alb Abb79006 Human ser Aav68578 Human alb Abb79006 Se Iymphoc Abj00986 B Iymphoc Abj00986 B Iymphoc Abg33347 Human Ber Abg33347 Human Ber Abg33347 Human Ber

AAP93344
AAR05318
AAR05318
AAR0518
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AA020111
AA020111
AAW83946
AAR12406
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AAR13139

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DMEGLPQKH-NFSHCCGKAGFPRRLCFFYNKKANVGFLPPFPTL---DPEEKCQAYKNNS 142
                                                                                                                                                                192 SSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLL 251
                                                                                                                                                                                           203 SSSYQRNVCGALIKFGFKVLNSINVAVFSKKFPKIGFKDLTTLLEDVSSMYEGCCEGDVV 262
                                                                                                                                                                                                                                                                                      263 HCIRSQSQVVWHICSKQDSISSKIKVCCEKKTLEREACIINANKDDRPEGLSLREAKFTE 322
                                                                                                                                                                                                                                                                                                                                                                                  323 SENVCQERDSDPDKFFAEFIYEYSRRHPDLSTPELLRITKVYMDFLEDCCSRENPAGCYR 382
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                                                                        ETFLKKYLYBIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKA
                                                                                                 143 ESFLHLYMYEVARRNDFVFAPVLLAVAAWFEEAATTCCEQQQKATCFQAKAAPITQYLKA
                                                                                                                                                                                                                                                             252 ECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVE
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A Haverfield E.V., Uzzell T., Spoleky C.M., Bazartseren B.;
T "Serum abbumin of the mole salamanders Ambystoma maculatum and ambystoma texanum.";
Submitted (DEC-1999) to the EMBL/APST182; PAT5182; AAL56485.11;
R RBBL, APST1821; AAL56485.11;
C GO: 0005386; F:carrier activity; IEA.
R GO; GO: 0005386; F:carrier activity; IEA.
R GO; GO: 0006810; P:transport, IEA.
R GO; GO: 0006810; P:transport, IEA.
R HINTS; PRO00224; Serum_albumin.
R PÉAM; PRO0273; transport_prot; 3.
R PRINTS; PRO0802; SERUMALBUMIN.
R PROD002486; Serum_albumin; 1.
R SMARY; SMO0103; ALBUMIN; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
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30.5%; Score 630; DB 13; Length 624;
Best Local Similarity 33.7%; Pred. No. 4.1e-46;
Matches 125; Conservative 66; Mismatches 170; Indels 10
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25 624 SERUM ALBUMIN.
624 AA; 70321 MW; DE08533BF4953EF7 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTW-2003 (TrEMBLrel. 24, Last annotation update)
Serum albumin precursor.
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NCBI_TaxID=8304;
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SEQUENCE
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RN FORDERS FROW N. S. STRAIN-C57BL/G1, TISSUE-BOdy;
RN FORDERS FROW N. S. STRAIN-C57BL/G1, TISSUE-BOdy;
RX THE FANTOM CONSOLITION.
RA THE FANTOM CONSOLITION.
REALL, AROTOGOSI; BAC36150.1; -.
DR FANTOM FORDERS FOR CONTINUATION (Sensu Mammalia); IMP.
BY G0: G0:0001442; Procesterone metabolism; IMP.
BY G0: G0:0014449; Procesterone metabolism; IMP.
BY G0: G0:001953; P: Sextual Teproduction; IMP.
BY G0: G0:001953; P: Sextual Teproduction; IMP.
BY G0: G0:001953; Fransport prot; 3.
BY RINTS; PRO0802; SERUMALBUMN: 1.
BY RANAT; SMO0103; ALBUMIN; 1.
BY ROSITE; PRO0124; ALBUMIN; 2.
BOR PROSITE; PRO0124; ALBUMIN; 2.
BOR PROSITE; PRO0124; ALBUMIN; 2.
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165 EFLGHYIHKVASSHTTMYPPAILSFTLHFDGIVSHCCKDEATVGQCLSEKMPAHKEEVEH
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Alpha-fetoprotein precursor.
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KEEETLRHEIE 407
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TVATLRETYGEMADCCAKQEPERNECFLQHKDDN----PNLPRLVRPEVDVMCTAFHDNE 131
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                                                                         16 BENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
TISSUE=Kidney;
Straubberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026681; AAH26681.1; --
RMD; MAI:2429409; Afm.
MGD; MAI:2429409; Afm.
RGO; GO:0005815; C:extracellular space; IEA.
GO; GO:0005816; F:carrier activity; IEA.
RGO; GO:0005816; P:carrier activity; IEA.
RGO; GO:0005816; P:carrier activity; IEA.
R ProDom; PR00273; Lransport; Drot; 2.
RRINTS; PR00202; Lransport prot; 2.
RRINTS; PR00202; Lransport prot; 2.
RRART; SM00103; ALBUMALEUMIN; 1.
RPCOM; PR00212; ALBUMIN; 2.
RRART; RM0103; ALBUMIN; 2.
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66; Mismatches 167;
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01-JUN-2002 (TrEMBLrel. 21, Creat
01-JUN-2002 (TrEMBLrel. 21, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Hypothetical protein (Fragment).
        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 TVATLRETYGEMADCCAKQEPERNECFLQHKDDNP-NLPRLVRPEVDVMCTAFHDNEETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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"Molecular Cloning and Expression of Woodchuck Alpha-Fetoprotein.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY034049; AAKS5757.1;
SEQUENCE 608 AA; 67962 MW; EB46D7A37382B222 CRC64;
                                      Kim J.G., Nonneman D., Vallet J.L., Christenson R.K.;

Kim J.G., Nonneman D., Vallet J.L., Christenson R.K.;

"Mapping of the porcine alpha-fetoprotein (AFP) gene to SSCB.";

"Mapping of the porcine alpha-fetoprotein (AFP) gene to SCB.";

EMBL; AF51770; AAM66710.1;

R.G.; GO:0005615; C:extracellular space; IEA.

GO; GO:0005615; F:carrier activity; IEA.

R.G.; GO:0005810; P:transport; IEA.

R. GO; GO:0005810; P:transport JEA.

R. Ffam; PF00273; transport Drot; 3.

R. Pfam; PF00273; transport Drot; 3.

R. ProDom; PD002486; Serum albumin; 1.

R. SMART; SM00103; ALBUMIN; 2.

R. SEQUENCE 610 AA; G8624 MW; C985BEAD44963D5B CRC64;
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Alpha-fetoprotein.
Alpha-fetoprotein.
Bukarnota monax (Woodchuck).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
33.7%; Score 697.5; DB 6;
Best Local Similarity 36.4%; Pred. No. 5.5e-52;
Matches 136; Conservative 74; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 AA
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Best Local Similarity
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Euteleostomí; Canis.

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100 HEKEISEKYG-LADCCSQREEERHNCFLAHKKAAPPSIPPFQVAEPVTSCKAYEENRDMF 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 EENPKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLC
                                                                                                                                                                                                                         A FURUICHI M., Neo S., Hisasue M., Tsuchiya R., Watanabe M.,
Hashizaki K., Hisamatsu S., Yamada T.;
Hashizaki K., Hisamatsu S., Yamada T.;
"Canine alpha-fetoprotein cDNA";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB089789; BAC07513.1;
GO; GO:0005386; F:carriac activity; IEA.
R GO; GO:0005386; F:carriac activity; IEA.
R Interpro; IPR000264; Serum_albumin.
R Pfan; PF00273; transport prot; 3.
R PRINTS; PR00023; SERUMALBUMIN.
R PRINTS; PR00023; SERUMALBUMIN; 1.
R PRINTS; PR0002486; Serum_albumin; 1.
R PRINTS; PR0002486; Serum_albumin; 1.
R PRINTS; PR00013; ALBUMIN; 2.
R PROSITE; PS00213; ALBUMIN; 2.
R PROSITE; PS00213; ALBUMIN; 2.
R PROSITE; PS00213; ALBUMIN; 2.
                                                                                                                                                                                                                                                                                                                      databases
                                                                               Alpha-fetoprotein.
AFP.
Canis familiaris (Dog).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae;
Q8MJU5;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
34.4%; Score 712; DB 6; Le
Best Local Similarity 37.3%; Pred. No. 3.1e-53;
Matches 139; Conservative 70; Mismatches 162;
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EELEKYIQESQAL 411
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                                                                                                                                                                                         NCBI_TaxID=9615;
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QBMJ76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
                               208 GQCFNDKMPEHKQEVEYVCALQKHNCYILQDFKERALTAYKAVQASQKFPLASFENVQII 267
                                                                                                                                                                                              268 VPDTVHLHQTCCGGDMMACMLERMKLTAKICEKKDELATHLKECCDKFLLERSACIIRLP 327
                                                                                                                                                                                                                                                                                      VTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVE 294
                                                                                                                                                                                                                                                         NDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVILLRLAKTYE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 BAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAA 84
    VRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKA 175
                                                                                      A-CLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKL 234
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01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 24, Last sequence update)

01-UND-2003 (TrEMBLrel. 24, Last annotation update)

Albumin (Fragment).

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=129/SvevTAcfBr;
Van Reeth T., Dreze P.L., Gabant P., Szpirer J.;
Van Reeth T., Dreze P.L., Gabant P., Szpirer J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ77794; CAC81903.1; -..
GO; GO:0005515; C:extracellular space; IEA.
GO; GO:0005886; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IFR000264; Serum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 739; DB 11; Length 205; ilarity 69.6%; Pred. No. 3.7e-56; Conservative 26; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AA; 23624 MW; 0A982E85C7474BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                             355 TTLEKCCAAADPHECYAKVFDEFKPLVEEPQNL 387
                                                                                                                                                                                                                                                                                                                                                                        388 FFLKKCCAAEGHNECLAKTEESLKKEIESSVTL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Best Local Similarity
Matches 126; Conserv
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SEQUENCE
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RESULT 9

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Length 609;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 QDGEKIMSYICSQQDILSSKIADCCKLPILELGQCIIHAENDGKPEGLSPNLNRFLEERD
                                                                                        135 LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTEÇCQAADKAAÇLLPKLDELRDEGKASSA
                                                                                                                                                                                                                                                                                         195 KORLKCASLOKFGERAFKAWAVARLSORPPKAEFAEVSKLVTDLTKVHTECCHGDLLECA
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Alpha-fetoprotein.
Sub scrofa (Pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TAXID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCC SE DIT DE SE DIT SE
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57 ESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN-PNLPRL 115
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                                                                                                                                                                                                                                                                                                                                        CDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPN-LPRLVRPEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAMAVARLSQRFPKAEFAEVSKLVTDLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                        241 VHTECCHGDLLECADDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPA
                                                                                                                                                                                             CLKSLDTIFLDEICHEEGFAAKY-DLAACCAKAEVERKECLLAHKNATPGFIFDFQRPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ambystoma maculatum (Spotted salamander).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ambysion texanum.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF217183; AALS6666.1;
GO; GO:0005618; C:extracellular space; IEA.
GO; GO:000586; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000264; Serum albumin.
PEAM; PR000273; transport prot; 3.
RRINTS; PR00802; SERUMALBUMIN.
Probom; PD002486; Serum albumin; 1.
SWART; SMO0103; ALBUMN; 3.
RROSITE; PS00212; ALBUMN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.; "Serum albumin of the mole salamanders Ambystoma maculatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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9D66F57F174AC23F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Serum albumin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.9%; Pred. No. 9.7e-58;
Matches 153; Conservative 64; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 CKTDNPPECYGQAEADLKKHIAQFQEL 330
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626
70677 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
25
626 AA;
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ambystoma.
NCBI_TaxID=43114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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SIGNAL
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Q8UW05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 DVWCTAFHDNESTFLKKYLYE------TILEKCCAAADPHECYAK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKVHTECC---HGDLLECADDRADLA-KYIC--ENQDSIŞSKLKECCEKPLLEKSHCIAE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEVDETYVPKBFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDD 361
                                                                                                                                                                                                                                                                                                                                                                                      9
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B EQUURNEE FROM N.A.

Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;

Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;

Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;

"Partial coding sequence for Sphenodon punctatus 68 kDa albumin.";

"Partial coding sequence for Sphenodon punctatus 68 kDa albumin.";

"B COO. (1900 1) to the EMBL/GenBank/DDBJ databases.

"B COO. (1900 1) to the EMBL/GenBank/DDBJ databases.

"R GO, GO. (1900 1) to the EMBL/GenBank/DDBJ databases.

"R GO, GO. (1900 1) to the EMBL/GenBank/DDBJ databases.

"R GO, GO. (1900 1) to the EMBL/GenBank/DDBJ databases.

"R GO, GO. (1900 1) to the EMBL/GenBank).

"R InterPro', IRRO (1900 1) to the EMBL/GenBank).

"R PRODON; PRO (1900 1) to the EMBL/GenBank).

"R PRODON; PRO (1900 1) to the EMBL/GenBank).

"R PRODON; PRO (1900 1) to the EMBL/GenBank).

"R PRO (1900 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 VFDEFKPLVEEPQNLIKQ--NCELPBQLGEYKPQNALLVRYTKKVPQVSTPTLVEVSRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKT
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                                                                                                                                                                                                                                                                                                                                                                                      1 DAHKSEVAHREKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
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                                                                                                                                                                                                                                       Length 396;
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080IIA9;
080IIA9;
080IIA9;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 24, Last sequence update)
01-OCT-2002 (TrEMBLrel. 24, Last annotation update)
Serum albumin (Fragment).
Sphenodon punctarus (fatteria) (Tuatara, Sphenodon punctarus (fatteria) (Tuatara, Butel)
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
                                                                                                                                                                                                                                                                                                             42; Mismatches 121; Indels
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                                                                                                                                                                  756519C096463A9B CRC64;
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Best Local Similarity 45.3%; Pred. No. 3.6e-60;
Matches 148; Conservative 53; Mismatches 124;
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.9%; Pred. No. 6.7e-73;
Matches 196; Conservative 42; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 FAAFVEKCCKADDKETCFA---EEGKKLVAASQ 391
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                       Pfam, PF00273; transport prot;
PRINTS; PR00802; SERUMALBUMIN.
SMART; SM00103; ALBUMIN; 2.
PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 396 AA; 45159 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 LEGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LFGDKLCAIPNLRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNESTFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 GKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFFFKAEFAEVSKLVTDLTKVHTECCHG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 DLLECADDRAELAKYMCENQATISSKLQTCCDKPLLKKAHCLSEVEHDTMPADLPAIAAD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVESKDVCKNYAEAKDVFLGMFLYBYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.";
Nature 420:553-573 (2002).
EMBL; AK050644; BAC33501; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 HRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHT
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER 1 1
SEQÜENCE 576 AA; 65002 MW; F85733E99AE37F04 CRC64;
                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005816; F:carrier activity; IEA.
GO; GO:0006810; F:carrier activity; IEA.
GO; GO:0006810; F:carrier activity; IEA.
INTEPPO; IEA000064; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMLEBUMIN.
ProDom: PD002486; Serum_albumin; 1.
SWART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
                                                                                                                                                                                         576 AA
361 CAAADPHECYAKVFDEFKPLVEEPQNL 387
                          385 CAEANPPACYGTVLAEFQPLVEEPKNL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J, TISSUE-Thymus;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYAKVFDEFKPLVEEPONL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || | || || || || || || || || || CYGTVLAEFQPLVEEPKNL 379
                                                                                                                                                                                                                                    ...mak-2003 (TrEMBLrel. 23, 01-0CT-2003 (TrEMBLrel. 23, Albumin 1 (Fragment).
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 RDAHKSEVAHR-----FKDLGEENFKAMAVARLSQRFPKABFAEVSKLVTDLTKVHTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 CHGDILECADDRADIAKYICENQDSISSKIKECCEKPILEKSHCIAEVENDEMPADLPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 CHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYBTTLEKCCAAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to serum albumin precursor.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                          Similar to alpha-fetoprotein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9
                                                                                                                                                                                                                                                                                                                       Straubberg R., Strauberg R., ARH4789.1, - GO, GO.0005615; C:extracellular space; IEA. GO, GO.0005186; F:carrier activity; IEA. GO, GO.0005886; F:carrier activity; IEA. InterPro; IPR000264; Serum_albumin. Rema, PR000273; transport prot; 2. PRINTS; PR008023; SERUMALBUMIN. ProDom; PD002486; Serum_albumin; 1. SRRAT; SM00103; ALBUMIN; 2. SRGUENCE 417 AA, 47360 MW; 1657648335E74E8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
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Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO35695; ARH55969.1; -
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005386; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IRR000264; Serum_albumin.
                                               01-00N-2003 (TrEMBLral. 24, Created)
01-00N-2003 (TrEMBLral. 24, Last sequence update)
01-0CT-2003 (TrEMBLral. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
46.2%; Score 956; DB 4;
Best Local Similarity 90.6%; Pred. No. 1.3e-74;
Matches 183; Conservative 3; Mismatches 10.
417 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHECYAKVFDEFKPLVEEPONL 219
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                             NCBI_TaxID=9606;
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121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCOAADKAACLLP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKC 384
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It mainter 420:563-573 (2002).

Recommendation of the Mouse of the Mouse of the Recommendation of the Rec
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                                                325 DLPSLAADFVEDKEVCKNYAEAKDVFLGTFLYSYARRHPDYSVALLLRLAKKYEATLEKC
                      DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLLRLAKTYETTLEKC
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                          608
                                                                                                                                             361 CAAADPHECYAKVFDEFKPLVEEPONL 387
                                                                                                                                                                             CAEADPSACYGKVLDEFOPLVEEPKNL
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                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
                                                                                                                             VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                                                                                                                                                                             241 IHKECCHGDLLECADDREDLAKYICENQDSISTKLKECCGKPVLEKSHCISEVERDELPA 300
                                                                                                                                                                                                                                                                                                                                 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
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Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6183;
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OSMAN A., Ashahi H., Stadecker M.J., Loverde P.T.;
OSMAN A., Ashahi H., Stadecker M.J., Loverde P.T.;
OSMAN A., Ashahi H., Stadecker M.J., Loverde P.T.;
OSMAN A., Stadecker M.J., Loverde P.T.;
EMBL, Albumin precursor noncologis a novel T helper cell immunogenic component in murine infection with Schistosoma mansoni.";
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL, AF418550; AALOBS79.1;
OG. GO:0005615; C:extracellular space; IEA.
GO: GO:0005610; P:transport; IEA.
InterPro; IPRO00264; Serum_albumin.
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PRINTS; PR00802; SERUMALBUMIN.
Probom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 2.

PROSTITE; P800212; ALBUMIN; 2.
SEQUENCE 608 AA; 68225 MW; ESEABB28EIC66E54 CRC64;
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Last annotation update)
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76.5%; Pred. No. 2.6e-137;
tive 53; Mismatches 38;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-UTM-2003 (TrEMBLrel. 24,
Albumin.
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Best Local Similarity
Matches 296; Conserv
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 19, 2004, 11:37:09; Search time 149.368 Seconds (without alignments) 817.479 Million cell updates/sec US-09-832-929-18\_COPY\_1\_387 2068 1 DAHKSEVAHRFKDLGEENFK......ECYAKVFDEFKPLVEEPQNL 387 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Run on:

Total number of hits satisfying chosen parameters: 1017041 segs, 315518202 residues Searched:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_25:\*

1: sp\_archea:\*

3: sp\_fungi:\*

4: sp\_fungi:\*

5: sp\_maman:\*

6: sp\_mamman:\*

7: sp\_mhc:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

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8: sp\_ortebrate:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARIES

	חסיידתיידים		Q7ysg3 felis silve	Q95vb7 schistosoma	Q8c7h3 mus musculu	Q8c7c7 mus musculu	Q86yg0 homo sapien	Q8iuk7 homo sapien	Q8jia9 sphenodon p	Q8uw05 ambystoma m	Q8cg74 mus musculu	Q8mjus canis famil	Q8mj76 sus scrofa	Q7tsf3 marmota mon	Q8r0j9 mus musculu	Q8uw06 ambystoma t	Qabkes mus musculu	Q8bk56 mus musculu
SE TARRESO S	£		Q7YSG3	Q95VB7	<b>Q8</b> С7 <b>H3</b>	Q8C7C7	Q86YG0	Q8IUK7	Q8JIA9	QSUWOS	Q8CG74	QBMJUS	Q8MJ76	Q7TSF3	Q8R0J9	QSUWO6	Q8BK65	Q8BK56
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	% Query Match Length DR		584	608	608	576	417	396	527	626	205	609	610	608	417	624	605	605
	% Ouery Match		83.2	81.3	9.94	74.6	46.2	45.3	38.2	36.9	35.7	34.4	33.7	33.2	32.7	30.5	29.7	29.4
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9H5X6Ö	091134	QBJIA7	QBJIA8	Q9W6F5	Q7TS97	042279	Q95MC2	Q83ZS7	074669	Q9JMX8	Q9TRA5	09ZLV0	025262	074668	Q8YK55	005060	Q8MS79	Q9VU94	Q9UVY2	Q9QVA1	001794	889060	001828	P78734	Q12075	Q81D09	061194	1 Q61182
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591			409.5			275			••	150		-44		146.5				120.5	_	111	Ч	110	110	•	109	0	8	08
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# ALIGNMENTS

PRELIMINARY; PRI	OCT-2003 OCT-2003 umin (Fraç	Felis silvestris catus (Cat). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis. 11.1	SEQUENCE FROM N.A. TISSUE-Liver; Reininger R., Swohoda I., Rohle B., Hauswirth A.W., Valent P.,	Rumpold H., Valenca R., Spitzauer S., "Escherichia coli expression and purification of recombinant car	Dibmini-ige recognition, induction or basopini activation and lymphoproliferative responses in atopic patients "; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. "SMBL; AJ487677; CAD32275.1;	JN 1EK 1 1 EGOUENCE 564 AA, 65908 MW, B51002F12902C9CE CRC64;	Query Match 83.2%; Score 1721; DB 6; Length 584; Best Local Similarity 80.1%; Pred. No. 8.4e-141; Matches 310; Conservative 36; Mismatches 41; Indels 0; Gaps 0;	1 DAHKSEVAHRFKDLGEBNFKALVLIAFAQYLQQCFFEDHVKLVNEVTEFAKTCVADESAE 60	BIAHRFNDLGEBHFRGLVLVAFSQYLQQCPFBDHVKLVNBVTEFANGCVAL	61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLFRLVRPEV 120	61 NCEKSLHELFGDKLCTVASLRDKYGEMADCCEKKEPERNECFLQHKDDNPGFGQLVTPEA 120	121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
NLT 1 SG3 Q7YSG3 Q7YSG3; 01-OCT-2	01-OCT-2 01-OCT-2 Albumin ALB.	Felis si Eukaryot Mammalia NCBI Tax	SEQUENCE TISSUE=L	Rumpold "Escheri	albumin: lymphopr Submitte EMBL; AJ	SEQUENCE	Query Match Best Local Matches 31	ч	н'	61	61	121
RESULT Q7YSG3 ID Q AC Q DT	SEA	80008	R R R	RR	RRR	S S	QWK	ò	DP	ò	qq	ò

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241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
241 VHTECCHGDILECADDRADIAKYICENQDSISSKIKECCEKPLLEKSHCIAEVENDEMPA 300
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Search completed: April 19, 2004, 12:54:56 Job time : 247.316 secs

us-09-832-929-18.rapb

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; LOCATION: (1)...(585)
; OTHER INFORMATION: ACETYLATION
US-10-319-263-2
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ORGANISM: Homo sapiens
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NAME/KEY: MOD_RES
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| Sequence 1, Application US/10319263
| Sequence 1, Application US/10319263
| Publication No. US20030180820A1
| GENERAL INFORMATION|
| APPLICANT: Bar-Or M.D., David
| APPLICANT: Bar-Or M.D., Edward
| APPLICANT: Winkler M.D., James V.
| TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Kits for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Kits for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Kits for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Kits for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Kits for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION NUMBER: 00/105,383
| PRIOR FILING DATE: 1998-10-02
| PRIOR FILING DATE: 1998-10-03
| PRIOR FILING DATE: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLLRLAKTYETTLEKC 360
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                                                                                                   361 CAAADPHECYAKVFDERKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
                                                                                                                                                                                             PTLVEVSRNLGKVGSKCCKHPRAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
                                                          CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFONALLVRYTKKVPQVST
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100.0%; Score 3103; DB 14; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.2e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                     KEQLKAVMDDFAAFVEKCCKADDKETCPAEEGKKLVAASQAALGL 585
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-319-263-1
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Sequence 2, Application US/10319263

Publication No. US20030180820A1

Sequence 1, Application US/10319263

Publication No. US20030180820A1

SERVERAL INFORMATION:
APPLICANT: Bar-Or M.D., David
APPLICANT: Bar-Or M.D., James V.
TITLE OF INVENTION: Kits
FILE OF INVENTION: MABER: US/10/319,263

CURRENT FILING DATE: 1999-01-11

PRIOR APPLICATION NUMBER: 60/115,392

PRIOR APPLICATION NUMBER: 60/102,738

PRIOR APPLICATION NUMBER: 09/165,926

PRIOR APPLICATION NUMBER: 09/165,926

PRIOR FILING DATE: 1998-10-02

PRIOR FILING DATE: 1998-10-02

PRIOR FILING DATE: 1998-10-02

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 2

LENGTHARE: PATENTIN VET: 2.0

LENGTHARE: PATENTIN VET: 2.0

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US-10-153-604A-5

| Sequence 5, Application US/10153604A
| Sublication No. US20030143191A1
| GENERAL INFORMATION:
| APPLICATE Bellet al. |
| TILLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
| TILLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
| TILLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
| TILLE OF INVENTION: OF APPLICATION NUMBER: US/10/153,604A
| PRIOR PILING DATE: 2001-05-25
| PRIOR PILING DATE: 2001-05-25
| NUMBER OF SEQ ID NOS: 137
| SEQ ID NO 5
| LENGTH: 585
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Best Local Similarity 100.
Matches 585; Conservative
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US-10-153-604A-5
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Publication No. US20020142814A1

GRUERAL INFORMATION:
APPLICANT: Ball et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PFS56
CURRENT APPLICATION WUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

FRIOR APPLICATION NUMBER: 60/293,212

FRIOR SPELING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PATENTH VERSION 3.1

SEQ ID NO 5

LENGTH: 585
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Best Local Similarity 100.0
Matches 585, Conservative
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Sequence 31, Application US/10425000

| Bedication No. US2004005277A1
| Bedication No. US2004005277A1
| GENERAL INFORMATION:
| APPLICANT: Cameron, Beatrice
| APPLICANT: Cameron, Beatrice
| APPLICANT: Blanche, Francise
| TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
| TITLE OF INVENTION: Anglogenesis
| TITLE OF INVENTION: Anglogenes
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APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
TITLE OF INVENTION: Prancia
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REFERENCE: ST01027-4
FILE REFERENCE: ST01027-4
CURRENT APPLICATION NUMBER: US/10/424,999
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Atentin version 3.2
SEQ ID NO 11
LENGTH: 585
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100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.2e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0;
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CTHER INFORMATION: Fusion protein human abrogen

US-10-424-999-11
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Publication No. US20040052810A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; Score 3103; DB 11;
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0; Mismatches 0;
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US-09-833-245-18

Sequence 18, Application US/0983245

PUBLICATION NO. US20040010134A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF546PCT

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR APPLICATION NUMBER: 60/226, 931

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PALON OF SEQ ID NOS: 2267

SEQ ID NO 18

LENGTH: 585
  Query Match
Best Local Similarity 100.0%;
Matches 585; Conservative 0
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CORGANISM: Homo Sapiens
US-09-833-245-18
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                                                                                               Gaps
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                                                    Query Match

100.0%; Score 3103; DB 10; Length 585;

Best Local Similarity 100.0%; Pred. No. 4.2e-269;

Matches 585; Conservative 0; Mismatches 0; Indels 0;
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Sequence 16, Application US/09833118

Sequence 16, Application US/09833118

Sequence 16, US20030219875A1

GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF544 bumin Fusion Proteins
FILE REFERENCE: PF544 bumin Fusion Proteins
FILE REFERENCE: PF544 bumin Fusion Proteins
FILE REFERENCE: PF545 bumin Fusion Proteins
FILE REFERENCE: PF545 bumin Fusion Proteins
FILE APPLICATION NUMBER: 60/229,358

PRIOR APPLICATION NUMBER: 60/226,931

PRIOR APPLICATION NUMBER: 60/199,384

PRIOR APPLICATION NUMBER: 60/199,384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 18

LENGTH: 585

TYPE: PRIOR SAPIGES

CRANISM: Homo Sapiens
US-09-833-118-18
; ORGANISM: Homo Sapiens
US-09-832-501-18
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100.0%; Score 3103; DB 11; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.2e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0;
Length 585
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100.0%; Score 3103; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.2e-269;
Matches 585; Conservative 0; Mismatches 0;
 ; ORGANISM: HomoSapiens
US-09-932-322-445
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US-09-932-322-445

Sequence 445, Application US/09932322

Publication No. US20030194743A1

GENERAL INFORMATION:
APPLICANT: Beltzer, James P.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
FILE REFERENCE: Dx.018.1 PCT; DXX-018.1 US

CURRENT APPLICATION NUMBER: US/09/932,322

CURRENT FILING DATE: 2001-08-17

SOFTWARE: PatentIn version 3.1

SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 585
                                                                                         TYPE: PRT CAGANISM: Homo Sapiens US-09-833-117-18.
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Gaps

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Length 585;

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Sequence 18, Application US/09812501
| Publication No. US20030199043A1 |
| GENERAL INFORMATION: |
| APPLICANT: Ballance, David J. |
| APPLICANT: Ballance, David J. |
| APPLICANT: Sleep, Darrell |
| APPLICANT: Sleep, Darrell |
| APPLICANT: Prior, Christopher P. |
| TITLE OF INVENTION: Albumin Fusion Proteins |
| TITLE REFERENCE: PF542 |
| CURRENT APPLICATION NUMBER: US/09/832,501 |
| CURRENT APPLICATION NUMBER: 60/229,358 |
| PRIOR APPLICATION NUMBER: 60/229,358 |
| PRIOR APPLICATION NUMBER: 60/1929,384 |
| PRIOR PILING DATE: 2000-04-12 |
| PRIOR PILING DATE: 2000-04-25 |
| TYPE: PRI
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EQ ID NO 445 LENGTH: 585 TYPE: PRT

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181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
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US-09-833-117-18
Sequence 18, Application US/09833117
Publication No. US20030171267A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Prior, Christopher P.
APPLICANT: Prior, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins FILE REFERENCE: PF543
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12
PRIOR FILING DATE: 2000-12-1
PRIOR FILING DATE: 2000-12-1
PRIOR FILING DATE: 2000-12-1
PRIOR FILING DATE: 2000-12-1
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
ILYPE: PRI
TYPE: PRI
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Best Local Similarity 100.
Matches 585, Conservative
                                                                                                                                  ; ORGANISM: Homo Sapiens
US-09-833-041-18
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100.0%; Score 3103; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.2e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0;
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US-09-833-041-18
Sequence 18, Application US/09633041
Sequence 18, Application US/09633041
Publication No. US20030125247A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Reselvine, William A.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF545
CURRENT APPLICATION NUMBER: US/09/833,041
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 26
   FILING DATE: 19-DEC-1996
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANII-SENSE: NO
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APPLICANT: House Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
APPLICANT: PROPER C.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A
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                                                                                                                                         Length 585;
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                                                                                                                                       100.0%; Score 3103; DB 9; 100.0%; Pred. No. 4.2e-269;
                                                                                                                                                                                         0; Mismatches
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                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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US-09-912-613-445

Bequance 445, Application US/09912613

Publication No. US20030091565A1

GENERAL INFORMATION:
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US-09-932-613-445
                                                                                                                                                                  Similarity
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Matches 585; C
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US-09-929-552-2
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE ADDRESS: 36
CITY: Washington
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: PORPY
COMPUTER: IBM PC COMPAGIBLE
COMPUTER: IBM PC COMPAGIBLE
COMPUTER: IBM PC COMPAGIBLE
COMPUTER: BM PC COMPAGIBLE
COMPUTER: PC COMPAGIBLE
COMPUTER: PREADABLE
SYNTHAM: PC COMPAGIBLE
COMPUTER: PREADABLE

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3; DB 10; Length 4.2e-269;
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Publication No. US20030104578A1
GENERAL INFORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/091,873
PILING DATE: 25-UNA-1998
APPLICATION NUMBER: PCT/GB96/03164
                                                                                                0; Mismatches
Score 3103;
Pred. No. 4.
100.0%;
                                                  Similarity 100.
35; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

 Run on:
 April 19, 2004, 12:00:25;
 Search time 246.316 Seconds (without alignments) 654.724 Million cell updates/sec

 Title:
 US-09-832-929-18

 Perfect score:
 3103

 Sequence:
 1 DAHKSBVAHRFKDLGEBNFK......TCFAEEGKKLVAASQAALGL 585

 Scoring table:
 BLOSUM62

 Gapop 10.0 , Gapext 0.5

 Searched:
 1124875 segs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_PWB PUB.pep:\*

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18: /cgn2\_6/ptodata/2/pubpaa/USO0\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 2, Appli	Sequence 445, App	Sequence 26, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 445, App	Sequence 18, Appl	18, 7	Sequence 18, Appl	11,	Sequence 31, Appl	Seguence 5, Appli	Sequence 5, Appli	H	7
ΠD	US-09-929-552-2	US-09-932-613-445	US-09-984-010-26	US-09-833-041-18	US-09-833-117-18	US-09-932-322-445	US-09-832-501-18	US-09-833-118-18	US-09-833-245-18	US-10-424-999-11	US-10-425-000-31	US-10-153-064-5	US-10-153-604A-5	US-10-319-263-1	US-10-319-263-2
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% Query Match Length DB	585	585	585	585	585	585	585	585	585	585	585	585	585	585	585
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	3103	3103	3103	3103	3103	3103	3103	3103	3103	3103	3103	3103	3103	3103	3103
Result No.	г	7	m	4	Ŋ	v	7	ω	σı	10	11	12	13	14	15

LENGTH: 585 amino acids

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US-10-414-469-1	US-10-414-469-2	10-413	10-4	10-413-	10-413-	-10	us	US-10-233-67	US-10-46	US-09-98	US-09-919	US-10-153-064-7	0-153	365		3-10	0-237	US-10-237-866-2	-10 - 237	37	US-10-433		US-10-433-	US-10	US-10-433	0	53-	.0 - 153	US-10-153-604A-132
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0	100.0
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# ALIGNMENTS

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RESULT 1
US-09-99-55-2
US-09-99-55-2

18-equence 2, Application US/09929552
Patent No. US20020123080A1
GENERAL INFORMATION:
CENTER INFORMATION:
COTOR, ANA M.
TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCE ADERSES:
ADDRESSEE: Montgomery Street, Suite 2200
STREET: 220 Montgomer No. 200
STREET: 220 Montgomer: 14-Mg-2001
COMPUTER: 1BM PC Compatible
OPERATION NUMBER: 08/09/929,552
FILING DATE: 19-DEC-1956
ATTORNEY/AGRY INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
TELEPHONE: GLARACTENISTICS:
SEQUENCE CHARACTENISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B Lymphocyte stimulator binding polypeptide.
                                                                                           PTLVEVSRNLGKVGSKCCKHPBAKRMPCABDYLSVVLNQLCVLHBKTPVSDRVTKCCTES
                                 PTLVEVSRNIGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
                                                                       LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKBRQIKKQTALVELVKHKPKAT
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Score 3103; DB 5; Length 585; Pred. No. 1.5e-254;

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Query Match Best Local Similarity

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Job time : 348.086 secs
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                                                                 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKABFAEVSKLVTDLTK
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                               DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                      NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                           DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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The present invention relates to albumin fusion proteins comprising a the albumin fusion proteins are useful for treating, preventing, or HA).

The albumin fusion proteins are useful for treating, preventing, or ameliorating various disorders. Such disorders include immune disorders, and incorders, include immune disorders, autoimmune disorders, lood-related disorders, respiratory disorders, neurological disorders, endortine disorders, reproductive disorders, neurological disorders, endortine disorders, reproductive disorders, astrointestinal disorders, infectious disease, and wound healing. Therapeutic proteins can be stabilised to extend shelf infe and/or retain the proteins can be stabilised to extend shelf the protein to albumin or its fragment or variant. In addition the use of albumin fusion proteins reduces the need to formulate protein solutions with large excesses of carrier proteins to prevent loss of therapeutic protein due to factors such as binding to the container. The extension of shelf life was tested by measuring biological activity (Nb2 cell protein remaining after incubation in cell culture media for up to 3 weeks. At week 3 there was still approximately 95% cell proliferation compared to no activity of unfused hGH. The present sequence represents the mature form of HSA which can be used to produce the albumin fusion mature of HSA which can be used to produce the albumin fusion by proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                New albumin fusion proteins with extended shelf life, useful for treating leukemia, warts, hepatitis, multiple sclerosis and AIDS, comprises therapeutic protein fused to albumin.
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100.0%; Score 3103; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.5e-254;
Matches 585; Conservative 0; Mismatches 0;
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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the potential for inhibiting cancer cell proliferation and for e
biopsied tumors, comprises employing albumin-derived peptide.
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Pred. No. 1.5e-254;
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N-PSDB; AAD11488.
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Albumin fusion proteins are stabilised therapeutic proteins e.g. antibodies to C5, C242 and CD80 useful for treating various diseases and disorders such as non-Hodgkin's lymphoma, cancer, obseity, transplant rejection, type I diabetes mellitus, rheumatoid arthitis and psoriasis. Fusing albumin to therapeutic proteins stabilises the therapeutic protein stabilises the invitro or in vivo biological activity. It also reduces the need to formulate protein solutions with large excesses of carrier proteins to prevent loss of the interpretation proteins due to factors such as binding to the container. The fusion proteins are easily dispensed with a simple formulation requiring minimal post storage manipulation. The fusion of therapeutic proteins sequence represents the mature human albumin (HA) protein which is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New albumin fusion proteins, useful for treating diseases and disorders such as cancer, comprise therapeutic protein fused to albumin.
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437. .448
461. .477
476. .487
492. .511
/note= "flexible inter-gubdomain linker region"
512. .585
514. .559
558. .567
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                                                                                                                                                                                                                                                                                                                            12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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Best Local Similarity 100.
Matches 585; Conservative
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                                                                                                                                                                                                                                                                                                                         Turner AJ;
              461. 475 /-
/label= Loop_X
478. 486
/label= Loop_XI
560. 566
/label= Loop_XI
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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(PRIN-) PRINCIPIA PHARM CORP
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N-PSDB; AAD22287.
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361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST

CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFBQLGEYKFQNALLVRYTKKVPQVST

421 PILVEVSRNIGKVGSKCCKHPEAKRAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT

PILVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES

421

LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT

481 541 541

KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL

Human mature albumin protein SEQ ID NO:18.

01-AUG-2002 ABB79006;

ABB79006 standard; protein; 585 AA

241 VHTECCHGDILECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300

301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC

301

70.77.07

MOII Apr 13

361

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d 75. .91
d 90. .101
d 90. .101
//note= "flexible inter-subdomain linker region"
120. .194
//label= subdomain
d 148. .177
195. .387
//label= subdomain
d 265. .253
d 265. .279
d 278. .289
                                                              Human; growth hormone; hGH; albumin; human serum albumin; HSA; albumin fusion protein; cytostatic; anorectic; immunosuppressive; antidiabetic; antitheumatic; antiatrhritic; psoriatic; cancer; non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis; type I diabetes mellitus; rheumatoid arthritis.
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1. .105
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53. .62
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388. .491
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DVMCTAFHDNEETFLKKKLYBIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180

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KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK

DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE

Query Match
100.0%; Score 3103; DB 4; Length
Best Local Similarity 100.0%; Pred. No. 1.5e-254;
Matches 585; Conservative 0; Mismatches 0; Indels

. 0

Length 585;

NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNFNLFRLVRFEV

VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAZVENDEMPA 300 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

180

360 360

420 420 480 480 540

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241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                         DVMCTAFHDNBBTFLKKYLYBIARRHPYFYAPELLFFAKRYKAAFTBCCQAADKAACLLP
                                                                                                                              CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
                                                                                                                                                                                                                                                                                                                                                    481 LVNRRPCFSALEVDETYVPKEFNABTFFFHADICTLSBKERQIKKQTALVELVKHKPKAT
                                                                                                                                                                 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC
                                                                                                                                                                                                                                                                              PILVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
                                                                                                                                                                                                                                                                                                 PTLVEVSRNIGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
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                                                                         KIDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFABVSKLVTDLTK
DVMCTAFHDNEETFLKKYYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders.
                                                                                                                                             LOOP_VIII
                                                                                                     461. 475 - 478 / label= Loop_X 478 . 486 / label= Loop_X / label= Loop_XI
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| 170. 176
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| 247. 252
| 1abel = Loop_V
                                                                                                                                                                                                                                           560. .566
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                                                                                                                  Loop_VII
        'label = Loop_III
                                                                         266. .277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 9; 380pp; English.
                                                                                                                                                                                                                                                                                                                                                                      12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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N-PSDB; AAD21638.
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Human, albumin, HA, fusion protein; immune system disorder; syphilis; transplant rejection; blood related disorder; myocardial infarction; hyperproliferative disorder; acute myeloid leukaemia; renal disorder; glomerulonephritis; cardiovascular disorder; arrhythmia; rhinitis; respiratory disorder; neurological disease; Alzhelmer's disease; endocrine disorder; pheocytochroma; reproductive system disorder; measles; gastrointestinal disorder; irritable bowel syndrome; HIV; human immunodeficiency virus; wound healing; renal cell carcinoma;
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76. .89
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                                               Human albumin (HA) protein.
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Query Match 100.0%; Score 3103; DB 4; Length 585; Best Local Similarity 100.0%; Pred. No. 1.5e-254; Matches 585; Conservative 0; Mismatches 0; Indels 0

Sequence 585 AA;

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NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLGHKDDNPNLPRLVRPEV

DAHKSEVAHRFKDLGEBNFKALVLIAFAQYLQQCPFBDHVKLVNEVTEFAKTCVADESAE

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The invention relates to human albumin (HA) fusion proteins and their corresponding nucleic acid sequences. Therapeutic proteins fused to albumin or its fragments have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid infarction), hyperproliferative disorders (e.g. childhood acute myeloid cleukaemia, metastatic renal cell carcinoma, metastatic melanoma, and lighant melanoma, ranal cell carcinoma, renal disorders (e.g. arrhythmias), candiovascular disorders (e.g. arrhythmias), capiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. iritable bowel syndrome), HIV chuman immunodeficiency virus) infection and wound healing. Nucleic acide encoding albumin fusion protein is used in gene therapy. The present
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            location/Qualifiers
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560. .566
/label= Loop_XII
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25-APR-2000, 2000US-0199384P.
21-DEC-2000, 2000US-0256931P.
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/label= Lo
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N-PSDB; AAD20005.
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Score 3103; DB 4; Length 585; Pred. No. 1.5e-254;

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Query Match Best Local Similarity

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The present invention relates to albumin fusion proteins, which comprise a therapeuric protein and albumin. The present sequence is the protein sequence for mature human serum albumin (HA), which was used to generate the fusion proteins of the present invention. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases Adisorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) hyperproliferative disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid leukemia), arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. syphilis),
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                                                                                                                                                                            CAAADPHECYAKVFDEFKPLVBEPQNLIKQNCELFBQLGEYKFQNALLVRYTKKVPQVST
                         CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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, human serum albumin, HSA, yeast codon bias, host cell; oligonucleotide; expression vector.

Yeast codon-biased recombinant human serum albumin

Recombinant;

overlapping

sapiens

Synthetic

CN1239103-A 22-DEC-1999

(first

28-JUL-2000

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The present sequence represents human albumin protein. The specification describes a method for the continuous detection of ischemic states. The method comprises detecting and quantifying the existence of an alteration of the serum protein albumin. The method comprises contacting an alteration biological sample containing albumin from the patient with an excess quantity of a metal ion salt, where the metal ion binds to the Vterminus of naturally occurring human albumin, to form a mixture containing bound metal ions bound metal ions bound to the albumin, to form a mixture containing bound metal ions bound to the albumin Vterminus. The amount of bound metal ions is correlated to a known value to determine the occurrence or non-occurrence of an ischemic event. The methods are useful for detection of ischemic states. The methods are also useful for distinguishing perioperative ischemia from ischemia caused by , amongst other things, myocardial infarctions and progressive coronary artery disease
                       i for the continuous detection of ischemic states comprises and quantifying the existence of an alteration of the serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 585;
                                                                                                                                    Disclosure, Page 97-100; 105pp; English
                          method for the
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 100.0%; Score 3103; DB 3;
100.0%; Pred. No. 1.5e-254;
ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
Matches 585, Conservative
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standard; protein; 585

AAY83946

AAY83946 ID AAY8 XX RESULT 7

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The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonucleotide fragments that were extended. This sequence represents the complete sequence of the HSA encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression vector, yeast host cells carrying the recombinant expression vector, process for producing human serum albumin in the yeast host cell,
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Pred. No. 1.5e-254;
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ifor preparing recombined human serum albumin comprising yeast sex codons - uses a recombinant DNA technique.

BIOENGINEERING CO

(HAIJ-) HAIJI

Lu D;

Li S,

WPI; 2000-351198/31. N-PSDB; AAA10091.

Process biased

98CN-00102506 98CN-00102506

17-JUN-1998; 17-JUN-1998; Disclosure, Fig 1, 44pp, Chinese.

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                                                                                                                                                                                                                                                                                                                                                                     sequence of a human albumin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a serum albumin-growth hormone fusion protein useful to treat growth hormone related diseases such as Down's syndrome. This sequence represents a HSA protein related to the serum albumingrowth hormone protein of the invention
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                      CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
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                                                                                                                                                                                                                                                                                                                                                     HSA protein sequence related to the growth hormone protein.
                                                                                                                                                                                              KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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100.0%; Score 3103; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.5e-254;
Matches 585; Conservative 0; Mismatches 0;
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N-PSDB; AAK99568.
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19-DEC-1996;
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VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
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KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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llarity 100.0%; Pred. No. 1.5e-254;
Conservative 0; Mismatches 0;
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                                                                                              AAR80301 standard; protein;
                                                                                                                                                                                           entry)
                                                                                                                                                                         (revised)
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N-PSDB; AAQ98695.
                                                                                                                                                                                           (first
                                                                                                                                                                                                                              Human serum albumin
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Best Local Similarity
Matches 585; Conserv
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                                                                                                                                                                       25-MAR-2003
17-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                Pragments A-C of HSA are expressed as fusion proteins with the signal peptide of E. coli alkaline phosphatase. The fragments are selected for their specific properties. The C-terminal truncated fragment, B, does not bind long-chain fatty acids but does bind to various medicines at the central region. The N-terminal truncated fragment, C, has good stability in protein folding. The central segment, A, has characteristics of both B and C. See also ARQ06096. (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PP field.)
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                                                                                                                                                                                                                                                                       - used
                                                                                                                                                                                                                                                                          human serum albumin fragments
                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 8; 24pp; Japanese
                                                                                              89JP-00217540,
                                                                                                                                      88JP-00250926.
                                                                                                                                                                                                                                                                                            stable folding of protein(s)
                                                                                                                                                                                                              WPI; 1990-317325/42.
N-PSDB; AAQ06099.
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                    JP02227079-A
                                                                                              25-AUG-1989;
                                                                                                                                      06-OCT-1988;
                                                           10-SEP-1990
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                                                                                                                          1 DAHKSEVAHRPKDLGEENPKALVLIAPAQYLQQCPFEDHVKLVNEVTEPAKTCVADESAE
produced using the sequence incorporated into a suitable controllers, and transfered to a yeast
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                                                                        100.0%; Score 3103; DB 2;
100.0%; Pred. No. 1.5e-254;
ive 0; Mismatches 0;
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Best Local Similarity
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  Mature HSA-A may |
plasmid vector wit
expression system
                                                      Sequence 585 AA;
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16-APR-1991
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                                                                                                      DLPSLAADFVESKDVCKNYAEAKDVFLCMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC
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       DAHKSEVAHRFKDLGBENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                           DAHKSEVAHRFKDLGBENFKALVLIAFAQYLQQCPFBDHVKLVNEVTEFAKTCVADESAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human serum albumin; HSA-A; yeast; ds
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Mature protein of human serum albumin (see corresp. AAN90128). Used to make new N-terminal fragments which are used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                   Human serum albumin; mature protein; new polypeptides; plasma
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Best Local Similarity 100.0%; Pred. No. 1.5e-254;
Matches 585; Conservative 0; Mismatches 0; Indels 0
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plasma expanders.
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N-PSDB; AAN90128.
Sequence 585 AA;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity 47.7%; Pred. No. 2.8e-75;
Matches 186; Conservative 80; Mismatches 124; Indels 0
                                                                             SEQUENCE FROM N.A.

Metcalf V.J. Brennan S.O., George P.M., Chambers G.K.;
Metcalf V.J. Brennan S.O., George P.M., Chambers G.K.;
Metcalf V.J. Brennan E.O., George P.M., Chambers G.K.;
Extractal mRNA sequence for tuatara A/B serum albumin.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF315973; AAM46106.1, -
EMBL, AF315973; AAM46106.1, -
EMBL, AF315973; AAM46106.1, -
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EKCCQAENKQECFSTEGEKLTQEGKALLGV 392
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The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

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"To 770 full-length cDNAs.";

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"To 60,770 full-length cDNAs.";

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SEQUENCE 605 AA; 67409 MW; CF3509A9EC146110 CRC64;
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GBJIA7;
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-UVN-2003 (TrEMBLrel. 24, Last annotation update)
A/B over-sized serum albumin (Fragment).
Sphenodon punctatus (Hatteria) (Tuatara).
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QBJIA7
ID QBJIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 HETELSNKYG-LSGCCSQSGVERHQCLLARKKTAPASVPFQFPEPAESCKARERRAVF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 LKKYLYEIARRHPYFYAPELLFPAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 KQRLKÇASLQKFGERAFKAWAVARLSQRFPKAEFABVSKLVTDLTKVHTECCHGDLLECA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKD 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 EKNVLSIATITFIQFVPEATEEE----VNKMTSDVLAAMKKNSGDGCLESQLSVFLDEIC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 BENFKALVLIAFAQYLQQCPFEDHVKLVNBVTBFAKTCVADESAENCDKSLHTLFGDKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
34.9%; Score 1082; DB 11; Length 605;
Best Local Similarity 35.7%; Pred. No. 5.1e-78;
Matches 204; Conservative 120; Mismatches 241; Indels 6
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STRAIN=CS7BL/6J; TISSUB=Placenta, and Extraembryonic tissue;
MEDLINE=22354683; PubMed=12466851;
    GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
GO; GO:0042448; P:progeterone metabolism; IMP.
GO; GO:0019553; P:sexual reproduction; IMP.
InterPro; IPR000264; Serum_albumin.
PRam; PR00273; Transport_Drot; 3.
PRINTS; PR00802; SERUMALBUMIN.
PRODOM; PD002486; Serum_albumin; 1.
PRODOM; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
SEQUENCE 605 AA; 67322 MW; 048B7A4A8B01EA4B CRC64;
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                                                                                      135
                                               100 HEKEIFEKYG-LSDCCSRSGEERHSCLPAHKKAAPALPPFQAPEPATSCKAYEEDRETFM 158
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                                                                                                              QRLKCASLQKFGERAFKAWAVARLSQRFPKAEFABVSKLVTDLTKVHTECCHGDLLECAD
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                                                                                                                                                                                                                                                                 KCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE
                                                                                                                                                                                                                                                                              136 KKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAK
                                                                                                                                                                                        CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFD
EENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLC
            TVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNESTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ambystoma texanum (Smallmouth salamander).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.; "Serum albumin of the mole salamanders Ambystoma maculatum and Ambystoma texanum."; Submitted (DEC-1999) to the FWPT //----.
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Last annotation update)
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ETCCQGQEQEVCFAEEGPKLISKTRDALGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00212; ALBUMIN;
Signal.
SIGNAL 1 24
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01-MAR-2002 (
01-JUN-2003 (
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                                                                                                                                                                                                                                                                                                                                                       312 SKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYA
                                                                                                                                                                                                                                                                                                                                                                                                                               KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPV-SDRVTKCCTESLVNRRPCFSA
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                                                                                                                                                           225 VCAVQKHNCYILQNFNERALRASKAAHACSKFPHASFENVQRLTDGIVHLHQTCCGGDMM
                                                                                                         45 IGVEHAKALAMALFSQMLSKCPHHEQVQRVRVRNVMDIADLCSRGAKHGDCGKSVMTIILNE
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STRAIN-CS7BL/6J; TISSUE=Body;

MEDINE=2234683; PubMed=12466851;

MEDINE=2234683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

The FANTOM Consortium,

"Analysis of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of 10,700 full-length CDMAs.

Nature 420:563-573(2002).

RIME, ARCHOGS; BACS36190.1; -.

MED; MI:87951; Afp.

GO; GO:0005615; C:extracellular space; IDA.
                                                                                       LGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDK
                                                                                                                                                                                               133 TFLKKYLYBIARRHPYFYAPBLLFFAKRYKAAFTBCCO-AADKAACLLPKLDBLRDBGKA
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                                                             12;
                                   624;
                                   Length
                                                              Indels
SERUM ALBUMIN.
DE08533BF4953EF7 CRC64;
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Last sequence update)
Last annotation update)
                                  Query Match
Best Local Similarity 37.7%; Pred. No. 2.1e-78;
Matches 214; Conservative 102; Mismatches 240;
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624 S
70321 MW;
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624 AA;
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SEQUENCE
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ID Q8BK65
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PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 610 AA; 68624 MW;
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                                                                                                                                                                              VTDLTKVHTECCHGDLLECADDRADLAKY I CENQDS I SSKLKECCEKPLLEKSHCI AEVE
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                                                                     1 DAHKSEVAHRPKDL----GEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVAD
                                                                                    EGHVDNPPHLIGDLIPMIGVDNSKGLVLAAVSQMLPLCPYEBHLQRVEDVMQIADLCAKG
                                                                                                                                                                 VRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKA
                                                                                                                                                                                                              176 A-CLLPKLDELRDEGKASSAKQRLKÇASLQKFGERAFKAWAVARLSQRFPKAEFABVSKL
                                                Gaps
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A Kim J.G., Nonneman D., Vallet J.L., Christenson R.K.;
A Kim J.G., Nonneman D., Vallet J.L., Christenson R.K.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
B RBL; AFS1770; AAM6510.1;
R GO; GO:0005186; P:carrier space; IEA.
R GO; GO:0005186; P:carrier activity; IEA.
R GO; GO:0005186; P:transport, IEA.
R GO; GO:000518; Extransport DTC: 3.
R Pfam; PF00273; transport DTC: 3.
R PRINTS; RRO8022; SERUM.IBUMIN.
R Probom; PD002486; Serum albumin; 1.
R SMART; SM00103; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                               9
                          DB 13; Length 626;
                                                Indels
  9D66F57F174AC23F CRC64;
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Last annotation update)
                      40.0%; Score 1242; DB 13;
larity 40.1%; Pred. No. 8.5e-91;
Conservative 110; Mismatches 238;
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   70677 MW;
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                                     Local Similarity
es 237; Conserv
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    SEQUENCE
                           Query Match
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Q8MJ76;
                                         Best Loca
Matches
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                                                                                                                        TVATLRETYGEMADCCAKQEPERNECFLQHKDDNP-NLPRLVRPEVDVMCTAFHDNEETF
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                                                                                                                                                                                                                                                                                                                                                                                      195 KORLKCASLOKFGERAFKAWAVARLSORPPKAEFABVSKLVTDLTKVHTECCHGDLLECA
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                                                                                              EENFKALVLIAPAQYLQQCPFEDHVKLVNEVTEPAKTCVADESAENCDKSLHTLFGDKLC
                                                   Gaps
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SEQUENCE FROM N.A.

Lin H.L., Chen P.J., Wu. H.L., Lee R.S., Chen D.S.;

"Molecular Cloning and Expression of Woodchuck Alpha-Fetoprotein.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY034049; AAKS57577.1;

SEQUENCE 608 AA; 67962 MW; EB46D7A37382B222 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Sciuridae, Sciurinae;
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  6; Length 610;
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38.1%; Score 1183.5; DB 11; Lengt
Best Local Similarity 39.3%; Pred. No. 3.9e-86;
Matches 224; Conservative 108; Mismatches 237; Indels
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Query Match 39.3%; Score 1218.5; DB 6; Best Local Similarity 39.7%; Pred. No. 6.2e-89; Matches 227; Conservative 117; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||||: ::| ||||||| |: ::||:||:
LLEKCCQGQBQEVCFAEBGPALISKTRASLGV 610
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Marmota monax (Woodchuck).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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279 QDGEKIMSYICSQQDILSSKIADCCKLPILELGQCIIHAENDGKPEGLSPNINRFLEERD 338
                                                                                                                                                                                                                                                                                                                                                    : : ||:|: | |||:| | ||:||| 339 FNQPSSREKDLFWARFTYEYSRHTKLAVPVVLRVAKGYQELLEKCSQSENPLECQDKGE 398
                                                                                                                                      195 KORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTKVHTECCHGDLLECA 254
                                                                                                                                                                                                                                                         255 DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKD 314
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                                                                                                                                                                                                        435 SKCCKHPEAKRMPCAEDYLSVVINOLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD
40 EMNLVDLATIFFAQFVQEATYKEVSKMVKDILTVIEKSTGSEQPGGCLENQLPAFLEEIC
                                                            135 LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLFKLDELRDEGKASSA
                                    76 TVATLRETYGEMADCCAKQEPERNECFLOHKD-DNPNLPRLVRPEVDVMCTAFHDNEETF
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
"Serum albumin of the mole salamanders Ambystoma maculatum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ambystoma texanum.";
submitted (DBC-19596 to the EMBL/GenBank/DDBJ databases.
EMBL; AF217183: AALS646.1; -.
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005386; F:carrier activity; IEA.
GO; GO:00053810; P:transport; IEA.
InterPro; IPR000264; Serum_albumin.
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Last sequence update)
Last annotation update)
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LEKCCQGQEQEACFEEEGPKLISKTRAALGV 609
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SERUM ALBUMIN.
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PRINTS; FRONGOZ; SERUWALBUMIN.
SMART; SMOOLO3; ALBUMIN; 1
SMART; SMOOLO3; ALBUMIN; 2.
PROSITE; PSOO212; ALBUMIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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626
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SIGNAL
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                                                                                                                                  KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
                                                                                                                                                     DIPSLAADFVESKDVCKNYAZAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYBTTLEKC 360
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                                                            DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
                                                                                 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
 CLKSLDTIFLDEICHEEGFAAKY-DLAACCAKAEVERKECLLAHKNATPGFIPAFQRFGI 63
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Furucchi M., Meo S., Hisasue M., Tsuchiya R., Watanabe M., Hashizaki K., Hisamatsu S., Yamada T.;

Hashizaki K., Hisamatsu S., Yamada T.;

"Canine alpha-fetoprotein CDNA.";

Submitted (AMC22002) to the EMBL/GenBank/DDBU databases.

EMBL, AB089789; BAC07513.1;

GO, GO.0005615; Ciextracellular space; IEA.

GO, GO.0005186; Ficarrier activity; IEA.

InterPro; IRR000264; Serum_albumin.

ProDom; PR00203; Fransport infa.

PRINTS; PR000021; Serum_albumin.

ProDom; PD002486; Serum_albumin; 1.

SNRAT; SM00103; ALBUMIN; 2.

SRQUENCE 609 AA; 68782 MW; BE4B8250C5AF2AF0 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
40.0%; Score 1242; DB 6; 1
Best Local Similarity 40.5%; Pred. No. 8.2e-91;
Matches 231; Conservative 113; Mismatches 225;
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DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLF 180
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Sphenodontia, Sphenodontidae; Sphenodon.
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01-OCT-2002 (TrEMBirel. 22, Created)
01-OCT-2002 (TrEMBirel. 22, Last sequence update)
01-UN-2003 (TrEMBirel. 24, Last annotation update)
Serum albumin (Fragment).
                                                                                                                                   DVMCTAFHDNEETFLKKYL----
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SEQUENCE 527 AA; 59711 MW;
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Best Local Simi
Matches 240;
                    61
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                                                                                                                                                                           186 RDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKABFAEVSKLVTDLTKVHTEC
                                                                                                                                                                                                        CHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSL
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                                                                                                                                     Gaps
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 6.7e-141;
0; Mismatches 0; Indels 213;
                                                                                                Length 417;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases. Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC035969; AAH35969.1; --
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005816; P:carriar activity; IEA.
GO; GO:0006810; P:carriar. activity; IEA.
InterPro; IPR000264; Serum_albumin.
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ProDom; PD002486; Serum_albumin; 1.
SMART; SM0103; ALBUMIN; 2.
PROSITE; PS0212; ALBUMIN; 2.
PROSITE; P 4012; ALBUMIN; 2.
SEQUENCE 417 AA; 47360 MW; 16E764833EEF4E8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 AVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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                                                                                                                                       10;
                                                                                           Query Match
Best Local Similarity 95.2%; Pred. No. 6.5e-151;
Matches 381; Conservative 3; Mismatches 10;
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PRINTS; PR00802; SERUVALBUMIN.
PRART; SM00103; ALBUMIN; 2.
PROS;TE; PS00212; ALBUMIN; 2.
SEQUENCE 396 AA; 45159 MW; 756
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llarity 63.6%;
Conservative
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Best Local Similarity
Matches 372; Conserv
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TISSUE=Liver;
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                                                                                                                     CABANPPACYGTVLAEFQPLVEBFKNLVKTNCDLYBKLGGYGFQNAILVRYTQKAPQVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LVNRRPCFSALEVDETYVPKEFNAETPTFHADICTLSEKERQIKKQTALVELVKHKPKAT
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DAHKSEVAHRPKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                    NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPRLVRPEV
                                                                                                        DVMCTAPHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
                                                                                                                                                          KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK
                                                                                                                                                                                                               VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA
                                                                                                                                                                                                                                                                   DLPSLAADFVESKDVCKNYABAKDVFLGMFLYBYARRHPDYSVVLLLRLAKTYETTLEKC
                                                                                                                                                                                                                                                                                                                       CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
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STRAIN-CSTBL/6J; TISSUB=Thymus;
STRAIN-CSTBL/6J; PubMed=12466851;
The FANTOM Consortium,
The RIXEM Genome Exploration Research Group Phase I & II Team;
Thanysis of the mouse transcriptome based on functional annotation (60,770 full-length cDNa.",
Nature 420:563-573(2002).
EMBL, AKOSG44; BASC31360.1;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583
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Last annotation update)
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GO; GO:0005615; C:extracellular space; IEA
GO; GO:0005386; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000264; Serum_albumin.
Pfan; PR00823; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD0002486; Serum_albumin.
SNART; SM00103; ALBUMIN; 3.
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01-OCT-2003 (TrEMBLrel. 23,
Albumin 1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 DNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCOAADKAACLLPKLDELRDE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 SALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKOTALAELVKHKPKATAEQLKTVM
                                                                                                                                                                                                                                                                         1 NRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKASSAKQRIKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                       Length 576;
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Strauberg R.;
Submitted (BEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041789; AAH41789.1; -.
EMBL; BC041789; AAH41789.1; -.
EGO; GO:0005615; C: extracellular space; IEA.
GO; GO:0005816; F: cartrier activity; IEA.
GO; GO:0006810; P: transport; IEA.
InterPro; IRR00264; Serum albumin.
Pfam; PF00273; transport pro;
PRINTS; PR00802; SERUMALEUMIN.
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Last annotation update)
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al Similarity 72.2%; Pred. No. 2.5e-178;
415; Conservative 79; Mismatches 81;
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                                                           F85733E99AE37F04
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Similar to alpha-fetoprotein.
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                                                        576 AA; 65002 MW;
PROSITE: PS00212; ALBUMIN; 3.
NON TER 1 1
SEQUENCE 576 AA; 65002 MW;
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Best Local
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               DVMCTAFHDNEETFLKKYLYSIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
                              DLPSLAADFVEDKEVCKOYAEAKDVFLGTFLYEYARRHPDYSVALLLRLAKKYEATLEKC
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                                                                                                                                                                                                                                                                                                                    PTLVEAARNLGKVGSKCCVLPEAQRLPCVEDYISAILNRVCVLHEKTPVSEQVTKCCTGS
                                                                                                                                                                                                                                                            481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT
                                                                      KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK
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The FANYOW Consortium,
The FANYOW Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 50,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BMED, AKOS0248; BAC34145.1; -...
MGD; MGI:87991; Alb1.
GQ; GQ:0005515; C:extracellular space; IEA.
GQ; GQ:0005386; F:carrier activity; IEA.
GQ; GQ:0005810; P:transport; IEA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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ilarity 72.2%; Pred. No. 2.5e-181;
Conservative 80; Mismatches 82;
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Pfam; PR00275; transport proc; 3.
PRINTS; PR00802; SERUMALEUMIN
PRODOM; PD002486; Serum albumin; 1.
SWART; SMO0103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
SEQUENCE 608 AA; 68722 MW; 292F60
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Schistosoma.
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80.7%; Score 2504; DB 5;
Best Local Similarity 76.3%; Pred. No. 9.9e-192;
Matches 445; Conservative 79; Mismatches 59;
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Schistosomatoidea, Schistosomatidae,
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40.3%; Score 1249.5; DB 1; Length 609;
Best Local Similarity 39.9%; Pred. No. 5.5e-73;
Matches 235; Conservative 116; Mismatches 231; Indels 7;
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-> G (in dbsNP-1057173).
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.W., Cargura M.J., Skalska U., Smailus D.B., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences,", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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"Human alpha-fetoprotein primary structure: a mass spectrometric
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Tanaoki T.,
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MEDLINE-78001760; Pubmed=71198;
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                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).

-!- FUNCTION: Binds copper, nickel, and fatty acids as well as, and bilirubin less well than, serum albumin. Only a small percentage (less than 2.8) of the human APP shows estrogen-binding properties.
-!- SUBUNIT: Dimeric and trimeric forms have been found in addition to the monomeric form.
-!- SUBCILIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Plasma. Synthesized by the fetal liver and
                        Adyagi Y., Ikenaka T., Ichida F.;
Abha-Feroprotein as a carrier protein in plasma and its bilirubin-
binding ability ";
Cancer Res. 39:3571-3574(1979).
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Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
"Tyrosine sulfation of proteins from the human hepatoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00112; ALBUMIN; 2. Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel; Signal; Polymorphism.
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Pfam; PR00273; transport prot; 3.
PRNUTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum albumin; 1.
SWART; SM00103; ALBUMIN; 3.
MEDLINE=80001710; PubMed=89900; Tchida F.;
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EMBL; M10950; AAAS1675.1; --
EMBL; W1014; CAA24758.1; --
EMBL; M16110; AAB58754.1; --
EMBL; EC027881; AAH37881.1; --
EMBL; Z19532; CAA73592.1; --
PIR; A26644; FPHU.
HSSP; P02768; IE78.
GlycoSuiteDB: P02771; --
Siena-2DPAGB; P02771; --
Genew; HGNC:317; AFP.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;
"Primary structures of human alpha-fetoprotein and its mRNA.",
Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).
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MEDLINE=87185438; PubMed=2436661;
MEDLINE=87185438; PubMed=2436661;
MEDLINE=87185438; A.;
MEDLINE=87185438; A.;
MEDLINE=87185438; A.;
A. Complete sequence of the human alpha-fetoprotein gene.";
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
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-!- FUNCTION: Binds copper, nickel, and fatty acids as well as, and bilitubin less well than, serum albumin.
-!- SUBGNIT: Dimeric and trimeric forms have been found in addition to the monomeric form (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Plasma. Synthesized by the fetal liver and
                                   Nishio H., Gibbs P.E., Minghetti P.P., Zielinski R., Dugaiczyk A.; "The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to that of gorilla but distinct differences from that of
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InterPro; IPR000264; Serum albumin.
Pfam; PF00273; transport_prot; 3.
Pfam; PF00273; transport_prot; 3.
PRINTS; PR0002486; Serum_albumin.
ProDom; PD002486; Serum_albumin; 1.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 2.
Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel; Signal.
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C032987CAD0E672B CRC64;
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-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
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Conservative 115; Mismatches
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                MEDLINE=96032345; PubMed=7557431;
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                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-28 FROM N.A.
MEDLINE=83161037; PubMed=6187737;
Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.;
"The 5' noncoding and flanking regions of the avian very low density
apolipoprotein II and serum albumin genes. Homologies with the egg
white protein genes.";
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R EMBL; V00381; CAA23680.1; -.

R PIR; S1571; AGCHS.

R HSSP; PO2768; LETS.

R HSSP; PO2768; LETS.

R Pfam; PF00273; transport prot; 3.

R Probom; PD00248; Serum albumin.

R Probom; PD00248; Serum albumin.

R Probom; PD00248; Serum albumin; 1.

SMART; SM00103; ALBUMIN; 3.

R PROSITE; PS00212; ALBUMIN; 3.

Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.

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                                                                                                                                                                                                                                                               of chicken
                Cassady A.I., Salkild C.K., Baverstock P., Wallace J.C., Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                Rosen A.M., Geller D.M.; "Chicken microsomal albumin: amino terminal sequence
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J. Biol. Chem. 258:4556-4564 (1983).
[3]
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MEDLINE=78019943; PubMed=911327;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-APP.
                                                                                                                                                            50.2%; Score 1557.5; DB 1; Length llarity 46.7%; Pred. No. 1e-92; Conservative 118; Mismatches 192; Indels
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=93142044; PubMed=1286668;

MEDLINE=93142044; PubMed=1286668;

MIGLOMETTI C.S., Taylor J., Tollaksen S.L.;

MOUSE liver protein database: a catalog of proteins detected by two-dimensional gelectrophoresis.";

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Electrophoresis 13:970-991(192).

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EMBL; MIGLEI; AAA31190.1; -
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SWISS-ZDPAGE; P07724; MOUSE.
SWISS-ZDPAGE; P07724; MOUSE.
MGD; MGI:87991; Alb1.
InterPro; IPR000264; Serum albumin.
Pfam; PF00773; transport prot; 3.
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Mol. Biol. Evol. 2:347-358(1985)
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InterPro; IPR00264; Serum albumin.
Pfam; PP00273; transport proc; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat;
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Matches 430; Conserv
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RECUENCE TISSUB=Tongue;

REALWAGGO, PubMed=11217851;

RECUENCE TISSUB=TONGUE;

REALWAGGO, PubMed=11217851;

REALWAGGO, T. SHINDSAWA A., SHIDHA K., KORNO H., Adachi J., Fukuda S., Yamanaka I., Adacha K., Makaido T., Roukawa T., Salto R., Adacha K., Makaido T., Roukawa T., Salto R., Radica T., Romo H., Rasukawa T., Salto R., Radica T., Romo H., Rasukawa T., Salto R., Radica T., Pubmin T., Gasselled S., Yamanaka I., Radica M., Marsuc Y., Nikaido I., Pesole G., Quackenbush J., Radica K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Askai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Askai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Askai K., Nikaido I., Peladrarelli R., Barsh G., Askai K., Natolionni L., Mashima J., Hume D.A., Kamiya M., Lee N.H., R. Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Asaeaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., R. Saaki H., Toyo-Oka K., Wang K.H., Masegawa Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Marshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Hayashiami Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Hayashiami Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Hayashiami Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Hayashiami Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Hayashiami Y., Kawaji H., Kohtsuki S., R. Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayashiami Y., Hayas
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MIDINE=2238257; PubMed=1247932;

Alterubler R.D., Collins F.S., Wagner L., Shemene C.M., Schuler G.D.,

Alterhul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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An Expleton M., Soares M.B., Bonaldo M.F., Carvin G.M., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F.,

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Branstein M.J., Usdin T.B., Tonaldo M.F., Carrinci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

Raha S.S., McBwan P.J., McKernan K.J., Malak J.A., Gunaratne P.H.,

Brass S.A., McBwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachiguez A.C., Grimwood J., Schmutz J., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalsku U., Smailus D.E.,

Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rachiguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rachiguez A.C., Grims S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Liver;
van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
542 EQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583
                                                                     P07724; Q61802;
01-APR-1988 (Rel. 07, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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Mus musculus (Mouse).
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121 DVMCTAFHDNEETFLKKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLF
                                                                        KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSORFPKABFAEVSKLVTDLTK
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Incleic Acids Res. 16:9045-9045 (1988).
Incleic Acids Res. 16:9045-9045 (1988).
Incleic Acids Res. 16:9045-9045 (1988).
Include a paperity for water, Ca (2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
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7; Mismatches 70; Indels
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EMBL; M36787; AAA30988.1; --
EMBL; M36787; AAA30988.1; --
EMBL; M36787; AAA30988.1; --
InterPro; IPR000264; Serum_albumin.
Ffam; PF00273; Transport prof; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PR00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCGI_TaxID=9823,
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78.2%; Score 2426; DB 1;
Best Local Similarity 73.4%; Pred. No. 2.2e-148;
Matches 428; Conservative 82; Mismatches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79001617; PubMed=80265;
A Acyagi Y., Ikenaka T., Ichida F.;
A copper(II) binding ability of human alpha-fetoprotein.";
Tocoper(II) binding ability of human alpha-fetoprotein.";
Cancer Res. 38:3483-346(1978)
C. I- FUNCTION: Serum albumin, the main protein of plasma, has a good
Dinding capacity for water, Ca(2+), Wa(+), K(+), fatty acids,
hormones, bilirubin and drugs. Its main function is the regulation
C. I- FUNCTION: NP regulates fat digestion, lipid absorption, and
blood flow (Potential).
C. ISUNCELLULAR LOCATION: Secreted.
C. ITSSUE SPECIFICITY: Plasma.
C. ITSSUE SPECIFICITY: Plasma.
C. ISINILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                      SECUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.,
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                                                                                 Isemura S., Ikenaka T.; "Amino acid sequences of fragments I and II obtained by cyanogen
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=8194805; PubMed=2437111;
Carraway R.E., Mitra S.P., Cochrane D.E.;
Structure of a biologically active neurotensin-related peptide
obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262:5968-5973(1987).
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NEUROTENSIN-RELATED PEPTIDE
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PIR; A93812; ABRTS.
HSSP; P02768; IERS.
InterPro; IRR000264; Serum albumin.
Pfam; PF00273; transport prot; 3.
PRINTS. PRO0002; SERUMLEBUMIN.
ProDom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSTIE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
SIGNAL
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                                                                                                                                    rat serum albumin.";
                                SEQUENCE OF 25-222.
MEDLINE=78109429; PubMed=564345;
                                                                                                                                    bromide cleavage of rat seru
J. Biochem. 83:35-48(1978).
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Caprinae; Ovis.
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COPPER (BY SIMILARITY).
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                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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SERUM ALBUMIN.
      607 AA
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PIR, S06936; ABSHS.
HISSP, PO2768; BE7B.
InterPro; IPR000264; Serum albumin.
PRINTS, PR008020; SERVEMALBUMIN.
PRODOM; PR00103; ALBUMIN.
PROSTIE; PS0012; ALBUMIN.
PROSTIE; PS00212; ALBUMIN.
SMART; SM0103; ALBUMIN.
SMART; SM0103; Lipid-binding; Repeat;
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P02770; P11382,
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
5erum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
                                                                                                                                                                                                                                                                                                                                  CAKEDPHACYATVEDKLKHLVDEPQNLIKKNCELFEKHGEYGFQNALIVRYTRKAPQVST
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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SEQUENCE OF 1-38, AND PROCESSING.
MEDLINE=77249657; PubMed=893447;
Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.,
"Rat liver pre-proalbumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
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  Length 607;
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78.4%; Score 2432.5; DB 1; 75.0%; Pred. No. 8.4e-149; iive 73; Mismatches 72; ]
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J. Biol. Chem. 252:6846-6855(1977)
     Query Match
Best Local Similarity 75.03
Matches 437; Conservative
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                                                               VHKECCHGDLLECADDRADLAKYICDNQDTISSKLKECCDKPLLEKSHCIAEVEKDAIPE 323
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                             VHTECCHGDLLECADDRADLAKYICENQDS1SSKLKECCEKPLLEKSHCIAEVENDEMPA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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(Rel. 33, Last sequence up
(Rel. 41, Last annotation
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Pfam; PF00273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                  68914 MW;
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-!- TISSUE SPECIFICITY: Figsuma.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M73993; AAA51411.1; -.
EMBL; X58989; CAA41735.1; -.
EMBL; X17769; CAA76847.1; -.
EMBL; AF542068; AAN17824.1; -.
EMBL; P02768; 1E7B.
InterPro; IPRO00264; Serum albumin.
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607 AA;
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"Structure of serum albumin: disulfide bridges.",

"Structure of serum albumin, the main protein of plasma, has a good

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good

binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,

hormones, bilirubin and drugs. Its main function is the regulation

of the colloidal osmotic pressure of blood.
-!- SUBCEBLUMAR LOCATION: Secreted.
                                                                                                                                                                          MEDLINE=80024278; PubMed=488109; McGillivray R.T.A., Chung D.W., Davie E.W.; McGillivray R.T.A., Chung D.W., Davie E.W.; Booynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin."; Eur. J. Biochem. 98:477-485(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND REVISIONS TO 118-119 AND 180.
MEDLINE=91083649; PubMed=2266975;
Hirayama K., AkaBhi S., Furuya M., Fukuhara K.-I.;
Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 25-41.
MEDIATR=88267456; PubMed=3389500;
MEDIATR=88267456; PubMed=3389500;
Haich J.C., Lin F.F., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical isoclectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";
Anal. Biochem. 170:1-8(1988).
                                                                                Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  bovine
                                                                                                                                                                                                                                                                                                                                            MEDLINE-82023364; PubMed=7283978;
Reed R.G., Putnam F.W., Peters T. Jr.;
"Sequence of residues 400-403 of bovine serum albumin.";
Biochem. J. 191:867-868(1980).
                             Barry T., Power S., Gannon F.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 "The complete cDNA sequence of bovine serum albumin."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=77134075; PubMed=843354;
Patterson J.E., Geller D.M.;
Bovine microsomal albumin: amino terminal sequence proalbumin.";
                                                                                                                                                                                                                                         SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 74:1220-1226(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 173:639-646(1990).
                                                                                                                                                                                                                                                                                                                  Submitted (APR-1975) to the PIR data bank
                                                                                                             SEQUENCE FROM N.A., AND VARIANT THR-214.
      SEQUENCE FROM N.A., AND VARIANT THR-214
                                                                                                                                                                                                                                                  Brown J.R.;
"Structure of bovine serum albumin.";
Fed. Proc. 34:591-591(1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1998) to Swiss-Prot
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                    rissum=Liver;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PR00802; SERUMALBUNIN.
Prodom; PD002486; Serum albumin; 1.
SNART; SN00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
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C -> K (IN REF. 6).

KP -> PC (IN REF. 6).

ST -> TS (IN REF. 6).

K -> A (IN REF. 6).

K -> B (IN REF. 6).

K -> B (IN REF. 6).

K -> B (IN REF. 6).
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ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
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MEDLINE=9345495;

MEDLINE=9345495;

Probadeduk E.W., Norton E.J., Twigg P.D., Carter D.C.;

HO J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

HO J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;

To a to 27-nm resolution.";

The to 0.27-nm resolution.";

The to 0.27-nm resolution.";

The to 0.27-nm resolution.";

The to 0.27-nm and cuge. Its main function is the regulation of the colloidal osmotic pressure of blood.

The colloidal osmotic pressure of blood.

THISSUE SPECIFICITY: Plasma.

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50S LVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQTALVELLKHKPKAT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g; Repeat; Signal; Copper; Allergen.
BY SIMILARITY.
BY SIMILARITY.
SERUM ALEUMIN.
ALBUMIN 1.
ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                   Equus caballus (Horse).
Edkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
                                           541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583
                                                           01-UTN-1994 (Rel. 29, Created)
01-UTN-1994 (Rel. 29, Last sequence update)
01-UTN-1994 (Rel. 22, Last annotation update)
Serum albumin precursor (Allergen Equ c 3).
                                                                                                                                         607 AA
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PIR; S3403; ABHOS.
HSSP; PO2766; BFDB.
InterPro; IPR00264; Serum_albumin.
PFRINCS: PR00205; SERUMLEMUIN.
PRODOM; PR00205; SERUMLABUMIN.
PRODENS: PR00215; ALBUMIN.
SMART; SM0103; ALBUMIN.
SMART; SM0103; ALBUMIN.
SIGNAL
PROSETE; PS00212; ALBUMIN.
SIGNAL
PROPER
19 24 BY SIMILA
CHAIN 25 204 ALBUMIN 1
DOMAIN 25 204 ALBUMIN 1
DOMAIN 403 ALBUMIN 2
DOMAIN 403 ALBUMIN 2
DISULPID 114 125
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DISULPID 191 200
DISULPID 191 200
DISULPID 191 200
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID=9913;
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                                                                                                                                                    DB 1; Length 607;
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                                                                                                                                                                                  Indels
                                                                                                                      68598 MW; 256F6E830A1B90C5 CRC64;
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581
607 AA;
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Best Local Similarity
Matches 445; Conserv
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TISSUE-Salivary gland;

MEDINE-94201492; PubMed=7512102;

MEDINE-94201492; PubMed=7512102;

Michines S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,

Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,

Muchl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;

Molecular characterization of dog albumin as a cross-reactive

a lalergen...

J Allergy Clin. Immunol. 93:614-627(1994).

C -: FUNCTION: Serum albumin, the main protein of plasma, has a good

binding capacity for water, Ca(2+), Na(+), fatty acids,

hormones, bilitubin and drugs. Its main function is the regulation

of the colloidal osmotic pressure of blood.

C -: SUBCELIULAR IOCATION: Secreted.

-: SIMILARITY: Belongs to the ALB/AFF/VDB family.

-: SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-EROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-48.
MEDLINE=75011422; PubMed=4414013;
Dixon J.W., Sarkar B.;
"Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-24) of dog serum albumin.";
J. Biol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 25-38.
TISSUE=Heart;
TISSUE=98163340; PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                                         Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                            TISSUB-Liver;
MEDLINE=20148667; PubMed=10669848;
Pandjaitan B., Swoboda I., Brandejsky-Pichler F., Rumpold H., Valenta R., Spitzauer S.;
"Escherichia coli expression and purification of recombinant dog albumin, a cross-reactive animal allergen.";
J. Allergy Clin. Immunol. 105:279-285(2000).
                                                                                                                                                    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
 10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Can f 3).
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SMART; SM00103; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dog heart proteins.";
Electrophoresis 18:2795-2802(1997)
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PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1
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                                                                                                             SEQUENCE FROM N.A.
STRAIN=Beagle; TISSUE=Liver;
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                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=9615;
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                       Repeat; Signal; Copper; Allergen.
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PROSITE; PS00212; ALBUMIN;
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                                                                                                                                                                                                                                                                                                                                                                        TENTIFICATION (1)
SEQUENCE FROM N.A.

MEDINES-6194824; PubMed=8647469;
MEDINES-6194824; PubMed=8647469;
MEDINES-6194824; PubMed=8647469;
MEDINES-6194824; PubMed=8647469;
MIGEN C., Grigioni F., Kohnen M., Hentges F.;
Meding cape encoding cat (Felis domesticus) serum albumin.";
Gene 169:259-256 (1996).

In Gene 169:259-256 (1996).

In Gene 169:259-256 (1996).

In FINITY SETULAR LOCATION: Server of blood.

In SUBCELLULAR LOCATION: Secreted.

In SUBCELLULAR LOCATION: Secreted.

In MILERGEN: Causes an allergic reaction in human.

In ALLERGEN: Causes an allergic reaction in human.

In SIMILARITY: Belongs to the ALBAAFFVOR family.
                                                                                                                                       540
                                                                                                                                     CAAADPHECYAKVFDEFQPLVEEPQNLVKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
                                                                                                       CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
                                                                                             PILVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
                                                                                                                                                                                                                                                                                                                                   Felis silvestris catus (Cat).
Sukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pissipedia; Felidae; Felis.
NCBI_TaxID=9685;
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SERUM ALBUMIN.
ALBUMIN 1.
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                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serum albumin precursor (Allergen Fel d 2).
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1828; D02768; 1E7B.
IASEP: P02768; 1E7B.
IASEP: P02768; 1E7B.
IASEN; P02069; Examaport prot; 3.
PRINTS; PROMOSO; ERRUALEUMIN.
PRINTS; PROMOSO; ERRUALEUMIN.
SNART; SMO0103; ALBUMIN; 3.
PROSITE; PSO0121; ALBUMIN; 3.
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82.0%; Pred. No. 8.1e-161;
ive 52; Mismatches 53; Indels
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ID ALBU CANFA STANDARD;
AC P49822; 071705; Q9TSZ4;
DT 01-00T-1996 (Rel. 34, Created)
DT 16-0CT-2001 (Rel. 40, Last sequence update)
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InterPro; IPR00264; Serum albumin.
Pfam; PP00273; transport prot; 3.
PRINTS; PR00802; SERUMLBUMIN.
ProDom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; P800212; ALBUMIN; 3.
PROSITE; P800212; ALBUMIN; 3.
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-i- TISSUE SPECIFICITY: Plasma.
-i- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-i- SIMILARITY: Contains 3 albumin domains.
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93.5%; Pred. No. 1.8
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-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELLULAR LOCATION: Secreted.
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N-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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MEDLINE=22388257; PubMed=12477932,

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Strausberg R.D., Colling E.A., Groue L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Galba R.A.,

Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mithing M., Madan J.W., Green E.D., Dickson M.C.,

Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Moner and many and moneral and yeis of more than 15,000 full-length
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Pergamon Press, New York (1979).
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el protein database: update
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Biochem. J. 171:453-459(1978).
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MEDLINE=86140099; PubMed=2419329;
Urano Y., Watanabe K., Sakai M., Tamaoki T.;
The human albumin gene. Characterization of the 5' and region the polymorphic gene transcripts.";
J. Biol. Chem. 261:3244-3251(1986).
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MEDLINE=76187907; PubMed=1225573;
Meloun B., Moravek L., Kostka V.;
"Complete amino acid sequence of human serum albumin.";
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences.";
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Corbett J.M., Wheeler C.H., Baker C.S., Ya
"The human myocardial two-dimensional gel
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SEQUENCE OF 222-229.
MEDLINE=76257808; PubMed=955075;
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MEDLINE=78186630; PubMed=656055;
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FBBS Lett. 66:173-175(1976).
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TISSUB-Liver;
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VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
MEDLINE=22190239; PubMed=1347703;
MIDCHIOLI, Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.;
"Two alloalbumins with identical electrophoretic mobility are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peach R.J., Brennan S.O.,
"Structural characterization of a glycoprotein variant of human serum
albumin: albumin Casebrook (494 Asp--Asn).";
Biochim. Biophys. Acta 1097:49-54 [1991).
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MEDLINE=90115852; PubMed=2104980;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
Blibumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106. MEDLINE=91062352; Pubmed=2247440; Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J., Watkins S., Purnam F.W.;
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MEDLINE-92052189; PubMed-1946412;
VISE)
VISES
VARIANT CANTERBURY ASN-337.
MEDLINE=8715/7744; PubMed=3828358;
Brennan S.O., Herbert P.;
Brennan S.O., Herbert D.;
Arbumin Canterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin.;
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Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
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                                                                                                                                                         VARIANTS NAG-2 AND NAG-3.
MEDLINE=88068523; PubMed=3479777;
Takbashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita
Satoh C., Neel J.V.;
                                                                                                                                                                                                                                                                                                                   VARIANTS NAG-1, HIR-1, HIR-2 AND TOCHIGI.
MEDLINE-89345611; PubMed=2762316;
Arai K., Madison J., Huss K., Ishioka N., Satoh C., Insel J.V., Sakurabayashi I., Putnam F.W.;
Ponne substitutions in Japanese alloabumins.";
Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
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Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987)
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VARIANT VENEZIA.
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OM protein - protein search, using sw model

Run on:

April 19, 2004, 11:25:34 ; Search time 42.6731 Seconds (without alignments) 713.823 Million cell updates/sec

Title: Perfect score:

US-09-832-929-18 3103 1 DAHKSEVAHRFKDLGEENFK.....TCFAEBGKKLVAASQAALGL 585

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	homo sa	macaca	feli	canis	P35747 equus cabal				P02770 rattus norv			P07724 mus musculu	P19121 gallus gall	Q28789 pan troglod	P02771 homo sapien	P28050 gorilla gor		P49066 equus cabal	P08759 xenopus lae			рощ		rattus	Balmo	Q03156 salmo salar		Q91274 petromyzon	P02774 homo sapien	276 x	9 oryc	514 mus	Q99pl5 mus musculu
SUMMAKIES	ID	ALBU HUMAN	ALBU MACMU	ALBU_FELCA	ALBU_CANFA	ALBU_HORSE	ALBU_BOVIN	ALBU_RABIT	ALBU_SHEEP	ALBU_RAT	ALBU_PIG	ALBU MERUN	ALBU_MOUSE	ALBU_CHICK	FETA_PANTR	FETA HUMAN	FETA_GORGO	ALB2_XENLA	FETA_HORSE	ALB1_XENLA	FETA_MOUSE	FETA_RAT	AFAM HUMAN	AFAM_MOUSE	AFAM_RAT		ALB2_SALSA			VTDB_HUMAN	VIDE RAT	VTDB_RABIT	VTDB_MOUSE	RRB1_MOUSE
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de	Query Match	100.0	94.8	84.4	82.6	79.8	79.0	78.8	78.4	78.2	7.77	76.9	9.91	50.2	40.4	40.3	40.0	38.8	38.7	37.5	34.9	34.4	34.0	30.4	29.9	24.1	23.9	22.5	14.2	12.4	12.3	12.2	12.0	4. 9.
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Q8nf91 homo sapien Q9p2e9 homo sapien Q08696 drosophila Q18439 homo sapien P15749 homo sapien P4544 homo sapien Q50898 gallus gall Q19788 parlus gall Q14789 homo sapien O75962 homo sapien
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# ALIGNMENTS

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Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata, J. Bur. J. Biochem. 146, 489-486, 1985
Bur. J. Biochem. 146, 489-486, 1985
A;Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilizatio
A;Reference number: A05288; MUID:85126974; PMID:3971963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   two Xenopus albumin genes. Dele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74K albumin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 Haequence revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: B41682; S02693; A05288
R;Moskaitis, J.E; Sargent, T.D; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.
Mol. Endocrinol. 3, 464-473, 1989
A;Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic during development.
A;Reference number: A41682; MUID:89313788; PMID:2747653
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C;Keywords: carrier protein; duplication; gjycoprotein; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
VEBPUTSCEAYEEDRETFMAKKIYEIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVE
                                                                                  CFOTKAATVTKELRESSLLNQHACAVMKNFGTRTFQAITVTKLSQKFTKVNFTEIQKLVJ
                                                                                                                                                              261 DVAHVHEHCCRGDVLDCLQDGEKIMSYICSQQDTLSNKITECCKLTTLERGQCIIHAEND
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A,Redidues: 3-607 <MOS.
A;Cross-references: MB:M21442; NID:g213930; PIDN:AAA49637.1; PID:g213931
A;Cross-references: BE:M21442; NID:g213930; PIDN:AAA49637.1; PID:g213931
B;Schorpp, M.; Doebbeling, U.; Wagner, U.; Ryffel, G.U.
J. Mol. Biol. 199, 83-93, 1988
A;Title: 5'-flanking and B. 'Proximal exon regions of the two Xenopus alb
A;Reference number: 802692; MUID:88172470; PMID:2451026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: not compared with conceptual translation; Molecule type: DNA; Residues: 1-48 <SCH>; Cross-references: EMBL: 226826
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;Residues: 459-502,'L',504-557 <WOL>
;Cross-references: GB:M28276
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F;25-607/Product: 74K serum albumin #status predicted <MAT>
F;22-01/Domain: serum albumin repeat homology <SA1>
F;22-0395/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;30/Finding alte: copper (His) #status predicted
F;30/Finding alte: copper (His) #status predicted
F;80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392
F;256/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                         HKHIADVYTALTERTFKGLTLAIVSQNLQKCSLEELSKLVNEINDFAKSCINDKTPE-C
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.larity 39.3%; Pred. No. 3.3e-72;
Conservative 108; Mismatches 239;
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ne : 73.3019 secs
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A, interpose 29/1; 46/2; 200/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 5: C; Superfamily: serum albumin; serum albumin repeat homology (C; Keywords: embryo; feuus; globulin; glycoprotein; metal binding; plasma (C; Keywords: embryo; feuus; globulin; glycoprotein; metal binding; plasma (F; 11-16/) Domain: signal sequence #status predicted <SIG. F; 19-609/Product: alpha-fetoprotein #status predicted <MAT. F; 19-609/Product: albha-fetoprotein #status predicted <MAT. F; 21-394/Domain: serum albumin repeat homology <SA2. F; 21-394/Domain: serum albumin repeat homology <SA2. F; 21-394/Domain: serum albumin repeat homology <SA2. F; 21-394/Jonain: serum albumin repeat homology <SA2. F; 21-394/Jug-193, 192-201, 224-270, 269-277, 289-303, 302-313, 384-393, 416-462, 461-47. F; 21-394/Binding site: bliirubin (Lys) #status predicted F; 251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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VPBPVTSCEAYEEDRETFMNKFIYEIARRHPFLYAPTILLWAARYDKIIPSCCKAENAVE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-fetoprotein precursor - gorilla
C,Species: Gorilla gorilla (gorilla)
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 HRNEYGIASILDSYQCTAEISLADIATIFFAQFVQEATYKEVSKAVKDALTAIBKPTGDE
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R;Ryan, S.C.; Zielinski, R.; Dugaiczyk, A.
Genomics 9, 60-72, 1991

A;Title: Structure of the gorilla alpha-fetoprotein gene and the diverger A;Reference number: A37970; MUD:91169517; PMID:1706310

A;Reference number: A37970; MUD:91169517; PMID:1706310

A;Residues: 1-609 - RYA>
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A, Molecule type: protein
A, Residues: 'S'. 20-24, 'Q', 26-30, 'A', 32-35, 'E', 37-39 <RUO>
A, Residues: 'S'. 20-24, 'Q', 26-30, 'A', 32-35, 'E', 37-39 <RUO>
Baol. Chem. 260, 5055-5060, 1985
J. Tile: The human alpha-fetoprotein gene. Sequence organization and the 5' flanking reg
A, Reference number: A95250; MUID:8812629; PMID:2580830
A, Contents: annotation; gene, exons and introns
R; Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A, Title: Copper(II)-binding ability of human alpha-fetoprotein.
A, Reference number: A90759; MUID:79001617; PMID:80265
A, Contents: annotation; metal binding
R; Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 39, 357-3574, 1979
A, Title: alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding abil A; Reference number: A90759; MUID:80001710; PMID:89900
A, Contents: annotation, bilirubin binding
C, Comment: AFP is synthesized by the fetal liver and yolk sac. It occurs in the plasma C
C, Comment: AFP is synthesized by the fetal liver and yolk sac. It occurs in the bilirubin contents after birth. The serum level in and fatty acids as well as, and the bilirubin
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A; Molecule type: protein

A; Residues: 'S', 20-30, 'A, 32-37,'A' ADD'

B; Residues: 'S', 20-30, 'B, Vaheri, A.; Seppala, M.; Virolainen, M.; Konttinen, A.

Johns Hopkins Med. J. Suppl. 3, 249-255, 1974

Johns Hopkins Med. J. Suppl. 3, 249-255, 1974

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A; Reference number: A33042; MUID:75018719; PMID:4138095
                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                  and characterization of monomeric
                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Comparative chemical structure of human alpha-fetoproteins from fetal serum A;Reference number: A90757; MUID:78001760; PMID:71198
A;Accession: A90757
                                                                                                                                                                                                                                    A;Molecule type: protein.
A;Residues: 'S', 20-22,'S', 24-35 <YAC>
A;Residues: 'S', 20-22,'S', 14-35 <YAC>
A;Note: dimeric and trimeric forms have been found in addition to the monomeric form R:Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 37, 3663-3667, 1977
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   A,Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609-8;Yachnin, S.; Hsu, R.; Heinrikson, R.L.; Miller, J.B.
Biochim. Biochyws. Acta 493, 418-428, 198-428, 198-48, A;Tille: Studies on human alpha-fetoprotein. Isolation and chara. A;Reference number: A90624; MUID:77242506; PMID:70228
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A;Cross-references: GDB:119660; OMIM:104150
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Best Local Similarity 39.9%; Pri
Matches 235; Conservative 116;
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A; Mostecus Cype: maxAs
A; Residues: 1-609 < MOR>
A; Cross-references: GB:J00077; NID:g311348; PIDN:CAA24758.1; PID:g31351
A; Cross-references: GB:J00077; NID:g311348; PIDN:CAA24758.1; PID:g31351
Gene 20, 415-422, 1982
A; Title: Structure and evolution of human alpha-fetoprotein deduced from partial sequer
A; Reference number: A91497; MUID:B3158778; PMID:G187626
A; References: GB:J00076
A; Residue type: mRNA
A; Residues: 429-556 < BRA>
A; Residues: 429-556 < BRA>
A; Residues: 429-556 < BRA>
A; Cross-references: GB:J00076
A; Pristile: Human alpha-fetoprotein primary structure: a mass spectrometric study.
A; Reference number: A23699; MUID:91242409; PMID:1709810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A26624
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: GB:M16110; NID:g773678; PIDN:AAB58754.1; PID:g178236
A;Cross-references: GB:M16110; NID:g773678; PIDN:AAB58754.1; PID:g178236
R;McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Krumlar, Hum. Mol. Genet. 2, 379-384, 1993
A;Title: A G-AS substitution in an HNF I binding site in the human alpha-fetoprotein genet. A;Reference number: 837655; MuID:93278385; PMID:7684942
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NyAlternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin
C;Species: Home sapiens (man)
C;Date: 19-Feb-1984 #sequence revision 19-Feb-1984 #text change 08-Dec-2000
C;Accession: A26624; 837655; A39861; A91497; A23699; A61480; A90624; A90757; A93042;
R;Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczyk, A.
Biochemistry 26, 1332-1343; 1987,
A;Title: Structure, polymorphism, and novel repeated DNA elements revealed by a complant and moder: A26624; MUID:87185438; PMID:2436661
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                                                                                          LEKCCAAADPHECYAKVFDEFKPLVEEPONLIKONCELFEQLGEYKFONALLVRYTKKVP
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A,Residues: 1-28 <MCV>
A,Residues: 1-28 <MCV>
A,Cross-references: EMEL:219532; NID:928527; PIDN:CAA79592.1; PID:928528
A,Cross-references: Emel.219532; NID:928527; PIDN:CAA79592.1; PID:928528
A,Note: the authors translated the codon TAT for residue 26 as Thr
R,Morinaga, T.; Sakai, M.; Wegmann, T.G.; TamaoKi, T.
R,Morinaga, T.; Sakai, M.; Wegmann, T.G.; TamaoKi, T.
A,Title: Primary structures of human alpha-fetoprotein and its mRNA.
A,Reference number: A93961; MUID:83273664; PMID:6192439
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A,Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
R,Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
J. Nucl. Med. Allied Sci. 34, 218-215, 1990
A;Title: Characterization of in vitro expressed human alpha-fetoprotein
A;Reference number: A61480; MUID:91225826; PMID:1709209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                537 PKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL
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A;Molecule type: protein
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A; Molecule type: mRNA
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CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiAccession: JG4258
R;Nishio, H; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczyk, A.
Gene 162, 213-220, 1995
A;Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to the A;Reference number: JC4258; MUID:96032345; PMID:7557431
A;Reference number: JC4258
A;Reference number: JC4258
A;Residues: 1-609 kNIS>
A;Cross-references: GE-121916; NID:9841311; PIDN:AAA91641.1; PID:9841312
A;Residues: 1-609 kNIS>
A;Cross-references: GE-121916; NID:9841311; PIDN:AAA91641.1; PID:9841312
C;Comment: This protein is a plasma protein produced in the fetal and neonatal liver and cinture properties: and structure.
C;Genetics:
A;Genetics:

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                                                                                                                              449
                                                                                                                                                                                                                         VNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATK 541
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      LPSLVEXYIEDKEVCKSFEAGHDAFWAEFVYEYSRRHPEFSIQLIMRIAKGYESLLEKCC
                                                                AAADPHECYAKVFDEFKPLVBEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP
                                                                                                                                                                                         422 TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESL
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Matches 236; Conserv
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A; Mcseidues: 1-28 eHRC>
A; Cross-references: GB: V00381; NID: G601066, 1977
B; Cross-references: GB: V00381; NID: G60-1066, 1977
B; Cross-reference: GB: V00381; NID: G60-1066, 1977
A; Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.
A; Reference number: A13451; MUID: 78019943; PMID: 911327
A; Accession: A13451
A; Molecule type: protein
A; Residues: 19-23, M', 25-30 < ROS>
C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, mones (weak bonds with these hormones promote their transfer across the membranes), thy C; Comment: Serum albumin; serum albumin repeat homology
C; Superfamily: serum albumin; serum predicted < SRO>
F; 1-18 (Domain: signal sequence #status predicted < MAT>
F; 25-619 (Domain: serum albumin repeat homology < SAA>
F; 25-619 (Domain: serum albumin repeat homology < SAA>
F; 25-398 (Domain: serum albumin repeat homology < SAA>
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A,Readudes: 1-615 cCAB.
A,Farchadudes: 1-615 cCAB.
A,Cross-references: BEBL:X60688, NID:g63747; PIDN:CAA43098.1; PID:g63748
R;Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
J. Biol. Chem. 258, 4556-4564, 1983
A,Title: The 5' noncoding and flanking regions of the avian very low density apolipopro
A,Reference number: A05078; MUID:83161037; PMID:6187737
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                                                                                                                                                                                                                                           Serum albumin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Dace: 31-Dec.1993 #sequence revision 31-Dec.1993 #text_change 22-Jun-1999
C;Accession: S15571; A05078; A13451
R;Cassady, A.1.; Salklid, C.K.; Baverstock, P.; Wallace, J.C.
submitted to the EMBL Data Library, July 1991
A;Reference number: 815571
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                           A; Accession: S15571
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A; Residues: 1448 < WIN.
B; Cross-references: GB:Midli; NID:g191764; PIDN:AAA37190.1; PID:g191765
R; Rocacacio, C; Deschartette, J; Meunier-Rotival, M.
Gene 88, 181-186, 1990
A; Title: Empty and occupied insertion site of the truncated LINE-1 repeat located in the A; Reference number: 148638; WUID:90269666; PMID:1971802
A; Reference number: 148638; WUID:90269666; PMID:1971802
A; Reference number: 148638
A; Residues: 379-453 < ROC.
A; Residues: 379-453 < ROC.
A; Residues: 379-453 < ROC.
A; Residues: 379-453 < ROC.
A; Cross-references: EMBL:X13060; NID:952939; PIDN:CAA31458.1; PID:9899334
C; Kaywords: carrier protein; duplication; metal binding; plasma
F; 1-104/Domain: serum albumin repeat homology (fragment) < SA1>
F; 123-296/Domain: serum albumin repeat homology (fragment) < SA3>
F; 315-453/Domain: serum albumin repeat homology (fragment) < SA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 405139; 148638
E;Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
Mol. Biol. Bvol. 2, 347.358, 1985
A;Rifle: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudog A;Reference number: A93055; Muid:88216123; PMID:2452956
A)Accession: A05139
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TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESL
                                  VNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATK
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60.0%; Score 1861; DB 2; Length 453;
Best Local Similarity 72.2%; Pred. No. 9.4e-116;
Matches 327; Conservative 64; Mismatches 62; Indels
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ò	421 PTLVEVSRNLGKVGSKCCKHPBAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480	ò	301 DIPSLAADFVESKDVÇKNYABAKDVFLGMFLYBYARRHPDYSVVLLLRLAKTYBTTLFKÇ 360
Ор	445 PTLVEAARNLGRVGTKCCTLPBAQRLPCVEDYLSAILNRLCVLHEKTPVSEKVTKCCSGS 504	qq	322 DINPLEHDFVEDKEVCKNYKEAKDVFLGTFLYEVSRRHPDYSVSLLLRIAKIYEATLEDC 381
Š 5	481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSBKERQIKKQTALVELVKHPKAT 540 [	à	CAAADPHECYAKVFDBFKPLVEBPQNLIKONCELFEGLGBYKFQNALLVRYTKKVPQVST
3		qq	382 CAKEDPPACYATVFDKFQPLVDEPKNLIKQNCELFEKLGEYGFQNALIVRYTKKVPQVST 441
පු දු	541 KEÇLKAMDDFAAFVEKCKADDKETCFAEBGKKLVAAAQAAL 583 ::	Qy Db	421 PTLVEVSRNIGKVGSKCCKHPEAKBMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480 
RESULT 8	,	ò	481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
ABPGS	numin predurent - pin (fragment)	qq	502 LVNRRPCFSALTPDETYKPKEFVSGTFTFHADLCTLPEDEKQIKKQTALVELLKHKPHAT 561
C,Specie	Outling Preceded.  8: Suc scrofa domestica (domestic pig) 11-Dec. 1993 #seconce revision 31-Dec-1993 #text change 22-Jun-1999	Š	
C, Access R; Weinst	ion: S01382; A61006 ock, J.; Baldwin, G.S.	Dp	:   :  : :     :
Nucleic A, Title:	Acids Res. 16, 9045, 1988 Nucleotide sequence of porcine liver albumin.	E	
A;Refere A:Access	nce number: S01382; MUID:89016582; PMID:3174440 ion: S01382	JC5838	
A;Status	: translation not shown	albumin C;Species	us (Mongolian jird)
A, Residu	TE CIPE: MINISTER STATES AND CALOTE, DIDN. CARAGOGO 1. DTD: GRA3798	C;Date: (C;Access:	rev
A; Cross- R; Limeba	references: Embligates; Milligates; Firm Carous, Firm Scott Scott Sakarya, H.; Chu, W.; Mackinnon, M.	R, Yoshida	1, K.; Seto-Ohshima, A.; Sinohara, H.
J. Bone A;Title:	Miner. Res. 4, 235-241, 1989 Serum albumin and its acid hydrolysis peptides dominate preparations of mineral	A;Title:	Arthle: Squencing of CDNA encoding serum albumin and its extrahepatic synthesis in the Arthle: Squencing of CDNA encoding serum albumin and its extrahepatic synthesis in the Arthle: Arthle: JC5838; MUID:98116663; PMID:9455485
A; Kerere A; Access	nce number: Actions; multi-ographog; multi-cross.	A; Access	
A; Residu	le type: protein es: 23-51,/X,/53-54;/XXXGY,/146,'E',148,'E',150-151,'XVN',155 <lim></lim>	A; Residues: A; Cross-ref	Estiques: 1-609 (2005) Cross-references: DDBJ:AB006197; NID:q2317277; PIDN:BAA21765.1; PID:g2317278
A; Note:	Mencal Source: denote transcer also found in bone albumin and other serum proteins are also found in bone of the liver so preproal himself thinds comper-	A; Experi	
C, Commer teroid h	ss th	F; 222-39	5/Domain: serum albumin repeat homology <sa2></sa2>
C;Superi C;Keywor F;1-16/D	C:Superfamily: serum albumin; serum albumin repeat homo-ogy C:Keywords: carrier protein; duplication; metal binding; plasma F:l-16/Domain: signal sequence (fragment) #status predicted <sig></sig>	Ouery Match Best Local	DB 2; Length 8-150; Trael
F;17-22/	Domain: propeptide #status predicted <pro> /Product: serum albumin #status predicted <mat></mat></pro>	Marches	450; Conservative 55; mismacches 0/; inders 0/ cags
F 27-195	/richards serum albumin repeat homology <8A1>	ò	2 AHKSEVAHREKDLGEENFKALVIJAFAQYLQQCPFEDHVKLNNEVTEFAKTCVADESAEN 61
F;410-58	11/Domain: Berum albumin repeat homology <883> 2000 - 11 Serum albumin repeat homology <883> 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201 - 201	වු	
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රු සි	61 NCDKSLHTLEGDKLCTVATLEETYGENADCCAKOBERRNBCFLCHKODNPHLFRLYRPEY 120	g &	
ò	121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180	Οp	267 TQECCHGDLLECADDRAELAKYMCENQASISSKLQACCDKEMLQKSQCLAEVEHDDMPAD 326
q	142 VALCADFQEDEÇKFWGKYLYEIARRHFYFYARELLYYAIIYKDVFSECCQAADKAACLLF 201	ò	LPSLAADFVESKDVCKNYABAXDVFLGMFLYBYARRHPDYSVVLLLRLAKTYETTLEKCC
λ,	KIDELEDEGKASSAKQRIKCASLQKPGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 2	ය ද	327 IFALTADFVEDKDVCKNYABAKDVFLGTFLYEYSRRHPEYSVSLLLRLAKKYEATLEKCC 386 363 abandheryakurnerkdijjerponijkonceljerolgevkfonallukvykkkvPovSTP 421
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A, roceincue; 1-7. ALBOS AND GROUPS NID: Q202828; PIDN: AAA40712.1; PID: 9554412
C, Superfamily: serum albumin; serum albumin repeat homology
C, Superfamily: serum albumin; serum albumin repeat homology
C, Seywords: carriar profetin; duplication; metal binding; plasma
E, 1-18/Domain: signal sequence #status experimental <BRO>
F;19-24/Domain: propeptide #status experimental <BRO>
F;19-24/Domain: propeptide #status experimental <BRO>
F;29-202/Domain: serum albumin repeat homology <BA>
F;21-394/Domain: serum albumin repeat homology <BA>
F;21-394/Domain: serum albumin repeat homology <BA>
F;21-395/Domain: serum albumin serum albumin repeat homology <BA>
F;27-305/Domain: serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin serum albumin
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A,Molecule type: protein
A,Residues: 166-173 <CAR>
R,Heard, J.
R,Heard, J.
A,Title: Determinants of rat albumin promoter tissue specificity analyzed by
A,Title: Determinants of rat albumin promoter tissue specificity analyzed by
A,Reference number: 157621; MUID:87286876; PMID:3475566
                Rilsemura, S.; Ikenaka, T.
J. Biochem. 79, 1183-1186, 1976
A.fitle: Pragmentation of rat serum albumin by cyanogen bromide cleavage and
A,Reference number: A91940; MUID:76260153; PMID:956149
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                                                                                                                                                             A; Molecule type: protein
A; Molecule type: protein
A; Residues: 223-288;572-608 <1S2>
A; Note: 262-Leu was also found
A; Note: 262-Leu was also found
R; Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
Cancer Res. 38, 3483-3486, 1978
A; Title: Copper(II) binding ability of human alpha-fetoprotein.
A; Reference number: A90758; MUID: 79001617; PMID: 80265
A; Contents: annotation; Copper binding
R; Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1800-1684, 1989
A; Title: Structures of histamine-releasing peptides formed by the a A; Reference number: A45800; MUID: 89341406; PMID: 2474609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: 157621
A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA
A, Residues: 1-5 < RES>
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Best Local Similarity 73.4'
Matches 428; Conservative
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NiAlternate names: preproalbumin
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Nagvinsy (Norway rat)
C;Species: Nagvinsy (Norway rat)
C;Species: Nagvinsy (Norway rat)
R;Sargent, T.D.; Yang, M.; Benner, J.
A;Reference number: A93872; MUD:8122722; PMID:701712
A;Reference number: A93872; MUD:8122722; PMID:7017712
A;Reference number: A93872; MUD:8122722; PMID:7017712
A;Reference number: A93872; MUD:8122722; PMID:85627; PIDN:CAA24532.1; PID:955628
A;Cross-references: GB:VO1222; GB:JO1698; NID:955627; PIDN:CAA24532.1; PID:955628
A;Reference number: A9211; MUD:77249657; PMID:893447
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A;Reference number: A9211; MUD:77249657; PMID:893447
A;Reference number: A9211; MUD:77249657; PMID:893447
A;Reference number: A9211; MUD:78109429; PMID:564345
A;Reference number: A9346; MUD:78109429; PMID:564345
A;Reference number: A93466; MUD:78109429; PMID:564345
A;Rocession: A93466
A;Reference number: A93466
A;Rocession: A93466
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Pred. No. 2e-153;
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Best Local Similarity 75.0%; Pr. Matches 437; Conservative 73;
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A.Molecule type: mRNA
A.Kesidues: 1-607 < ERO.
A.Fesidues: 1-607 < ERO.
A.Gross-references: BNBL:X17055, NID:g1386; PIDN:CAA34903.1; PID:g1387
A.Groment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
C.Comment: Serum albumin; serum albumin repeat homology promote their transfer across the memb:
C.Superfamily: serum albumin; serum albumin repeat homology
C.Keywords: carrier protein; duplication; metal binding; plasma
C.F.19.70main: signal sequence #status predicted < RGO.
F.19-24/Domain: serum albumin repeat homology < SA3.>
F.20-201/Domain: serum albumin repeat homology < SA3.>
F.20-333/Domain: serum albumin repeat homology < SA3.>
F.412-591/Domain: serum albumin repeat homology < SA3.>
F.412-591/Domain: serum albumin repeat homology < SA3.>
F.77/Binding site: copper (His) #status predicted
F.77/Binding site: bilirubin (Lys) #status predicted
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S06936
R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:9009888; PMID:2602160
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                                                                                                                                          25 DTHKSEIAHRFKDLGBEQFKGLVLIAFSQYLQQCPFDBHVKLVNELTEFAKTCVADESHA
                                                                                                                                                                                                                                           61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                                                                                                                                                                                                                    121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                    1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTK
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; Mismatches 70;
al Similarity 75.6%; Pro
441; Conservative 71;
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A;Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,'E
R,Brown, J.R.
Rubmitted to the Atlas, April 1975
A;Reference number: A94551
A;Accession: A94551
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A;Residues: 25-41,'H',43-57,59-64 <STR>
F;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1984
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A;Reference number: A45800; MUID:89341406; PMID:2474609
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A/Molecule: protein:
A/Molecule:
A/Momain: signal sequence #status experimental <SIG>
F/19-24/Domain: signal sequence #status experimental <PRO>
F/19-24/Domain: serum albumin #status experimental <MPT>
F/20-393/Domain: serum albumin repeat homology <SA2>
F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-393/Domain: serum albumin #status predicted
F/20-393/Domain: serum albumin #status predicted
F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-393/Domain: serum albumin repeat homology <SA3>
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F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-392/Domain: serum albumin repeat homology <SA3>
F/20-393/Domain: serum albumin repeat homology <SA3>
F/20-393/
                          R.HSieh, J.C., Lin, F.P., Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A.Title: Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing A.Title: Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing A.Reference number: A66808 MUID:88267456; PMID:3389500
A.Rocession: B60808
A.Molecule type: protein
A.Residues: 25-41 cHSI>
R.Atrawich, E.; Glincher, M.J.
R.Atrawich, E.; Glincher, M.J.
R.Atrawich, E.; Glincher, M.J.
R.Atritle: Tooth "enamelins' identified mainly as serum proteins. Major 'enamelin' is albha. A.Recession: S10780; MUID:90336641; PMID:2379503
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A; Residues: 163-172 (CAR>
B; Residues: 163-172 (CAR>
B; Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5568-5973, 1987
A; Title: Structure of a biologically active neurotensin-related peptide obtained from basecance number: A26693; MUID:87194805; PMID:2437111
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A; Residues: 165-172, 'L' <CA2>
R; Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem, J. 191, 867-868, 1980
A; Title: Sequence of residues 400-403 of bovine serum albumin.
A; Reference number: A90309; MUID:82023364; PMID:7283978
A; Accession: A90309
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Fed. Proc. 34, 591, 1975
A.Fille: Structure of bovine serum albumin.
A.Reference number: A91458
A.Accession: A91458
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A,Residues: 190-195 <BR2>
R,Brown, J.R.
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A;Residues: 402-433 <REE>
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540

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Length 607, Score 2432.5; DB 1; -1

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60 84 180

203

120 143 240

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VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
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79.8%; Score 2475.5; DB 1;
76.3%; Pred. No. 2.9e-156;
ive 69; Mismatches 68;
                                             Conservative
                           1 Similarity
445; Conser
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C;Species: Equus caballus (domestic horse)

C;Species: Equus caballus (domestic horse)

C;Species: Equus caballus (domestic horse)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999

C;Accession: S34053

R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.

Eur. J. Biochem. 215, 205-212, 1993

A;Reference number: S34053; MUID:93345495; PMID:8344202

A;Accession: S34053; MUID:93345495; PMID:8344202

A;Accession: S34053

A;Molecule type: mRNA

A;Residues: 1-607 <403

A;Accession: S34053

A;Molecule type: mRNA

A;Residues: 1-607 <403

A;Cross-references: GB:X74045; NID:9339571; PIDN:CAA52194.1; PID:9399672

C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, c;Superfamily: serum albumin; serum albumin repeat homology

C;Keywords: carrier protein; duplication; metal binding; plasma

F;1-18/Domain: signal sequence #status predicted <816>
F;1-24/Domain: signal sequence #status predicted <816>
F;1-24/Domain: propeptide #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816>
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F;25-60/C;Product: serum albumin #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816>
F;25-60/C;Product: serum albumin #status predicted <816<
F;25-60/C;Produ
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F,220-393/Domain: serum albumin repeat homology <8A2>
F,412-591/Domain: serum albumin repeat homology <8A3>
F,27/Binding site: copper (His) #status predicted
F,77/Binding site: copper (His) #status predicted
F,77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,
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                                                                                          DAHKSEVAHREKDIGEENEKALVI.IAFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAE
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         84.4%; Score 2620; DB 2; Secore 2620; Pred. No. 8.1e-166; ive 52; Mismatches 53;
                                                    478; Conservative
                                  Similarity
           Query Match
Best Local S:
Matches 478
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A; Molecule type: protein
A; Molecule type: protein
B; MacGillivray, R.1.4: 43-189, P., 191-213, T., 215-323, D., 325-393, TS', 396-607 < HIR>
B; MacGillivray, R.T.A.; Chung, D.W.; Davie, E.W.
Biochem. 98, 477-485, 1979
A; Tile: Biosynthesis of bovine plaema proteins in a cell-free system.
A; Reference number: A91258; MUID:80024278; PMID:488109
A; Accession: A91258
A; Molecule type: protein
Accession: Assession: Assession and revine Assession and confirmation of the Enrich Properties and revision of the probability of the properties of the properties of the properties of the primition of the properties of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the properties of the primition of the properties of the primition of the properties of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the primition of the p
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A; Experimental source: liver
C; Comment: This protein is the major protein component in plasma. It functions ein has 35 conserved cysteine residues.
C; Cyuperfamily: serum albumin; serum albumin repeat homology
C; Keywords: liver; plasma
C; Keywords: liver; plasma
F; 19-24/Domain: signal sequence #status predicted <SIG>F; 19-24/Domain: propeptide #status predicted <RRP>F; 25-608/Product: serum albumin repeat homology <SA1>F; 20-202/Domain: serum albumin repeat homology <SA2-594/Domain: serum albumin repeat homology <SA3>F; 21-394/Domain: serum albumin rep
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C;Species: Felis silvestris catus (domestic cat)
C;Date: 19-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
C;Accession: JG4660; S57632
R;Hilger, C; Grigioni, F; Hentges, F.
Gane 169, 295-296, 1996
A;Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A;Reference number: JG4660; MUID:96194824; PMID:8647469
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A;Residues: 1-608 <HI2>
A;Cross-references: EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g886485
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                                                       Match

Local Similarity 93.5%; Pred. No. 4e-187;

es 545; Conservative 23; Mismatches 15;
      <SA3>
   7;405-584/Domain: serum albumin repeat homology
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C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Accession: A47391
R;Watkins, S.; Sakamoto, Y.; Madison, U.; Davis, E.; Smith, D.G.; Dwulet, U.; Putnam, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in biliru
A;Reference number: A47391; MUID: 93211971; PMID: 8460152
A;Contents: B/B homozygote
A;Contents: B/B homozygote
A;Contents: Drellminary
A;Molecule type: mRNA; protein
A;Molecule type: mRNA; protein
A;Molecule type: mRNA; protein
A;Residues: 1600 cMAT>
A;Cross-references: GB: N90463; NID: 9342294; PIDN: AA3806.1; PID: 9342295
A;Cross-references: GB: Natura albumin repeat homology
C;Superfamily: serum albumin repeat homology cSA1>
F;21-194/Domain: serum albumin repeat homology cSA2>
F;166-174/Product: Kinetensin #status experimental <KIP>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;77/Binding site: copper (His) #status predicted
F;77/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,148-193,192-201,244-270,269-277,289-303,302-313,340-385,384-393,
F;214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
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                                                                                                                                                                                                      100.0%; Score 3103; DB 1;
100.0%; Pred. No. 9e-198;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 585; Conservative
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A, Residues: 166-173 < CAR.
R, Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
R, Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
B, Mochem. Blophys. Res. Commun. 136, 983-988, 1986
A, Title: The amino acid sequence of Kinetensin, a novel peptide isolated from pepsin-tre
A, Reference number: A03239; MUID:86242180; PMID:3087352
A, Accession: A03239; MUID:86242180; PMID:3087352
A, Molecule type: protein
A, Residues: 166-173, L' < MOG>
R, Gilliano, W.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S.
R, Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S.
R, ATitle: Mutations in genetic variants of human serum albumin found in Italy.
A, Accession: C38255
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
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A,Residues: 45-67,141-160,311-337,469-490,570-581 <PIN>
B;Kausler, E.; Spiteller, G.
Biol. Chem. Roppe-Seyler 372, 849-655, 1991
A,Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol A,Reference number: 817599, MUD: 92126241; PMID:1772598
A,Accession: 817599
A,Molecule type: protein
A,Residues: 25-54,354-357;431-447 <KAU>
A,Nolecule type: protein
A,Residues: 25-54,354-357;431-447 <KAU>
A,Nolecule type: protein
A,Residues: 25-84,354-357;431-447 <KAU>
A,Nolecule type: protein
A,Title: Structures of found
A,Title: Structures of histanine-releasing peptides formed by the action of acid proteas A,Reference number: A45800; MUD:89341406; PMID:2474609
A,Anolecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: 25-117, Mol. (120-154, Mol. ). B. Molecule type: 25-117, Molecule type: 120-117, Molecule type: 12
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A;Residues: 25-48 (**NES-**)
R;Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 595-599, 1993
A;Title: Mass spectrometric identification of modifications to human serum albumin treat
A;Reference number: S36882; MuID:93384321; PMID:8373198
                                                                                                                                                            A.Reference number: 088292
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: G01747
A.Accession: S55314
A.Accession: S55314
A.Accession: S55314
A,Note: this frame-shift variant is designated albumin Bazzano, four additional variants R;Menaya, J.; Parrilla, R.; Ayuso, M.S. submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 19-27 <LEDS
F.Meloun, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A,TitLe: Complete amino acid sequence of human serum albumin.
A,Reference number: 291420, MUID:76187907; PMID:1225573
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A; Residues: 76-111 < GAL1>
A; Accession B18125
A; Accession type: protein
A; Residues: 82-105, YK', 107-110 < GAL2>
A; Note: this variant is designated albumin Vibo Valentia
A; Molecule type: protein
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A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
B, Minchicotti. L., Gallando, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Porte
Biochim. Biophys. Acta 1119, 22-238, 1992
A, Title: Two alloablumins with identical electrophoretic mobility are produced by diffe
A, Recession: S21078
A, Molecule type: procein
A, Residues: 384-356, W. 138-378 eMID: 2190239; PMID: 1347703
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Reference number: A46756, MUID: 2334427; PMID: 1630489
A, Concents: annotation: Array crystafalography, 2.8 angstroms
A, Reference number: A34442
A, Robber, M.A.; Shockley, P.; Behrens, P.O.
A, Robber, M.A.; Shockley, P.; Behrens, P.O.
A, Robber, M.A.; Shockley, P.; Behrens, P.O.
A, Robber, M.A.; Stockley, P.; Behrens, P.O.
A, Reference number: A34442
A, Robber, M.A.; Stockley, P.; Behrens, P.O.
A, Reference number: A34939; MUID: 186350; PMID: 1877
A, Reference number: A39039; MUID: 186350; PMID: 1878
A, Robber, M.B.; Bedd, R.G.
A, Robber, M.B.; Bedd, R.G.
A, Robber, M.B.; Bedd, R.G.
A, Robber, M.B.; Bedd, R.G.
A, Robber, M.B.; Bedd, R.G.
A, Robber, M.B.; Bedd, R.G.
A, Rochenser: annotation; binding site
A, Rochenser: annotation; binding site
A, Rochenser: annotation; binding site
A, Rochenser: annotation; Benefit and Bollon, I.; eds., 11-27
A, Thus, Sechen annotation; gene position and active sites.
A, Thus, Robber, M.B.; Dugalczyk, A.
A, Thus, Robber, M.B.; Dugalczyk, A.
A, Reference number: A49408
A, Rochenser: annotation; gene positionarily-rela
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A;Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phosph A;Reference number: A56294; MUID:92183881; PMID:1544460
A;Contents: annotation
A;Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak C;Comment: A large number of variants of human serum albumin have been described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C)Genetics:
A)Genetics:
A)Gene
A;Note: this variant is designated albumin Torino
R;Minchlotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A;Tile: The structural characterization and bilirubin-binding properties of albumin He
A;Reference number: 833298; MUID:93292504; PMID:8513793
A;Accession: 833298
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model - protein search, using OM protein April 19, 2004, 11:37:59; Search time 71.3019 Seconds (without alignments) 789.208 Million cell updates/sec Run on:

US-09-832-929-18 3103 1 DAHKSEVAHRFKDLGEENFK......TCFAEEGKKLVAASQAALGL 585 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

88	Description	erum albumin	albumin		albumin			albumin	serum albumin prec	in - Mong	albumin	serum albumin prec	alpha-fetoprotein	alpha-fetoprotein	alpha-fetoprotein	74K albumin precur	albumin - dog (fra	68K serum albumin	alpha-fetoprotein	alpha-fetoprotein	afamin precursor -	serum albumin prec	precursor	albumin 1		ı		vitamin D-binding		vitamin D-binding
SUMMARIES	ΙΩ	ABHUS	A47391	S57632	ABHOS	ABBOS	ABSHS	ABRTS	ABPGS	JC5838	A05139	ABCHS	JC4258	FPHU	FPGO	ABXL72	I46986	ABXL68	FPMS	FPRT	A54906	859517	A53195	ABONS1	ABONS2	A37253	S27941	VYHUD	œ	A35327
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	% Query Match		94.8	84.4	79.8	78.8	78.4	78.2	77.7	76.9	60.09	50.2		40.3						34.4								12.4	12.4	12.0
	Score	3103	2942	2620	2475.5	2446.5	2432.5	2426	2411.5	2387	1861	1557.5	1253.5	1249.5	1242.5	1205	1181.5	1175.5	1084	1067	1055	928.5	928	747.5	742.5	669	440.5	386	œ	r
			73	ო	4	'n	ø	7	α	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 589-590, ALPRRVKNLLLQVKLP' <MAD>
A;Rosidues: 589-590, ALPRRVKNLLLQVKLP' <MAD>
A;Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

cag island protein	cag pathogenicity	calcium-binding pr	hypothetical prote	major surface glyc	cell surface glyco	hypothetical prote	sperm tail-specifi	kinesin homolog F2	major surface glyc	myosin heavy chain	cell-cycle-depende	glycoprotein A - P	hypothetical prote	giantin - human	embryonic muscle m
A71928	G64585	T30282	AG2558	JC2221	JC2300	T17272	551364	T06733	JC2217	D35815	PC4035	JC4091	A64465	I52300	A59236
N	N	7	~	0	N	7	~	7	N	N	N	N	N	~	N
1819	1927	1560	1348	1004	1083	1780	1390	1070	1076	1175	1017	1051	1005	3225	1927
5.9	υ 6,	4.6	4.4	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.1	4.1	4.1	4.1
184	184	141.5	137.5	134.5	134	134	133.5	132.5	131	130	129	128.5	128	. 128	126.5
30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

## ALIGNMENTS

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NALerance names: preproatbunin

NyAlerance names: preproatbunin

NyAlerance names: preproatbunin

NyAlerance names: preproatbunin

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens

C;Accession: A33743; A9336; I39427; I59286; I59313; G01747; S55314; A91420; S06422; S3

R;Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seebu

Nucleic Acids Res. 9, 6103-6114, 1981

A;Title: The sequence of human serum albumin CDNA and its expression in Escherichia col

A;Reference number: A93743; MUID:82081882; PMID:6171778

A;Accession: A33743

A;Accession: A33743

A;Residues: 1-419, 'K', 421-609 <LAW>
A;Coss.references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:CAA2

A;Cross.references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:CAA2

A;Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.

A;Residues: 1-120, 'G', 122-609 <br/>A;Residues: 1-120, 'G', 
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A;Retus: translation not shown
A;Retus: translation not shown
A;Residues: 1-26 <URA>
A;Residues: 1-26 <URA>
A;Residues: 1-26 <URA>
A;Cross-references: 0.7; Galliano, M.; Minchiotti, L.; Putnam, F.W.
B;Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994
A;Title: A nucleocide insertion and frameshift cause analbuminemia in an Italian family
A;Reference number: I59286; MUID:94181575; PMID:8134387
A;Accession: I59286
A;Status: translated from GB/EMBL/DDBJ
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A, Residues: 282-290, KSRFDLO, *MAT>
A, Residues: 282-290, KSRFDLO, *MAT>
A, Cross-references: GB: 569192, NID: 9546032; PIDN: AAB30282.1; PID: 9546033
A, Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia
R, Madison, J.; Galliano, M.; Matkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putnam,
Proc. Natl. Acad. Sci. US.A. 91, 6476-6480, 1994
A, Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl
A, Reference number: I59313; MUID: 94294404; PMID: 8022807
serum albumin precursor [validated] - human
                                                                                N;Alternate names: preproalbumin
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US-10-319-263-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFRKRYKAAFTECCQAADKAACLLF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
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                 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYSYARRHPDYSVVLLLRLAKTYETTLEKC 360
DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10319263
Publication No. US20030180820A1
GENERAL INFORMATION:
APPLICANT: Bar-Or M.D., David
APPLICANT: Lau Ph.D., Edward
APPLICANT: Winkler M.D., James V.
TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
TITLE OF INVENTION: Kits
FILE REFERENCE: ISCOO7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DAHKSBVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLDBLRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 2068; DB 14; Length 585; Best Local Similarity 100.0%; Pred. No. 2.3e-190; Matches 387; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                              RESULT 14
US-10-133-604A-5
US-10-133-604A-5
Sequence 5, Application US/10153604A
Publication No. US20030143191A1
GENERAL INFORMATION:
TILLE OF INVENTION:
FILE REFRENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,604A
CURRENT APLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin Version 3.1
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CAAADPHECYAKVFDEFKPLVBEPQNL 387
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                                                           CAAADPHECYAKVFDEFKPLVEEPONL 387
                                                                             TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0; Indels 0;
CURRENT APPLICATION NUMBER: US/10/119,263
CURRENT FILING DATE: 2002-12-13
PRIOR PAPLICATION NUMBER: 06/115,392
PRIOR PLING DATE: 1999-01-11
PRIOR PLING DATE: 1999-01-0.02
PRIOR PLING DATE: 1998-10-02
SOOTWARE: PARENT NUMBER: 09/165,581
NUMBER OF SEQ ID NOS: 2
SOOTWARE: PARENT NOS: 2
LENGTH: 585
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ORGANISM: Homo sapiens
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US-10-153-064-5
US-10-153-064-5
PUBLICATION NO. US20020142814A1
GENERAL INFORMATION:
TILLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
TILLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PFS56
CURRENT APPLICATION NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 66/293,212
PRIOR APPLICATION NUMBER: 66/293,212
NUMBER OF SEQ ID NOS: 137
SOCTWARE: Patentin version 3.1
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100.0%; Score 2068; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0;
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US-10-153-064-5
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LENGTH: 585
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100.0%; Score 2068; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Human derived fusion protein US-10-425-000-31
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FILE REFERENCE: STOIO127-8
CURRENT PEDELICATION NUMBER: US/10/425,000
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
LENGTH: 585
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ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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APPLICANT: Nesbit, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
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100.0%; Score 2068; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0;
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; Publication No. US20040052777A1
; GENERAL INFORMATION:
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US-10-425-000-31
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                      DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
                                                                                                                                           VHTECCHGDLLECADDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPA
 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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100.0%; Pred. No. 2.3e-190;
iive 0; Mismatches 0;
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US-09-833-245-18

Sequence 18, Application US/0983345

Publication No. US20040010134A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT FILING DATE: 2001-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-12-21

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-12-21

SPRIOR FILING DATE: 2000-12-21

SOFTWARE: PALENTING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PALENTING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SEQ ID NO 18

LENGTH: 585
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Best Local Similarity 100.
Matches: 387; Conservative
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US-09-833-245-18
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100.0%; Score 2068; DB 11; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0; Indels 0;
                                                                                                     Query Match 100.0%; Score 2068; DB 10; Length 585; Best Local Similarity 100.0%; Pred. No. 2.3e-190; Matches 387; Conservative 0; Mismatches 0; Indels 0;
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Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
Sequence 18, Application US/09833118
GENERAL INFORMATION:
APPLICANT: Reset in Albumin Fusion Proteins
FILE REFERENCE: PF54
GURRENT AFPLICATION NUMBER: US/09/833,118
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR PILING DATE: 2000-12-21
PRIOR PRING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
SPICE APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-12-21
SOFTWARE PAPELICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-12-21
SOFTWARE PAPELICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 35
LENGTH: 585
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; ORGANISM: Homo Sapiens
US-09-833-118-18
     ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-832-501-18
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APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony, Tony
APPLICANT: Fleming, Tony, Tony
APPLICANT: Fleming, Tony, Tony
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: Dyx-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT APPLICATION DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTHARE: PATENTING DATE: AND ASSEQ ID NO 445
LENGTH: 585
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Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0; Indels 0;
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Sequence 18, Application US/09832501
GENERAL INFORMATION:
APPLICANT: Slance, David J.
APPLICANT: Sleep, David J.
APPLICANT: Sadeghi, Homa
APPLICANT: Sadeghi, Homa
APPLICANT: Parent J.
APPLICANT: Sadeghi, Homa
APPLICANT: Print Cor, Christopher P.
TITE OF INVENTION: Albumin Pusion Proteins
FILE REFERENCE: PF542
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIN Ver. 2.1
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301 DLPSLAADFVESKDVCKNYABAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
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100.0%; Score 2068; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.3e-190;
Matches 387; Conservative 0; Mismatches 0;
                                                                                                                                                                         US-09-833-117-18
Sequence 18, Application US/09833117
Publication No. US2030171267A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Prior, Christopher P.
APPLICANT: Prior, Christopher P.
TILE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF543
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PARCH NOS: 36
SOFTWARE: PARCH NOS: 36
SEQ ID NO 18
LENTHERED
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                                                                                    361 CAAADPHECYAKVFDEFKPLVEEPQNL 387
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US-09-932-322-445
US-09-932-322-445
Sequence 445. Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Dyax Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo Sapiens
US-09-833-117-18
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                            DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
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Publication No. US20330125247A1
APPLICANT: Rosen, Craig A.
APPLICANT: Reseltine, William A.
ITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF545
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR APPLICATION NUMBER: 60/226,931
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 585
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ORGANISM: Homo Sapiens
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US-09-833-041-18
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSE: 11NNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP STREET: 1300 I Street, NW
CITY: Washington
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3135
COMPUTER READABLE FORM:
MEDIUM TYPE: ROPEDY disk
COMPUTER: IBW PC COMPATIBLE
COMPUTER: IBW PC COMPATIBLE
COMPUTER: IBW PC COMPATIBLE
COMPUTER: TATE: 100 PC COMPATIBLE
COMPUTER: TATE: 100 PC COMPATIBLE
COMPUTER: TATE: 100 PC COMPATIBLE
COMPUTER: TATE: 100 PC COMPATIBLE
COMPUTER: DATE: 100 PC COMPATIBLE
COMPUTER: 100 PATA:
APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-UN-1998
APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-UN-1998
APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-UN-1998
APPLICATION NUMBER: PCTY(896/03164
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
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                                                                                                        241 VHTBCCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                                                                                                                                                                                                                   VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                                                                                                                                                                                     DIPSLAADFVESKDVCKNYAEAKDVFLGMFLYBYARRHPDYSVVLLLRLAKTYETTLEKC 360
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                             121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTBCCQAADKAACLLP
DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/09984010
; Publication No. US20030104578A1
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT FUSION
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                         CAAADPHECYAKVFDEFKPLVEEPONL 387
                                                                                                                                                                                                                                                                                                                                                                    361 CAAADPHECYAKVFDEFKPLVEEPQNL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-984-010-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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APPLICANT: Baltzer, James P.
APPLICANT: Beltzer, James P.
APPLICANT: Beltzer, M. Daniel
APPLICANT: Potenty, M. Daniel
APPLICANT: Pleming, Tony J.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
FILE REPERENCE: Dyx-025.1 pc7; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
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                                                                                                                               Length 585;
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                                                                                                                             Query Match 100.0%; Score 2068; DB 9; Best Local Similarity 100.0%; Pred. No. 2.3e-190; Matches 387; Conservative 0; Mismatches 0;
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TOPOLOGY: Ilhear
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MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-929-552-2
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Publication No. US20030091565A1
GENERAL INFORMATION:
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US-09-932-613-445
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LENGTH: 585
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Sequence 18, Appl
Sequence 145, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 31, Appl
Sequence 31, Appl
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                                                                                              April 19, 2004, 12:00:25; Search time 162.947 Seconds (without alignments) 654.724 Million cell updates/sec
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Sequence 34,
Sequence 5,
                                                                                                                                                                      US-09-832-929-18_COPY_1_387
2068
1 DAHKSEVAHRFKDLGEENFK......ECYAKVFDEFKPLVEEPQNL 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

(cgn2 6/ptodata//pubpaa/USO7_PUBCOMB.pep:*

(cgn2 6/ptodata/2/pubpaa/BCT_NEW_PUB.pep:*

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-984-010-26
US-09-883-117-18
US-09-833-117-18
US-09-833-117-18
US-09-833-117-18
US-09-832-501-18
US-09-832-501-18
US-09-832-501-18
US-09-833-245-18
US-10-424-999-11
US-10-425-000-31
US-10-425-000-31
US-10-153-108-34
US-10-153-108-34
US-10-153-108-34
US-10-153-108-34
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                                                                                                                                                                                                                                                                                           1124875 segs, 275673149 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Segment	Segmen	Sequence	Sequence	Sequence	Sequence	Sequenc	Sequence	Sequence	Sequence	Seguenc	Sequence	Seguena	Seguence	Seguena	Sequence	Seguenc	Seguence	Sequence	Seguena	Sequen	Sequence	Sednenc	Sednen	Sequence	Sequence	Sequenc	Seguenc	Seguenc	Sequenc	
9-26	-10-414-469-	-10-414-469	10-413-831-	-10-413-83	-10-413-832-	-10-413-832	10-414-386-	-10-414-386-	-233-675A-	-10-462-2	-984-010-	-919-039-3	0-609-34	-10-153-06	-153-604A-	-10-365-623	19-984-186-	-10-237-667-	10-237-708-	-10-237-866-	-10-237-87	-10-237-624-	-10-433-10	-10-433-108-1	10-433-	-10-433-108-1	-10-433-108-	-10-153-064-133		
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### ALIGNMENTS

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RESULT.

US-09-99-552-2

1 Sequence 2, Application US/09929552

1 Sequence 2, Application US/09929552

1 Patent No. US200201202041

2 Sequence 2, Application Sequence 2, Application of Carlos GENERAL INFORMATION:

APPLICANT: Sonnenschein, Carlos APPLICANT: Sonnenschein, Carlos CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CONTRY: San Francisco

STATE: California CONTRY: United States of America CONTRY: United States of America COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

COMPUTER: READABLE FORM:

MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

COMPUTER: BPADABLE FORM:

MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

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MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

COMPUTER: BPADABLE FORM:

MEDIUM TYPE: Ploppy disk COMPUTER: BPADABLE FORM:

APPLICATION NUMBER: US/09/929,552

BTLING DATE: 14-Aug-2001

PRICECOMMUNICATION NUMBER: 32,837

REFERENCE CHARACTERISINGS

MAME: CATCOLL NUMBER: 32,837

TELERONMUNICATION NUMBER: 32,837

TELERONMUNICATION NUMBER: 32,837

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TELERONMUNICATION OF 2:

SEQUENCE CHARACTERISINGS

LENDART: BEBARCETION ACCIDENCE NUMBER: BBARCETION ACCIDENCE CHARACTERISINGS

LENDART: BBARCETISTINGS

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